Applying Faster R-CNN for Object Detection on Malaria Images

Import libs

In [1]:

```
from __future__ import division
from __future__ import print_function
from __future__ import absolute_import
import random
import pprint
import sys
import time
import numpy as np
from optparse import OptionParser
import pickle
import math
import cv2
import copy
from matplotlib import pyplot as plt
import tensorflow as tf
import pandas as pd
import os

from sklearn.metrics import average_precision_score

from keras import backend as K
from keras.optimizers import Adam, SGD, RMSprop
from keras.layers import Flatten, Dense, Input, Conv2D, MaxPooling2D, Dropout
from keras.layers import GlobalAveragePooling2D, GlobalMaxPooling2D, TimeDistributed
from keras.engine.topology import get_source_inputs
from keras.utils import layer_utils
from keras.utils.data_utils import get_file
from keras.objectives import categorical_crossentropy

from keras.models import Model
from keras.utils import generic_utils
from keras.engine import Layer, InputSpec
from keras import initializers, regularizers
```

```
Using TensorFlow backend.
```

Config setting

In [2]:

```
class Config:

        def __init__(self):

                # Print the process or not
                self.verbose = True

                # Name of base network
                self.network = 'vgg'

                # Setting for data augmentation
                self.use_horizontal_flips = False
                self.use_vertical_flips = False
                self.rot_90 = False

                # Anchor box scales
    # Note that if im_size is smaller, anchor_box_scales should be scaled
    # Original anchor_box_scales in the paper is [128, 256, 512]
                self.anchor_box_scales = [64, 128, 256]

                # Anchor box ratios
                self.anchor_box_ratios = [[1, 1], [1./math.sqrt(2), 2./math.sqrt(2)], [2./math.sqrt(2), 1./math.s
qrt(2)]]

                # Size to resize the smallest side of the image
                # Original setting in paper is 600. Set to 300 in here to save training time
                self.im_size = 300

                # image channel-wise mean to subtract
                self.img_channel_mean = [103.939, 116.779, 123.68]
                self.img_scaling_factor = 1.0

                # number of ROIs at once
                self.num_rois = 4

                # stride at the RPN (this depends on the network configuration)
                self.rpn_stride = 16

                self.balanced_classes = False

                # scaling the stdev
                self.std_scaling = 4.0
                self.classifier_regr_std = [8.0, 8.0, 4.0, 4.0]

                # overlaps for RPN
                self.rpn_min_overlap = 0.3
                self.rpn_max_overlap = 0.7

                # overlaps for classifier ROIs
                self.classifier_min_overlap = 0.1
                self.classifier_max_overlap = 0.5

                # placeholder for the class mapping, automatically generated by the parser
                self.class_mapping = None

                self.model_path = None
```

Parser the data from annotation file

In [3]:

```
def get_data(input_path):
        """Parser the data from annotation file

        Args:
                input_path: annotation file path

        Returns:
                all_data: list(filepath, width, height, list(bboxes))
                classes_count: dict{key:class_name, value:count_num}
                        e.g. {'Car': 2383, 'Mobile phone': 1108, 'Person': 3745}
                class_mapping: dict{key:class_name, value: idx}
                        e.g. {'Car': 0, 'Mobile phone': 1, 'Person': 2}
        """
        found_bg = False
        all_imgs = {}

        classes_count = {}

        class_mapping = {}
```

```
        visualise = True

        i = 1

        with open(input_path,'r') as f:

                print('Parsing annotation files')

                for line in f:

                        # Print process
                        sys.stdout.write('\r'+'idx=' + str(i))
                        i += 1

                        line_split = line.strip().split(',')

                        # Make sure the info saved in annotation file matching the format (path_filename, x1, y1,
x2, y2, class_name)
                        # Note:
                        #       One path_filename might has several classes (class_name)
                        #       x1, y1, x2, y2 are the pixel value of the origial image, not the ratio value
                        #       (x1, y1) top left coordinates; (x2, y2) bottom right coordinates
                        #   x1,y1-------------------
                        #       |                                               |
                        #       |                                               |
                        #       |                                               |
                        #       |                                               |
                        #       ----------------------x2,y2

                        (filename,x1,y1,x2,y2,class_name) = line_split

                        if class_name not in classes_count:
                                classes_count[class_name] = 1
                        else:
                                classes_count[class_name] += 1

                        if class_name not in class_mapping:
                                if class_name == 'bg' and found_bg == False:
                                        print('Found class name with special name bg. Will be treated as a backgr
ound region (this is usually for hard negative mining).')
                                        found_bg = True
                                class_mapping[class_name] = len(class_mapping)

                        if filename not in all_imgs:
                                all_imgs[filename] = {}

                                img = cv2.imread(filename)
                                (rows,cols) = img.shape[:2]
                                all_imgs[filename]['filepath'] = filename
                                all_imgs[filename]['width'] = cols
                                all_imgs[filename]['height'] = rows
                                all_imgs[filename]['bboxes'] = []
                                # if np.random.randint(0,6) > 0:
                                #       all_imgs[filename]['imageset'] = 'trainval'
                                # else:
                                #       all_imgs[filename]['imageset'] = 'test'

                        all_imgs[filename]['bboxes'].append({'class': class_name, 'x1': int(x1), 'x2': int(x2), '
y1': int(y1), 'y2': int(y2)})


                all_data = []
                for key in all_imgs:
                        all_data.append(all_imgs[key])

                # make sure the bg class is last in the list
                if found_bg:
                        if class_mapping['bg'] != len(class_mapping) - 1:
                                key_to_switch = [key for key in class_mapping.keys() if class_mapping[key] == len
(class_mapping)-1][0]
                                val_to_switch = class_mapping['bg']
                                class_mapping['bg'] = len(class_mapping) - 1
                                class_mapping[key_to_switch] = val_to_switch

                return all_data, classes_count, class_mapping
```

Define ROI Pooling Convolutional Layer

In [4]:

```
class RoiPoolingConv(Layer):
```

```
    '''ROI pooling layer for 2D inputs.
    See Spatial Pyramid Pooling in Deep Convolutional Networks for Visual Recognition,
    K. He, X. Zhang, S. Ren, J. Sun
    # Arguments
        pool_size: int
            Size of pooling region to use. pool_size = 7 will result in a 7x7 region.
        num_rois: number of regions of interest to be used
    # Input shape
        list of two 4D tensors [X_img,X_roi] with shape:
        X_img:
        `(1, rows, cols, channels)`
        X_roi:
        `(1,num_rois,4)` list of rois, with ordering (x,y,w,h)
    # Output shape
        3D tensor with shape:
        `(1, num_rois, channels, pool_size, pool_size)`
    '''
    def __init__(self, pool_size, num_rois, **kwargs):

        self.dim_ordering = K.image_dim_ordering()
        self.pool_size = pool_size
        self.num_rois = num_rois

        super(RoiPoolingConv, self).__init__(**kwargs)

    def build(self, input_shape):
        self.nb_channels = input_shape[0][3]

    def compute_output_shape(self, input_shape):
        return None, self.num_rois, self.pool_size, self.pool_size, self.nb_channels

    def call(self, x, mask=None):

        assert(len(x) == 2)

        # x[0] is image with shape (rows, cols, channels)
        img = x[0]

        # x[1] is roi with shape (num_rois,4) with ordering (x,y,w,h)
        rois = x[1]

        input_shape = K.shape(img)

        outputs = []

        for roi_idx in range(self.num_rois):

            x = rois[0, roi_idx, 0]
            y = rois[0, roi_idx, 1]
            w = rois[0, roi_idx, 2]
            h = rois[0, roi_idx, 3]

            x = K.cast(x, 'int32')
            y = K.cast(y, 'int32')
            w = K.cast(w, 'int32')
            h = K.cast(h, 'int32')

            # Resized roi of the image to pooling size (7x7)
            rs = tf.image.resize_images(img[:, y:y+h, x:x+w, :], (self.pool_size, self.pool_size))
            outputs.append(rs)


        final_output = K.concatenate(outputs, axis=0)

        # Reshape to (1, num_rois, pool_size, pool_size, nb_channels)
        # Might be (1, 4, 7, 7, 3)
        final_output = K.reshape(final_output, (1, self.num_rois, self.pool_size, self.pool_size, self.nb_channel
s))

        # permute_dimensions is similar to transpose
        final_output = K.permute_dimensions(final_output, (0, 1, 2, 3, 4))

        return final_output


    def get_config(self):
        config = {'pool_size': self.pool_size,
                  'num_rois': self.num_rois}
        base_config = super(RoiPoolingConv, self).get_config()
        return dict(list(base_config.items()) + list(config.items()))
```

Vgg-16 model

In [5]:

```
def get_img_output_length(width, height):
    def get_output_length(input_length):
        return input_length//16

    return get_output_length(width), get_output_length(height)

def nn_base(input_tensor=None, trainable=False):


    input_shape = (None, None, 3)

    if input_tensor is None:
        img_input = Input(shape=input_shape)
    else:
        if not K.is_keras_tensor(input_tensor):
            img_input = Input(tensor=input_tensor, shape=input_shape)
        else:
            img_input = input_tensor

    bn_axis = 3

    # Block 1
    x = Conv2D(64, (3, 3), activation='relu', padding='same', name='block1_conv1')(img_input)
    x = Conv2D(64, (3, 3), activation='relu', padding='same', name='block1_conv2')(x)
    x = MaxPooling2D((2, 2), strides=(2, 2), name='block1_pool')(x)

    # Block 2
    x = Conv2D(128, (3, 3), activation='relu', padding='same', name='block2_conv1')(x)
    x = Conv2D(128, (3, 3), activation='relu', padding='same', name='block2_conv2')(x)
    x = MaxPooling2D((2, 2), strides=(2, 2), name='block2_pool')(x)

    # Block 3
    x = Conv2D(256, (3, 3), activation='relu', padding='same', name='block3_conv1')(x)
    x = Conv2D(256, (3, 3), activation='relu', padding='same', name='block3_conv2')(x)
    x = Conv2D(256, (3, 3), activation='relu', padding='same', name='block3_conv3')(x)
    x = MaxPooling2D((2, 2), strides=(2, 2), name='block3_pool')(x)

    # Block 4
    x = Conv2D(512, (3, 3), activation='relu', padding='same', name='block4_conv1')(x)
    x = Conv2D(512, (3, 3), activation='relu', padding='same', name='block4_conv2')(x)
    x = Conv2D(512, (3, 3), activation='relu', padding='same', name='block4_conv3')(x)
    x = MaxPooling2D((2, 2), strides=(2, 2), name='block4_pool')(x)

    # Block 5
    x = Conv2D(512, (3, 3), activation='relu', padding='same', name='block5_conv1')(x)
    x = Conv2D(512, (3, 3), activation='relu', padding='same', name='block5_conv2')(x)
    x = Conv2D(512, (3, 3), activation='relu', padding='same', name='block5_conv3')(x)
    # x = MaxPooling2D((2, 2), strides=(2, 2), name='block5_pool')(x)

    return x
```

RPN layer

In [6]:

```
def rpn_layer(base_layers, num_anchors):
    """Create a rpn layer
        Step1: Pass through the feature map from base layer to a 3x3 512 channels convolutional layer
                Keep the padding 'same' to preserve the feature map's size
        Step2: Pass the step1 to two (1,1) convolutional layer to replace the fully connected layer
                classification layer: num_anchors (9 in here) channels for 0, 1 sigmoid activation output
                regression layer: num_anchors*4 (36 in here) channels for computing the regression of bboxes with
linear activation
    Args:
        base_layers: vgg in here
        num_anchors: 9 in here

    Returns:
        [x_class, x_regr, base_layers]
        x_class: classification for whether it's an object
        x_regr: bboxes regression
        base_layers: vgg in here
    """
    x = Conv2D(512, (3, 3), padding='same', activation='relu', kernel_initializer='normal', name='rpn_conv1')(bas
e_layers)

    x_class = Conv2D(num_anchors, (1, 1), activation='sigmoid', kernel_initializer='uniform', name='rpn_out_class
')(x)
    x_regr = Conv2D(num_anchors * 4, (1, 1), activation='linear', kernel_initializer='zero', name='rpn_out_regres
s')(x)

    return [x_class, x_regr, base_layers]
```

Classifier layer

In [7]:

```
def classifier_layer(base_layers, input_rois, num_rois, nb_classes = 4):
    """Create a classifier layer

    Args:
        base_layers: vgg
        input_rois: `(1,num_rois,4)` list of rois, with ordering (x,y,w,h)
        num_rois: number of rois to be processed in one time (4 in here)

    Returns:
        list(out_class, out_regr)
        out_class: classifier layer output
        out_regr: regression layer output
    """

    input_shape = (num_rois,7,7,512)

    pooling_regions = 7

    # out_roi_pool.shape = (1, num_rois, channels, pool_size, pool_size)
    # num_rois (4) 7x7 roi pooling
    out_roi_pool = RoiPoolingConv(pooling_regions, num_rois)([base_layers, input_rois])

    # Flatten the convlutional layer and connected to 2 FC and 2 dropout
    out = TimeDistributed(Flatten(name='flatten'))(out_roi_pool)
    out = TimeDistributed(Dense(4096, activation='relu', name='fc1'))(out)
    out = TimeDistributed(Dropout(0.5))(out)
    out = TimeDistributed(Dense(4096, activation='relu', name='fc2'))(out)
    out = TimeDistributed(Dropout(0.5))(out)

    # There are two output layer
    # out_class: softmax acivation function for classify the class name of the object
    # out_regr: linear activation function for bboxes coordinates regression
    out_class = TimeDistributed(Dense(nb_classes, activation='softmax', kernel_initializer='zero'), name='dense_c
lass_{}'.format(nb_classes))(out)
    # note: no regression target for bg class
    out_regr = TimeDistributed(Dense(4 * (nb_classes-1), activation='linear', kernel_initializer='zero'), name='d
ense_regress_{}'.format(nb_classes))(out)

    return [out_class, out_regr]
```

Calculate IoU (Intersection of Union)

In [8]:

```
def union(au, bu, area_intersection):
        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):
        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)

        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)
```

Calculate the rpn for all anchors of all images

In [9]:

```
def calc_rpn(C, img_data, width, height, resized_width, resized_height, img_length_calc_function):
        """(Important part!) Calculate the rpn for all anchors
                If feature map has shape 38x50=1900, there are 1900x9=17100 potential anchors

        Args:
                C: config
                img_data: augmented image data
                width: original image width (e.g. 600)
                height: original image height (e.g. 800)
                resized_width: resized image width according to C.im_size (e.g. 300)
                resized_height: resized image height according to C.im_size (e.g. 400)
                img_length_calc_function: function to calculate final layer's feature map (of base model) size ac
cording to input image size

        Returns:
                y_rpn_cls: list(num_bboxes, y_is_box_valid + y_rpn_overlap)
                        y_is_box_valid: 0 or 1 (0 means the box is invalid, 1 means the box is valid)
                        y_rpn_overlap: 0 or 1 (0 means the box is not an object, 1 means the box is an object)
                y_rpn_regr: list(num_bboxes, 4*y_rpn_overlap + y_rpn_regr)
                        y_rpn_regr: x1,y1,x2,y2 bunding boxes coordinates
        """
        downscale = float(C.rpn_stride)
        anchor_sizes = C.anchor_box_scales   # 128, 256, 512
        anchor_ratios = C.anchor_box_ratios  # 1:1, 1:2*sqrt(2), 2*sqrt(2):1
        num_anchors = len(anchor_sizes) * len(anchor_ratios) # 3x3=9

        # calculate the output map size based on the network architecture
        (output_width, output_height) = img_length_calc_function(resized_width, resized_height)

        n_anchratios = len(anchor_ratios)    # 3

        # initialise empty output objectives
        y_rpn_overlap = np.zeros((output_height, output_width, num_anchors))
        y_is_box_valid = np.zeros((output_height, output_width, num_anchors))
        y_rpn_regr = np.zeros((output_height, output_width, num_anchors * 4))

        num_bboxes = len(img_data['bboxes'])

        num_anchors_for_bbox = np.zeros(num_bboxes).astype(int)
        best_anchor_for_bbox = -1*np.ones((num_bboxes, 4)).astype(int)
        best_iou_for_bbox = np.zeros(num_bboxes).astype(np.float32)
        best_x_for_bbox = np.zeros((num_bboxes, 4)).astype(int)
        best_dx_for_bbox = np.zeros((num_bboxes, 4)).astype(np.float32)

        # get the GT box coordinates, and resize to account for image resizing
        gta = np.zeros((num_bboxes, 4))
        for bbox_num, bbox in enumerate(img_data['bboxes']):
                # get the GT box coordinates, and resize to account for image resizing
```

```
                gta[bbox_num, 0] = bbox['x1'] * (resized_width / float(width))

                gta[bbox_num, 1] = bbox['x2'] * (resized_width / float(width))
                gta[bbox_num, 2] = bbox['y1'] * (resized_height / float(height))
                gta[bbox_num, 3] = bbox['y2'] * (resized_height / float(height))

        # rpn ground truth

        for anchor_size_idx in range(len(anchor_sizes)):
                for anchor_ratio_idx in range(n_anchratios):
                        anchor_x = anchor_sizes[anchor_size_idx] * anchor_ratios[anchor_ratio_idx][0]
                        anchor_y = anchor_sizes[anchor_size_idx] * anchor_ratios[anchor_ratio_idx][1]

                        for ix in range(output_width):
                                # x-coordinates of the current anchor box
                                x1_anc = downscale * (ix + 0.5) - anchor_x / 2
                                x2_anc = downscale * (ix + 0.5) + anchor_x / 2

                                # ignore boxes that go across image boundaries
                                if x1_anc < 0 or x2_anc > resized_width:
                                        continue

                                for jy in range(output_height):

                                        # y-coordinates of the current anchor box
                                        y1_anc = downscale * (jy + 0.5) - anchor_y / 2
                                        y2_anc = downscale * (jy + 0.5) + anchor_y / 2

                                        # ignore boxes that go across image boundaries
                                        if y1_anc < 0 or y2_anc > resized_height:
                                                continue

                                        # bbox_type indicates whether an anchor should be a target
                                        # Initialize with 'negative'
                                        bbox_type = 'neg'

                                        # this is the best IOU for the (x,y) coord and the current anchor
                                        # note that this is different from the best IOU for a GT bbox
                                        best_iou_for_loc = 0.0

                                        for bbox_num in range(num_bboxes):

                                                # get IOU of the current GT box and the current anchor box
                                                curr_iou = iou([gta[bbox_num, 0], gta[bbox_num, 2], gta[bbox_num,
1], gta[bbox_num, 3]], [x1_anc, y1_anc, x2_anc, y2_anc])
                                                # calculate the regression targets if they will be needed
                                                if curr_iou > best_iou_for_bbox[bbox_num] or curr_iou > C.rpn_max
_overlap:
                                                        cx = (gta[bbox_num, 0] + gta[bbox_num, 1]) / 2.0
                                                        cy = (gta[bbox_num, 2] + gta[bbox_num, 3]) / 2.0
                                                        cxa = (x1_anc + x2_anc)/2.0
                                                        cya = (y1_anc + y2_anc)/2.0

                                                        # x,y are the center point of ground-truth bbox
                                                        # xa,ya are the center point of anchor bbox (xa=downscale
* (ix + 0.5); ya=downscale * (iy+0.5))
                                                        # w,h are the width and height of ground-truth bbox
                                                        # wa,ha are the width and height of anchor bboxe
                                                        # tx = (x - xa) / wa
                                                        # ty = (y - ya) / ha
                                                        # tw = log(w / wa)
                                                        # th = log(h / ha)
                                                        tx = (cx - cxa) / (x2_anc - x1_anc)
                                                        ty = (cy - cya) / (y2_anc - y1_anc)
                                                        tw = np.log((gta[bbox_num, 1] - gta[bbox_num, 0]) / (x2_a
nc - x1_anc))
                                                        th = np.log((gta[bbox_num, 3] - gta[bbox_num, 2]) / (y2_a
nc - y1_anc))

                                                if img_data['bboxes'][bbox_num]['class'] != 'bg':

                                                        # all GT boxes should be mapped to an anchor box, so we k
eep track of which anchor box was best
                                                        if curr_iou > best_iou_for_bbox[bbox_num]:
                                                                best_anchor_for_bbox[bbox_num] = [jy, ix, anchor_
ratio_idx, anchor_size_idx]
                                                                best_iou_for_bbox[bbox_num] = curr_iou
                                                                best_x_for_bbox[bbox_num,:] = [x1_anc, x2_anc, y1
_anc, y2_anc]
                                                                best_dx_for_bbox[bbox_num,:] = [tx, ty, tw, th]

                                                        # we set the anchor to positive if the IOU is >0.7 (it do
es not matter if there was another better box, it just indicates overlap)
                                                        if curr_iou > C.rpn_max_overlap:
```

```
                                                                bbox_type = 'pos'

                                                                num_anchors_for_bbox[bbox_num] += 1
                                                                # we update the regression layer target if this IOU is the best for the current (x,y) and anchor position
                                                                if curr_iou > best_iou_for_loc:
                                                                        best_iou_for_loc = curr_iou
                                                                        best_regr = (tx, ty, tw, th)

                                                        # if the IOU is >0.3 and <0.7, it is ambiguous and no included in the objective
                                                        if C.rpn_min_overlap < curr_iou < C.rpn_max_overlap:
                                                                # gray zone between neg and pos
                                                                if bbox_type != 'pos':
                                                                        bbox_type = 'neutral'

                                                # turn on or off outputs depending on IOUs
                                                if bbox_type == 'neg':
                                                        y_is_box_valid[jy, ix, anchor_ratio_idx + n_anchratios * anchor_size_idx] = 1
                                                        y_rpn_overlap[jy, ix, anchor_ratio_idx + n_anchratios * anchor_size_idx] = 0
                                                elif bbox_type == 'neutral':
                                                        y_is_box_valid[jy, ix, anchor_ratio_idx + n_anchratios * anchor_size_idx] = 0
                                                        y_rpn_overlap[jy, ix, anchor_ratio_idx + n_anchratios * anchor_size_idx] = 0
                                                elif bbox_type == 'pos':
                                                        y_is_box_valid[jy, ix, anchor_ratio_idx + n_anchratios * anchor_size_idx] = 1
                                                        y_rpn_overlap[jy, ix, anchor_ratio_idx + n_anchratios * anchor_size_idx] = 1
                                                        start = 4 * (anchor_ratio_idx + n_anchratios * anchor_size_idx)
                                                        y_rpn_regr[jy, ix, start:start+4] = best_regr

        # we ensure that every bbox has at least one positive RPN region

        for idx in range(num_anchors_for_bbox.shape[0]):
                if num_anchors_for_bbox[idx] == 0:
                        # no box with an IOU greater than zero ...
                        if best_anchor_for_bbox[idx, 0] == -1:
                                continue
                        y_is_box_valid[
                                best_anchor_for_bbox[idx,0], best_anchor_for_bbox[idx,1], best_anchor_for_bbox[idx,2] + n_anchratios *
                                best_anchor_for_bbox[idx,3]] = 1
                        y_rpn_overlap[
                                best_anchor_for_bbox[idx,0], best_anchor_for_bbox[idx,1], best_anchor_for_bbox[idx,2] + n_anchratios *
                                best_anchor_for_bbox[idx,3]] = 1
                        start = 4 * (best_anchor_for_bbox[idx,2] + n_anchratios * best_anchor_for_bbox[idx,3])
                        y_rpn_regr[
                                best_anchor_for_bbox[idx,0], best_anchor_for_bbox[idx,1], start:start+4] = best_dx_for_bbox[idx, :]

        y_rpn_overlap = np.transpose(y_rpn_overlap, (2, 0, 1))
        y_rpn_overlap = np.expand_dims(y_rpn_overlap, axis=0)

        y_is_box_valid = np.transpose(y_is_box_valid, (2, 0, 1))
        y_is_box_valid = np.expand_dims(y_is_box_valid, axis=0)

        y_rpn_regr = np.transpose(y_rpn_regr, (2, 0, 1))
        y_rpn_regr = np.expand_dims(y_rpn_regr, axis=0)

        pos_locs = np.where(np.logical_and(y_rpn_overlap[0, :, :, :] == 1, y_is_box_valid[0, :, :, :] == 1))
        neg_locs = np.where(np.logical_and(y_rpn_overlap[0, :, :, :] == 0, y_is_box_valid[0, :, :, :] == 1))

        num_pos = len(pos_locs[0])

        # one issue is that the RPN has many more negative than positive regions, so we turn off some of the negative
        # regions. We also limit it to 256 regions.
        num_regions = 256

        if len(pos_locs[0]) > num_regions/2:
                val_locs = random.sample(range(len(pos_locs[0])), len(pos_locs[0]) - num_regions/2)
                y_is_box_valid[0, pos_locs[0][val_locs], pos_locs[1][val_locs], pos_locs[2][val_locs]] = 0
                num_pos = num_regions/2

        if len(neg_locs[0]) + num_pos > num_regions:
                val_locs = random.sample(range(len(neg_locs[0])), len(neg_locs[0]) - num_pos)
                y_is_box_valid[0, neg_locs[0][val_locs], neg_locs[1][val_locs], neg_locs[2][val_locs]] = 0

        y_rpn_cls = np.concatenate([y_is_box_valid, y_rpn_overlap], axis=1)
```

```
        y_rpn_regr = np.concatenate([np.repeat(y_rpn_overlap, 4, axis=1), y_rpn_regr], axis=1)

        return np.copy(y_rpn_cls), np.copy(y_rpn_regr), num_pos
```

Get new image size and augment the image

In [10]:

```
def get_new_img_size(width, height, img_min_side=300):
	if width <= height:
		f = float(img_min_side) / width
		resized_height = int(f * height)
		resized_width = img_min_side
	else:
		f = float(img_min_side) / height
		resized_width = int(f * width)
		resized_height = img_min_side

	return resized_width, resized_height

def augment(img_data, config, augment=True):
	assert 'filepath' in img_data
	assert 'bboxes' in img_data
	assert 'width' in img_data
	assert 'height' in img_data

	img_data_aug = copy.deepcopy(img_data)

	img = cv2.imread(img_data_aug['filepath'])

	if augment:
		rows, cols = img.shape[:2]

		if config.use_horizontal_flips and np.random.randint(0, 2) == 0:
			img = cv2.flip(img, 1)
			for bbox in img_data_aug['bboxes']:
				x1 = bbox['x1']
				x2 = bbox['x2']
				bbox['x2'] = cols - x1
				bbox['x1'] = cols - x2

		if config.use_vertical_flips and np.random.randint(0, 2) == 0:
			img = cv2.flip(img, 0)
			for bbox in img_data_aug['bboxes']:
				y1 = bbox['y1']
				y2 = bbox['y2']
				bbox['y2'] = rows - y1
				bbox['y1'] = rows - y2

		if config.rot_90:
			angle = np.random.choice([0,90,180,270],1)[0]
			if angle == 270:
				img = np.transpose(img, (1,0,2))
				img = cv2.flip(img, 0)
			elif angle == 180:
				img = cv2.flip(img, -1)
			elif angle == 90:
				img = np.transpose(img, (1,0,2))
				img = cv2.flip(img, 1)
			elif angle == 0:
				pass

			for bbox in img_data_aug['bboxes']:
				x1 = bbox['x1']
				x2 = bbox['x2']
				y1 = bbox['y1']
				y2 = bbox['y2']
				if angle == 270:
					bbox['x1'] = y1
					bbox['x2'] = y2
					bbox['y1'] = cols - x2
					bbox['y2'] = cols - x1
				elif angle == 180:
					bbox['x2'] = cols - x1
					bbox['x1'] = cols - x2
					bbox['y2'] = rows - y1
					bbox['y1'] = rows - y2
				elif angle == 90:
					bbox['x1'] = rows - y2
					bbox['x2'] = rows - y1
					bbox['y1'] = x1
					bbox['y2'] = x2
				elif angle == 0:
					pass

	img_data_aug['width'] = img.shape[1]
	img_data_aug['height'] = img.shape[0]
	return img_data_aug, img
```

Generate the ground_truth anchors

In [11]:

```
def get_anchor_gt(all_img_data, C, img_length_calc_function, mode='train'):
	""" Yield the ground-truth anchors as Y (labels)

	Args:
		all_img_data: list(filepath, width, height, list(bboxes))
		C: config
		img_length_calc_function: function to calculate final layer's feature map (of base model) size ac
cording to input image size
		mode: 'train' or 'test'; 'train' mode need augmentation

	Returns:
		x_img: image data after resized and scaling (smallest size = 300px)
		Y: [y_rpn_cls, y_rpn_regr]
		img_data_aug: augmented image data (original image with augmentation)
		debug_img: show image for debug
		num_pos: show number of positive anchors for debug
	"""
	while True:

		for img_data in all_img_data:
			try:

				# read in image, and optionally add augmentation

				if mode == 'train':
					img_data_aug, x_img = augment(img_data, C, augment=True)
				else:
					img_data_aug, x_img = augment(img_data, C, augment=False)

				(width, height) = (img_data_aug['width'], img_data_aug['height'])
				(rows, cols, _) = x_img.shape

				assert cols == width
				assert rows == height

				# get image dimensions for resizing
				(resized_width, resized_height) = get_new_img_size(width, height, C.im_size)

				# resize the image so that smalles side is length = 300px
				x_img = cv2.resize(x_img, (resized_width, resized_height), interpolation=cv2.INTE
R_CUBIC)
				debug_img = x_img.copy()

				try:
					y_rpn_cls, y_rpn_regr, num_pos = calc_rpn(C, img_data_aug, width, height,
resized_width, resized_height, img_length_calc_function)
				except:
					continue

				# Zero-center by mean pixel, and preprocess image

				x_img = x_img[:,:, (2, 1, 0)]  # BGR -> RGB
				x_img = x_img.astype(np.float32)
				x_img[:, :, 0] -= C.img_channel_mean[0]
				x_img[:, :, 1] -= C.img_channel_mean[1]
				x_img[:, :, 2] -= C.img_channel_mean[2]
				x_img /= C.img_scaling_factor

				x_img = np.transpose(x_img, (2, 0, 1))
				x_img = np.expand_dims(x_img, axis=0)

				y_rpn_regr[:, y_rpn_regr.shape[1]//2:, :, :] *= C.std_scaling

				x_img = np.transpose(x_img, (0, 2, 3, 1))
				y_rpn_cls = np.transpose(y_rpn_cls, (0, 2, 3, 1))
				y_rpn_regr = np.transpose(y_rpn_regr, (0, 2, 3, 1))

				yield np.copy(x_img), [np.copy(y_rpn_cls), np.copy(y_rpn_regr)], img_data_aug, de
bug_img, num_pos

			except Exception as e:
				print(e)
				continue
```

In [12]:

```
def non_max_suppression_fast(boxes, probs, overlap_thresh=0.9, max_boxes=300):
	# code used from here: http://www.pyimagesearch.com/2015/02/16/faster-non-maximum-suppression-python/
```

```
        # if there are no boxes, return an empty list


    # Process explanation:
    #   Step 1: Sort the probs list
    #   Step 2: Find the larget prob 'Last' in the list and save it to the pick list
    #   Step 3: Calculate the IoU with 'Last' box and other boxes in the list. If the IoU is larger than overlap_
threshold, delete the box from list
    #   Step 4: Repeat step 2 and step 3 until there is no item in the probs list
        if len(boxes) == 0:
                return []

        # grab the coordinates of the bounding boxes
        x1 = boxes[:, 0]
        y1 = boxes[:, 1]
        x2 = boxes[:, 2]
        y2 = boxes[:, 3]

        np.testing.assert_array_less(x1, x2)
        np.testing.assert_array_less(y1, y2)

        # if the bounding boxes integers, convert them to floats --
        # this is important since we'll be doing a bunch of divisions
        if boxes.dtype.kind == "i":
                boxes = boxes.astype("float")

        # initialize the list of picked indexes
        pick = []

        # calculate the areas
        area = (x2 - x1) * (y2 - y1)

        # sort the bounding boxes
        idxs = np.argsort(probs)

        # keep looping while some indexes still remain in the indexes
        # list
        while len(idxs) > 0:
                # grab the last index in the indexes list and add the
                # index value to the list of picked indexes
                last = len(idxs) - 1
                i = idxs[last]
                pick.append(i)

                # find the intersection

                xx1_int = np.maximum(x1[i], x1[idxs[:last]])
                yy1_int = np.maximum(y1[i], y1[idxs[:last]])
                xx2_int = np.minimum(x2[i], x2[idxs[:last]])
                yy2_int = np.minimum(y2[i], y2[idxs[:last]])

                ww_int = np.maximum(0, xx2_int - xx1_int)
                hh_int = np.maximum(0, yy2_int - yy1_int)

                area_int = ww_int * hh_int

                # find the union
                area_union = area[i] + area[idxs[:last]] - area_int

                # compute the ratio of overlap
                overlap = area_int/(area_union + 1e-6)

                # delete all indexes from the index list that have
                idxs = np.delete(idxs, np.concatenate(([last],
                        np.where(overlap > overlap_thresh)[0])))

                if len(pick) >= max_boxes:
                        break

        # return only the bounding boxes that were picked using the integer data type
        boxes = boxes[pick].astype("int")
        probs = probs[pick]
        return boxes, probs

def apply_regr_np(X, T):
        """Apply regression layer to all anchors in one feature map

        Args:
                X: shape=(4, 18, 25) the current anchor type for all points in the feature map
                T: regression layer shape=(4, 18, 25)

        Returns:
                X: regressed position and size for current anchor
        """
```

```
        try:

                x = X[0, :, :]
                y = X[1, :, :]
                w = X[2, :, :]
                h = X[3, :, :]

                tx = T[0, :, :]
                ty = T[1, :, :]
                tw = T[2, :, :]
                th = T[3, :, :]

                cx = x + w/2.
                cy = y + h/2.
                cx1 = tx * w + cx
                cy1 = ty * h + cy

                w1 = np.exp(tw.astype(np.float64)) * w
                h1 = np.exp(th.astype(np.float64)) * h
                x1 = cx1 - w1/2.
                y1 = cy1 - h1/2.

                x1 = np.round(x1)
                y1 = np.round(y1)
                w1 = np.round(w1)
                h1 = np.round(h1)
                return np.stack([x1, y1, w1, h1])
        except Exception as e:
                print(e)
                return X

def apply_regr(x, y, w, h, tx, ty, tw, th):
    # Apply regression to x, y, w and h
        try:
                cx = x + w/2.
                cy = y + h/2.
                cx1 = tx * w + cx
                cy1 = ty * h + cy
                w1 = math.exp(tw) * w
                h1 = math.exp(th) * h
                x1 = cx1 - w1/2.
                y1 = cy1 - h1/2.
                x1 = int(round(x1))
                y1 = int(round(y1))
                w1 = int(round(w1))
                h1 = int(round(h1))

                return x1, y1, w1, h1

        except ValueError:
                return x, y, w, h
        except OverflowError:
                return x, y, w, h
        except Exception as e:
                print(e)
                return x, y, w, h
```

In [13]:

```
def rpn_to_roi(rpn_layer, regr_layer, C, dim_ordering, use_regr=True, max_boxes=300,overlap_thresh=0.9):
        """Convert rpn layer to roi bboxes

        Args: (num_anchors = 9)
                rpn_layer: output layer for rpn classification
                        shape (1, feature_map.height, feature_map.width, num_anchors)
                        Might be (1, 18, 25, 9) if resized image is 400 width and 300
                regr_layer: output layer for rpn regression
                        shape (1, feature_map.height, feature_map.width, num_anchors)
                        Might be (1, 18, 25, 36) if resized image is 400 width and 300
                C: config
                use_regr: Wether to use bboxes regression in rpn
                max_boxes: max bboxes number for non-max-suppression (NMS)
                overlap_thresh: If iou in NMS is larger than this threshold, drop the box

        Returns:
                result: boxes from non-max-suppression (shape=(300, 4))
                        boxes: coordinates for bboxes (on the feature map)
        """
        regr_layer = regr_layer / C.std_scaling

        anchor_sizes = C.anchor_box_scales   # (3 in here)
        anchor_ratios = C.anchor_box_ratios  # (3 in here)

        assert rpn_layer.shape[0] == 1
```

```
        (rows, cols) = rpn_layer.shape[1:3]

        curr_layer = 0

        # A.shape = (4, feature_map.height, feature_map.width, num_anchors)
        # Might be (4, 18, 25, 9) if resized image is 400 width and 300
        # A is the coordinates for 9 anchors for every point in the feature map
        # => all 18x25x9=4050 anchors cooridnates
        A = np.zeros((4, rpn_layer.shape[1], rpn_layer.shape[2], rpn_layer.shape[3]))

        for anchor_size in anchor_sizes:
                for anchor_ratio in anchor_ratios:
                        # anchor_x = (128 * 1) / 16 = 8  => width of current anchor
                        # anchor_y = (128 * 2) / 16 = 16 => height of current anchor
                        anchor_x = (anchor_size * anchor_ratio[0])/C.rpn_stride
                        anchor_y = (anchor_size * anchor_ratio[1])/C.rpn_stride

                        # curr_layer: 0~8 (9 anchors)
                        # the Kth anchor of all position in the feature map (9th in total)
                        regr = regr_layer[0, :, :, 4 * curr_layer:4 * curr_layer + 4] # shape => (18, 25, 4)
                        regr = np.transpose(regr, (2, 0, 1)) # shape => (4, 18, 25)

                        # Create 18x25 mesh grid
                        # For every point in x, there are all the y points and vice versa
                        # X.shape = (18, 25)
                        # Y.shape = (18, 25)
                        X, Y = np.meshgrid(np.arange(cols),np. arange(rows))

                        # Calculate anchor position and size for each feature map point
                        A[0, :, :, curr_layer] = X - anchor_x/2 # Top left x coordinate
                        A[1, :, :, curr_layer] = Y - anchor_y/2 # Top left y coordinate
                        A[2, :, :, curr_layer] = anchor_x       # width of current anchor
                        A[3, :, :, curr_layer] = anchor_y       # height of current anchor

                        # Apply regression to x, y, w and h if there is rpn regression layer
                        if use_regr:
                                A[:, :, :, curr_layer] = apply_regr_np(A[:, :, :, curr_layer], regr)

                        # Avoid width and height exceeding 1
                        A[2, :, :, curr_layer] = np.maximum(1, A[2, :, :, curr_layer])
                        A[3, :, :, curr_layer] = np.maximum(1, A[3, :, :, curr_layer])

                        # Convert (x, y , w, h) to (x1, y1, x2, y2)
                        # x1, y1 is top left coordinate
                        # x2, y2 is bottom right coordinate
                        A[2, :, :, curr_layer] += A[0, :, :, curr_layer]
                        A[3, :, :, curr_layer] += A[1, :, :, curr_layer]

                        # Avoid bboxes drawn outside the feature map
                        A[0, :, :, curr_layer] = np.maximum(0, A[0, :, :, curr_layer])
                        A[1, :, :, curr_layer] = np.maximum(0, A[1, :, :, curr_layer])
                        A[2, :, :, curr_layer] = np.minimum(cols-1, A[2, :, :, curr_layer])
                        A[3, :, :, curr_layer] = np.minimum(rows-1, A[3, :, :, curr_layer])

                        curr_layer += 1

        all_boxes = np.reshape(A.transpose((0, 3, 1, 2)), (4, -1)).transpose((1, 0))  # shape=(4050, 4)
        all_probs = rpn_layer.transpose((0, 3, 1, 2)).reshape((-1))                    # shape=(4050,)

        x1 = all_boxes[:, 0]
        y1 = all_boxes[:, 1]
        x2 = all_boxes[:, 2]
        y2 = all_boxes[:, 3]

        # Find out the bboxes which is illegal and delete them from bboxes list
        idxs = np.where((x1 - x2 >= 0) | (y1 - y2 >= 0))

        all_boxes = np.delete(all_boxes, idxs, 0)
        all_probs = np.delete(all_probs, idxs, 0)

        # Apply non_max_suppression
        # Only extract the bboxes. Don't need rpn probs in the later process
        result = non_max_suppression_fast(all_boxes, all_probs, overlap_thresh=overlap_thresh, max_boxes=max_boxe
s)[0]

        return result
```

Test Images and test annotation file paths

In [14]:

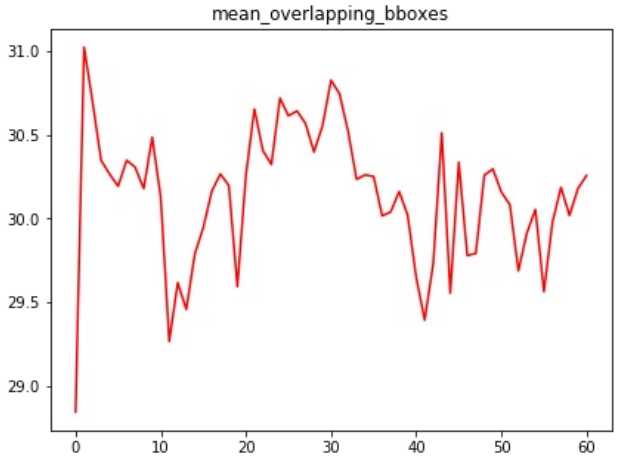
```
base_path = 'Dataset/Open Images Dataset v4 (Bounding Boxes)/'

test_path = 'Dataset/Open Images Dataset v4 (Bounding Boxes)/test_annotation.txt' # Test data (annotation file)

test_base_path = 'Dataset/Open Images Dataset v4 (Bounding Boxes)/test' # Directory to save the test images

config_output_filename = os.path.join(base_path, 'model_vgg_config.pickle')
```

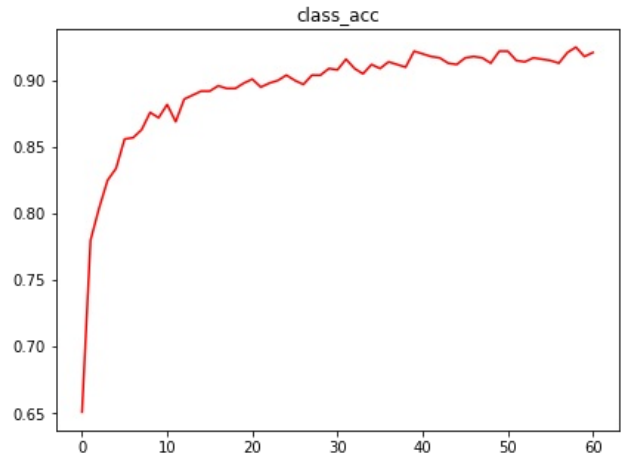
In [15]:

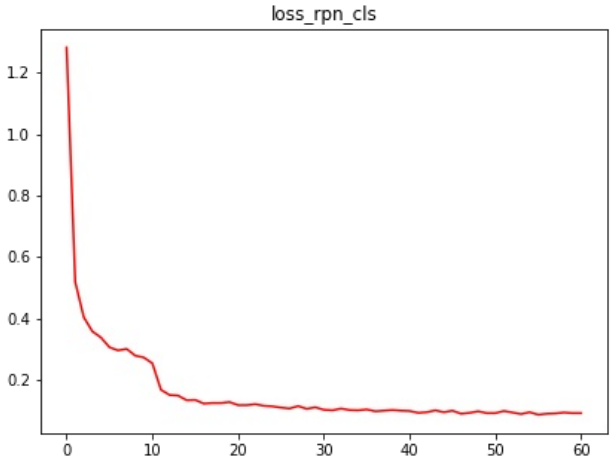
```
with open(config_output_filename, 'rb') as f_in:
        C = pickle.load(f_in)

# turn off any data augmentation at test time
C.use_horizontal_flips = False
C.use_vertical_flips = False
C.rot_90 = False
```

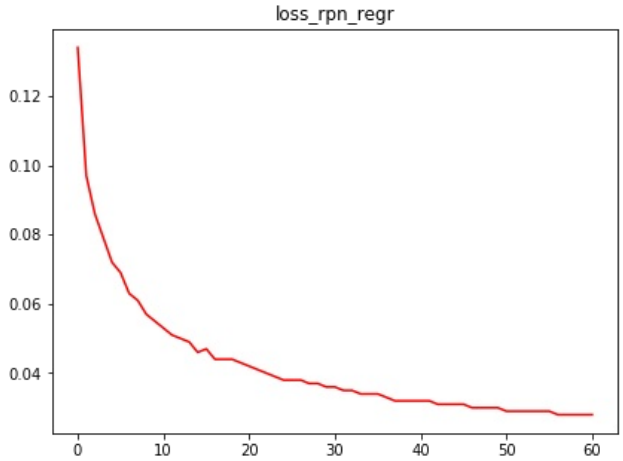
In [16]:

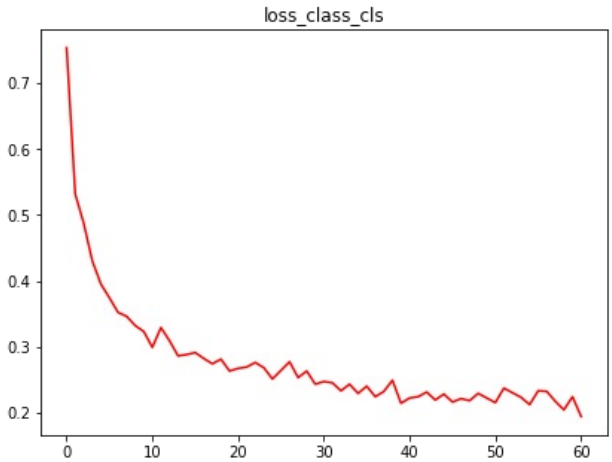
```
# Load the records
record_df = pd.read_csv(C.record_path)

r_epochs = len(record_df)

plt.figure(figsize=(15,5))
plt.subplot(1,2,1)
plt.plot(np.arange(0, r_epochs), record_df['mean_overlapping_bboxes'], 'r')
plt.title('mean_overlapping_bboxes')

plt.subplot(1,2,2)
plt.plot(np.arange(0, r_epochs), record_df['class_acc'], 'r')
plt.title('class_acc')

plt.show()

plt.figure(figsize=(15,5))

plt.subplot(1,2,1)
plt.plot(np.arange(0, r_epochs), record_df['loss_rpn_cls'], 'r')
plt.title('loss_rpn_cls')

plt.subplot(1,2,2)
plt.plot(np.arange(0, r_epochs), record_df['loss_rpn_regr'], 'r')
plt.title('loss_rpn_regr')
plt.show()
plt.figure(figsize=(15,5))
plt.subplot(1,2,1)
plt.plot(np.arange(0, r_epochs), record_df['loss_class_cls'], 'r')
plt.title('loss_class_cls')

plt.subplot(1,2,2)
plt.plot(np.arange(0, r_epochs), record_df['loss_class_regr'], 'r')
plt.title('loss_class_regr')
plt.show()
plt.figure(figsize=(15,5))
plt.subplot(1,2,1)
plt.plot(np.arange(0, r_epochs), record_df['curr_loss'], 'r')
plt.title('total_loss')

plt.subplot(1,2,2)
plt.plot(np.arange(0, r_epochs), record_df['elapsed_time'], 'r')
plt.title('elapsed_time')

plt.show()
```

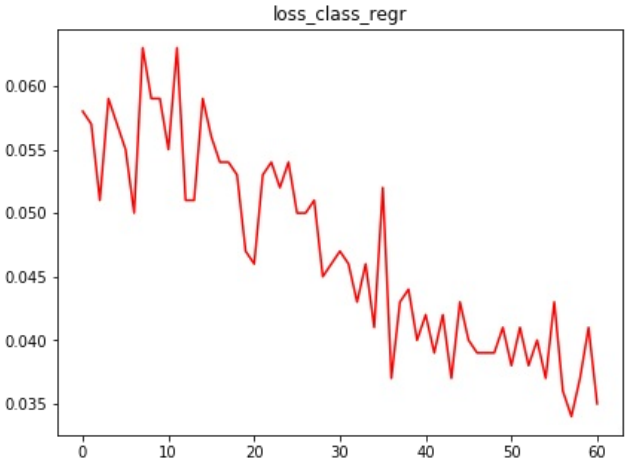

mean_overlapping_bboxes
31.0
30.5
30.0
29.5
29.0
0
10
20
30
40
50
60

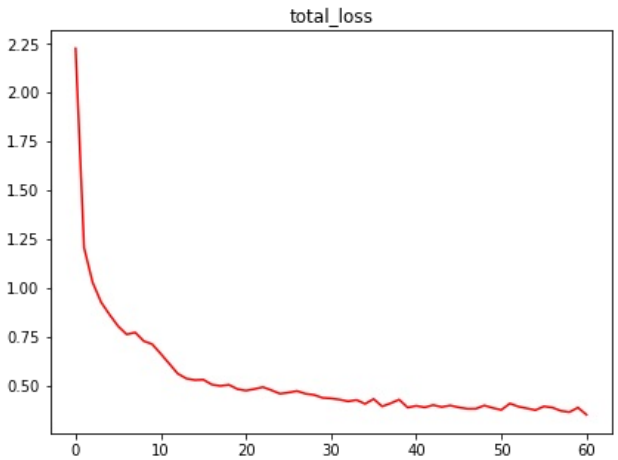

class_acc
0.90
0.85
0.80
0.75
0.70
0.65
0
10
20
30
40
50
60

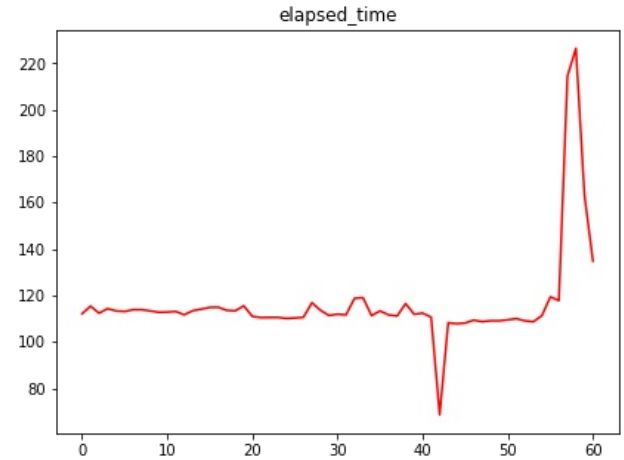

loss_rpn_cls
1.2
1.0
0.8
0.6
0.4
0.2
0
10
20
30
40
50
60


loss_rpn_regr
0.12
0.10
0.08
0.06
0.04
0
10
20
30
40
50
60


loss_class_cls
0.7
0.6
0.5
0.4
0.3
0.2
0
10
20
30
40
50
60


loss_class_regr
0.060
0.055
0.050
0.045
0.040
0.035
0
10
20
30
40
50
60


total_loss
2.25
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0
10
20
30
40
50
60


elapsed_time
220
200
180
160
140
120
100
80
0
10
20
30
40
50
60

Test

In [17]:

```
def format_img_size(img, C):
        """ formats the image size based on config """
        img_min_side = float(C.im_size)
        (height,width,_) = img.shape

        if width <= height:
                ratio = img_min_side/width
                new_height = int(ratio * height)
                new_width = int(img_min_side)
        else:
                ratio = img_min_side/height
                new_width = int(ratio * width)
                new_height = int(img_min_side)
        img = cv2.resize(img, (new_width, new_height), interpolation=cv2.INTER_CUBIC)
        return img, ratio

def format_img_channels(img, C):
        """ formats the image channels based on config """
        img = img[:, :, (2, 1, 0)]
        img = img.astype(np.float32)
        img[:, :, 0] -= C.img_channel_mean[0]
        img[:, :, 1] -= C.img_channel_mean[1]
        img[:, :, 2] -= C.img_channel_mean[2]
        img /= C.img_scaling_factor
        img = np.transpose(img, (2, 0, 1))
        img = np.expand_dims(img, axis=0)
        return img

def format_img(img, C):
        """ formats an image for model prediction based on config """
        img, ratio = format_img_size(img, C)
        img = format_img_channels(img, C)
        return img, ratio

# Method to transform the coordinates of the bounding box to its original size
def get_real_coordinates(ratio, x1, y1, x2, y2):

        real_x1 = int(round(x1 // ratio))
        real_y1 = int(round(y1 // ratio))
        real_x2 = int(round(x2 // ratio))
        real_y2 = int(round(y2 // ratio))

        return (real_x1, real_y1, real_x2 ,real_y2)
```

In [18]:

```
num_features = 512

input_shape_img = (None, None, 3)
input_shape_features = (None, None, num_features)

img_input = Input(shape=input_shape_img)
roi_input = Input(shape=(C.num_rois, 4))
feature_map_input = Input(shape=input_shape_features)

# define the base network (VGG here, can be Resnet50, Inception, etc)
shared_layers = nn_base(img_input, trainable=True)

# define the RPN, built on the base layers
num_anchors = len(C.anchor_box_scales) * len(C.anchor_box_ratios)
rpn_layers = rpn_layer(shared_layers, num_anchors)

classifier = classifier_layer(feature_map_input, roi_input, C.num_rois, nb_classes=len(C.class_mapping))

model_rpn = Model(img_input, rpn_layers)
model_classifier_only = Model([feature_map_input, roi_input], classifier)

model_classifier = Model([feature_map_input, roi_input], classifier)

print('Loading weights from {}'.format(C.model_path))
model_rpn.load_weights(C.model_path, by_name=True)
model_classifier.load_weights(C.model_path, by_name=True)

model_rpn.compile(optimizer='sgd', loss='mse')
model_classifier.compile(optimizer='sgd', loss='mse')
```

```
WARNING:tensorflow:From c:\users\srila\appdata\local\programs\python\python36\lib\site-packages\tens
orflow\python\framework\op_def_library.py:263: colocate_with (from tensorflow.python.framework.ops)
is deprecated and will be removed in a future version.
Instructions for updating:
Colocations handled automatically by placer.
WARNING:tensorflow:From c:\users\srila\appdata\local\programs\python\python36\lib\site-packages\kera
s\backend\tensorflow_backend.py:3445: calling dropout (from tensorflow.python.ops.nn_ops) with keep_
prob is deprecated and will be removed in a future version.
Instructions for updating:
Please use `rate` instead of `keep_prob`. Rate should be set to `rate = 1 - keep_prob`.
Loading weights from Dataset/Open Images Dataset v4 (Bounding Boxes)/model/model_frcnn_vgg.hdf5
```

In [19]:

```
# Switch key value for class mapping
class_mapping = C.class_mapping
class_mapping = {v: k for k, v in class_mapping.items()}
print(class_mapping)
class_to_color = {class_mapping[v]: np.random.randint(0, 255, 3) for v in class_mapping}
```

```
{0: 'red blood cell', 1: 'trophozoite', 2: 'schizont', 3: 'difficult', 4: 'ring', 5: 'leukocyte', 6:
'gametocyte', 7: 'bg'}
```

In [20]:

```
test_imgs = os.listdir(test_base_path)

imgs_path = []
for i in range(12):
        idx = np.random.randint(len(test_imgs))
        imgs_path.append(test_imgs[idx])

all_imgs = []

classes = {}
```

Sample test images with bounding boxes using trained model weights.

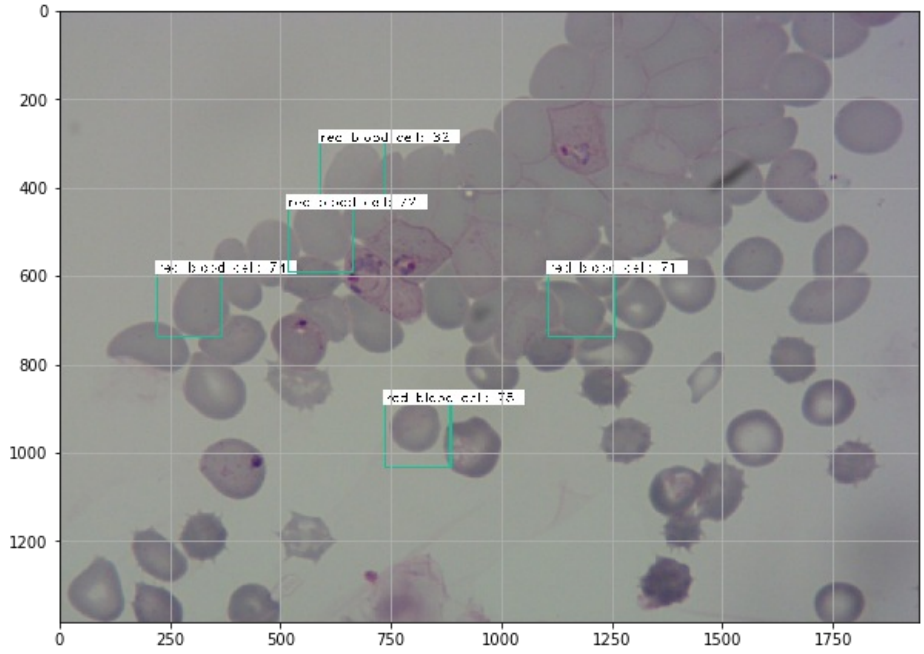
In [21]:

```
# If the box classification value is less than this, we ignore this box
bbox_threshold = 0.7

for idx, img_name in enumerate(imgs_path):
    if not img_name.lower().endswith(('.bmp', '.jpeg', '.jpg', '.png', '.tif', '.tiff')):
        continue
    print(img_name)
    st = time.time()
    filepath = os.path.join(test_base_path, img_name)
```

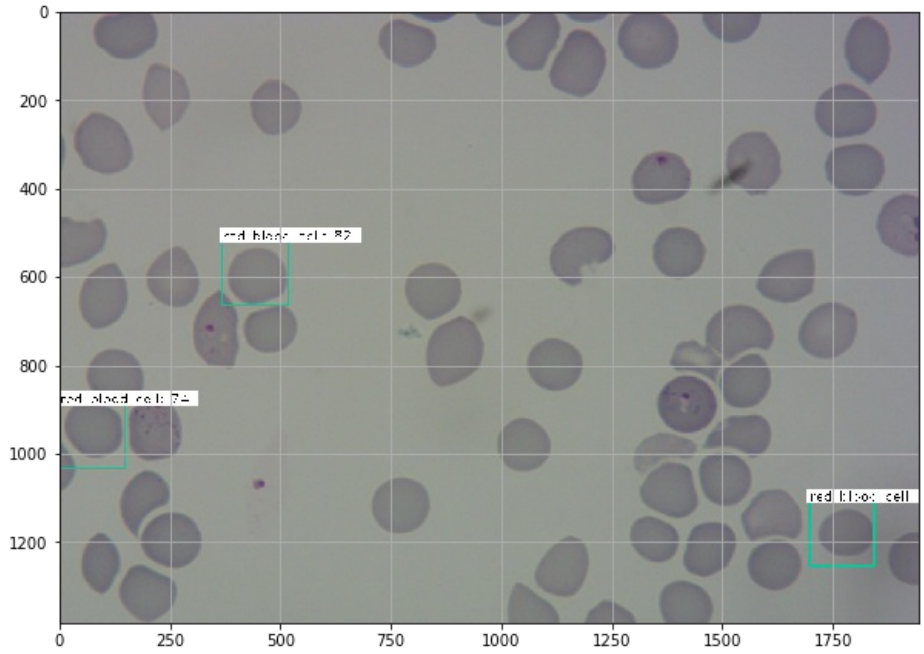
```
    img = cv2.imread(filepath)


    X, ratio = format_img(img, C)

    X = np.transpose(X, (0, 2, 3, 1))

    # get output layer Y1, Y2 from the RPN and the feature maps F
    # Y1: y_rpn_cls
    # Y2: y_rpn_regr
    [Y1, Y2, F] = model_rpn.predict(X)

    # Get bboxes by applying NMS
    # R.shape = (300, 4)
    R = rpn_to_roi(Y1, Y2, C, K.image_dim_ordering(), overlap_thresh=0.7)

    # convert from (x1,y1,x2,y2) to (x,y,w,h)
    R[:, 2] -= R[:, 0]
    R[:, 3] -= R[:, 1]

    # apply the spatial pyramid pooling to the proposed regions
    bboxes = {}
    probs = {}

    for jk in range(R.shape[0]//C.num_rois + 1):
        ROIs = np.expand_dims(R[C.num_rois*jk:C.num_rois*(jk+1), :], axis=0)
        if ROIs.shape[1] == 0:
            break

        if jk == R.shape[0]//C.num_rois:
            #pad R
            curr_shape = ROIs.shape
            target_shape = (curr_shape[0],C.num_rois,curr_shape[2])
            ROIs_padded = np.zeros(target_shape).astype(ROIs.dtype)
            ROIs_padded[:, :curr_shape[1], :] = ROIs
            ROIs_padded[0, curr_shape[1]:, :] = ROIs[0, 0, :]
            ROIs = ROIs_padded

        [P_cls, P_regr] = model_classifier_only.predict([F, ROIs])

        # Calculate bboxes coordinates on resized image
        for ii in range(P_cls.shape[1]):
            # Ignore 'bg' class
            if np.max(P_cls[0, ii, :]) < bbox_threshold or np.argmax(P_cls[0, ii, :]) == (P_cls.shape[2] - 1):
                continue

            cls_name = class_mapping[np.argmax(P_cls[0, ii, :])]

            if cls_name not in bboxes:
                bboxes[cls_name] = []
                probs[cls_name] = []

            (x, y, w, h) = ROIs[0, ii, :]

            cls_num = np.argmax(P_cls[0, ii, :])
            try:
                (tx, ty, tw, th) = P_regr[0, ii, 4*cls_num:4*(cls_num+1)]
                tx /= C.classifier_regr_std[0]
                ty /= C.classifier_regr_std[1]
                tw /= C.classifier_regr_std[2]
                th /= C.classifier_regr_std[3]
                x, y, w, h = apply_regr(x, y, w, h, tx, ty, tw, th)
            except:
                pass
            bboxes[cls_name].append([C.rpn_stride*x, C.rpn_stride*y, C.rpn_stride*(x+w), C.rpn_stride*(y+h)])
            probs[cls_name].append(np.max(P_cls[0, ii, :]))

    all_dets = []

    for key in bboxes:
        bbox = np.array(bboxes[key])

        new_boxes, new_probs = non_max_suppression_fast(bbox, np.array(probs[key]), overlap_thresh=0.2)
        for jk in range(new_boxes.shape[0]):
            (x1, y1, x2, y2) = new_boxes[jk,:]

            # Calculate real coordinates on original image
            (real_x1, real_y1, real_x2, real_y2) = get_real_coordinates(ratio, x1, y1, x2, y2)

            cv2.rectangle(img,(real_x1, real_y1), (real_x2, real_y2), (int(class_to_color[key][0]), int(class_to_
color[key][1]), int(class_to_color[key][2])),4)

            textLabel = '{}: {}'.format(key,int(100*new_probs[jk]))
            all_dets.append((key,100*new_probs[jk]))
```

```
            (retval,baseLine) = cv2.getTextSize(textLabel,cv2.FONT_HERSHEY_COMPLEX,1,1)
            textOrg = (real_x1, real_y1-0)

            cv2.rectangle(img, (textOrg[0] - 5, textOrg[1]+baseLine - 5), (textOrg[0]+retval[0] + 5, textOrg[1]-r
etval[1] - 5), (0, 0, 0), 1)
            cv2.rectangle(img, (textOrg[0] - 5,textOrg[1]+baseLine - 5), (textOrg[0]+retval[0] + 5, textOrg[1]-re
tval[1] - 5), (255, 255, 255), -1)
            cv2.putText(img, textLabel, textOrg, cv2.FONT_HERSHEY_DUPLEX, 1, (0, 0, 0), 1)

    print('Elapsed time = {}'.format(time.time() - st))
    print(all_dets)
    plt.figure(figsize=(10,10))
    plt.grid()
    plt.imshow(cv2.cvtColor(img,cv2.COLOR_BGR2RGB))
    plt.show()
```

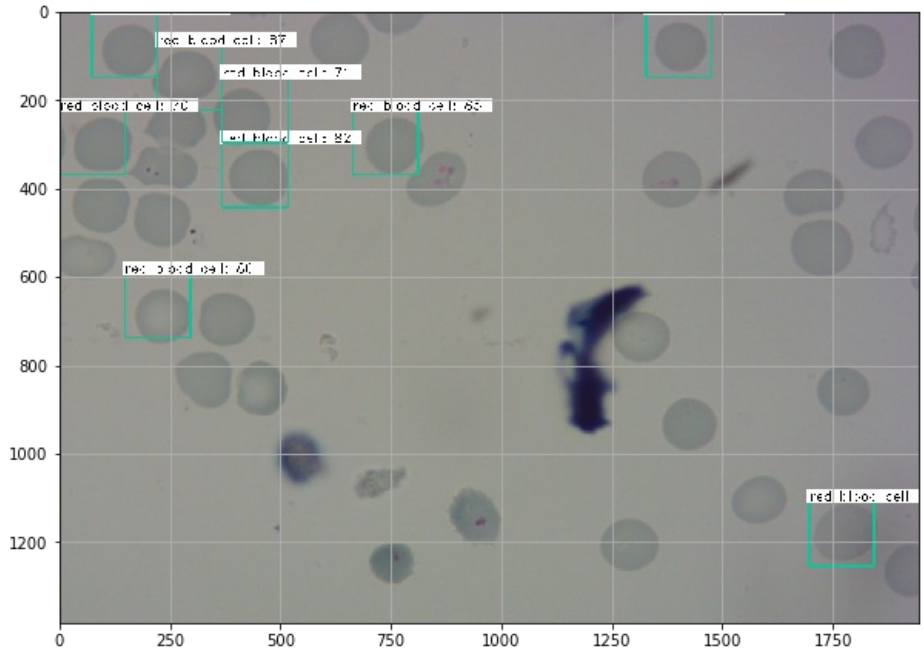
```
cea1cd9b-9b03-407b-ad8d-348155567dab.jpg
Elapsed time = 5.10888671875
[('red blood cell', 82.9387366771698), ('red blood cell', 78.72391939163208), ('red blood cell', 74.
12447333335876), ('red blood cell', 72.6984441280365), ('red blood cell', 71.28586173057556)]
```



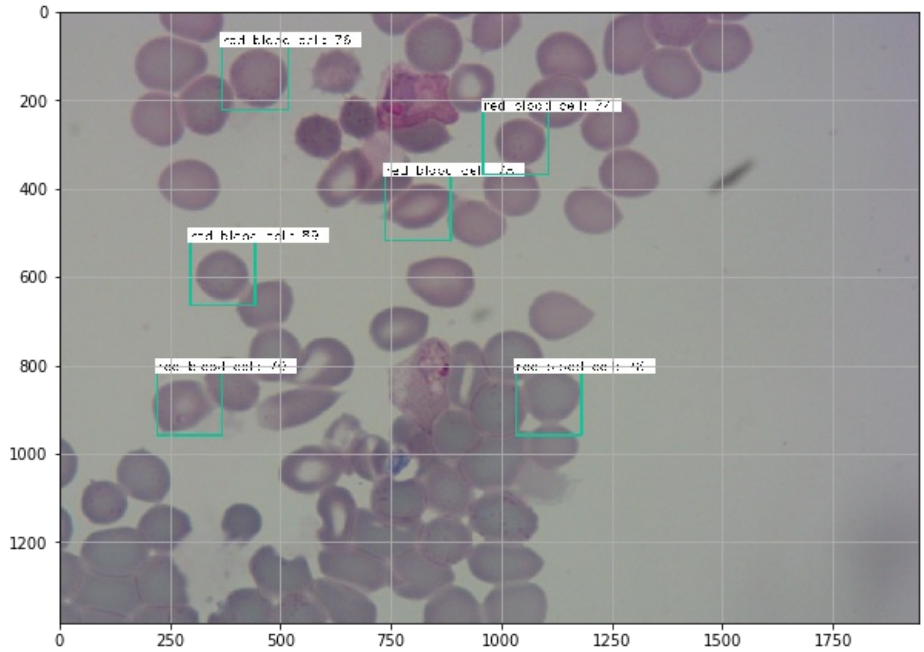

```
4dcd5df9-c56c-471b-8d44-fa4b1ca9a600.jpg
Elapsed time = 7.318870544433594
[('red blood cell', 82.68083930015564), ('red blood cell', 74.6269702911377), ('red blood cell', 71.
95661067962646)]
```



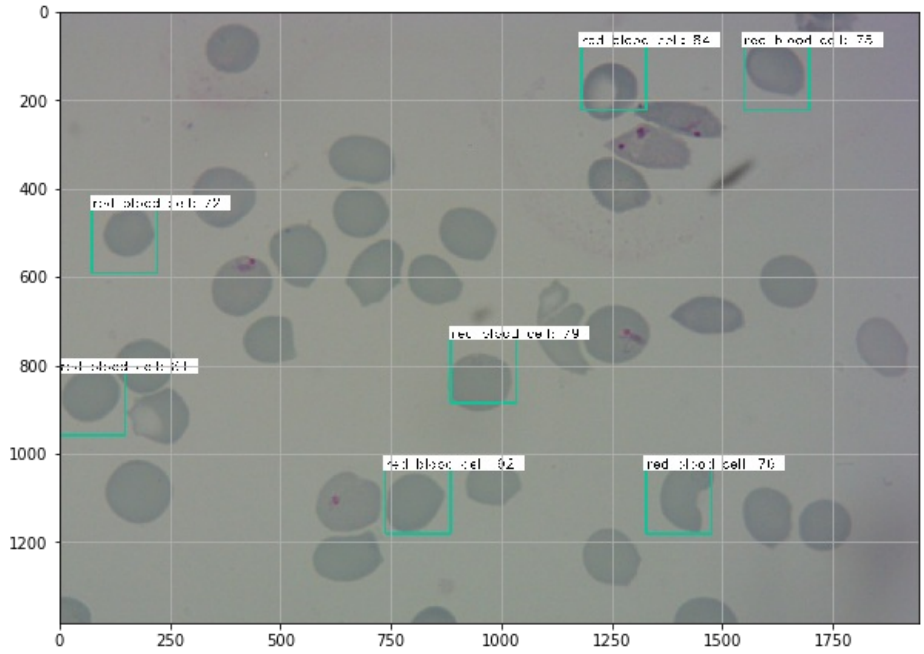
47112c6b-aaf6-488d-8f3b-f9ed0cce9a95.jpg
Elapsed time = 4.753338575363159
[('red blood cell', 91.29507541656494), ('red blood cell', 87.71923780441284), ('red blood cell', 85.2257251739502), ('red blood cell', 84.69824194908142), ('red blood cell', 82.75554180145264), ('red blood cell', 80.56358695030212), ('red blood cell', 75.86962580680847), ('red blood cell', 71.07610702514648), ('red blood cell', 70.17082571983337)]



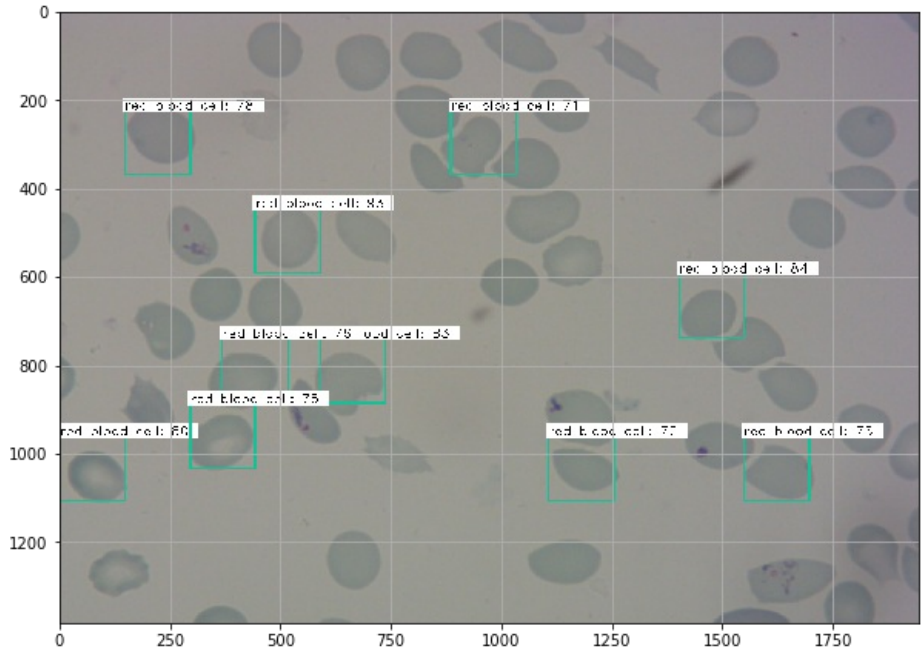
ebc4056e-d766-43cf-b6b4-5dac79d96e84.jpg
Elapsed time = 7.3694908618927
[('red blood cell', 89.45038318634033), ('red blood cell', 78.89096736907959), ('red blood cell', 78.53004336357117), ('red blood cell', 76.73243880271912), ('red blood cell', 74.2729663848877), ('red blood cell', 70.19702196121216)]



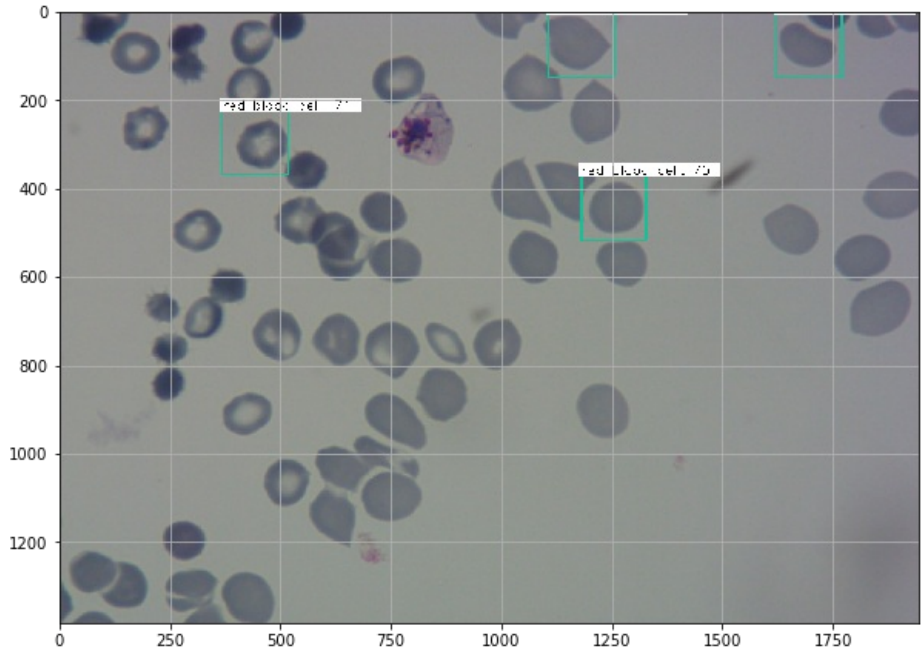
f08e873b-9617-42b3-9c7a-55d0e39c2663.jpg
Elapsed time = 5.426325798034668
[('red blood cell', 92.32266545295715), ('red blood cell', 84.2742919921875), ('red blood cell', 81.37965202331543), ('red blood cell', 79.36841249465942), ('red blood cell', 78.60924005508423), ('red blood cell', 76.39964818954468), ('red blood cell', 72.67778515815735)]



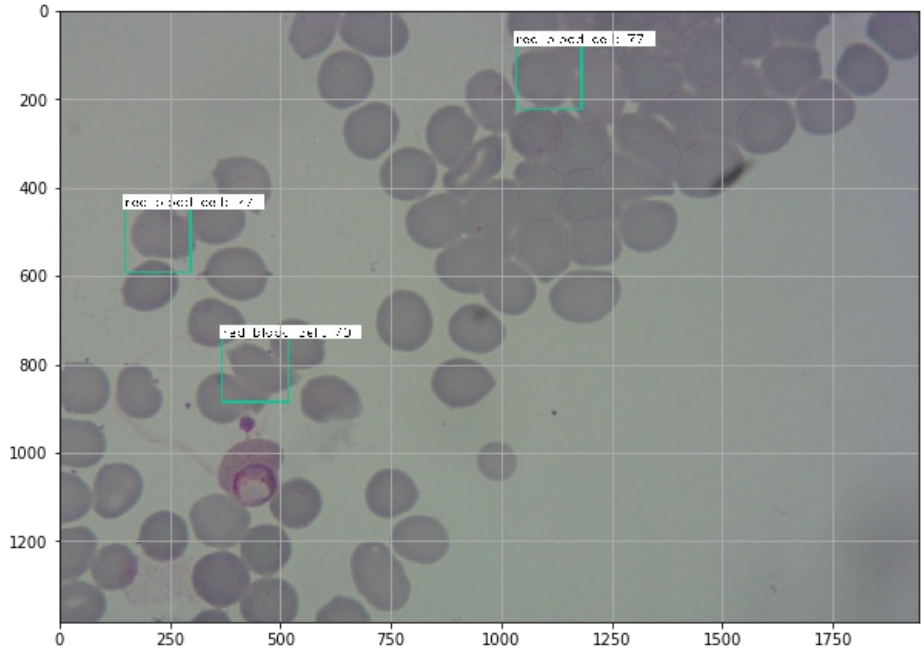
3147f1e4-6fc4-4eff-a9dd-ddeee5e2de13.jpg
Elapsed time = 7.714938402175903
[('red blood cell', 93.12155842781067), ('red blood cell', 84.8413348197937), ('red blood cell', 83.84708166122437), ('red blood cell', 80.63066601753235), ('red blood cell', 78.7824034690857), ('red blood cell', 76.40061974525452), ('red blood cell', 75.04188418388367), ('red blood cell', 73.95653128623962), ('red blood cell', 72.88896441459656), ('red blood cell', 71.16767764091492)]



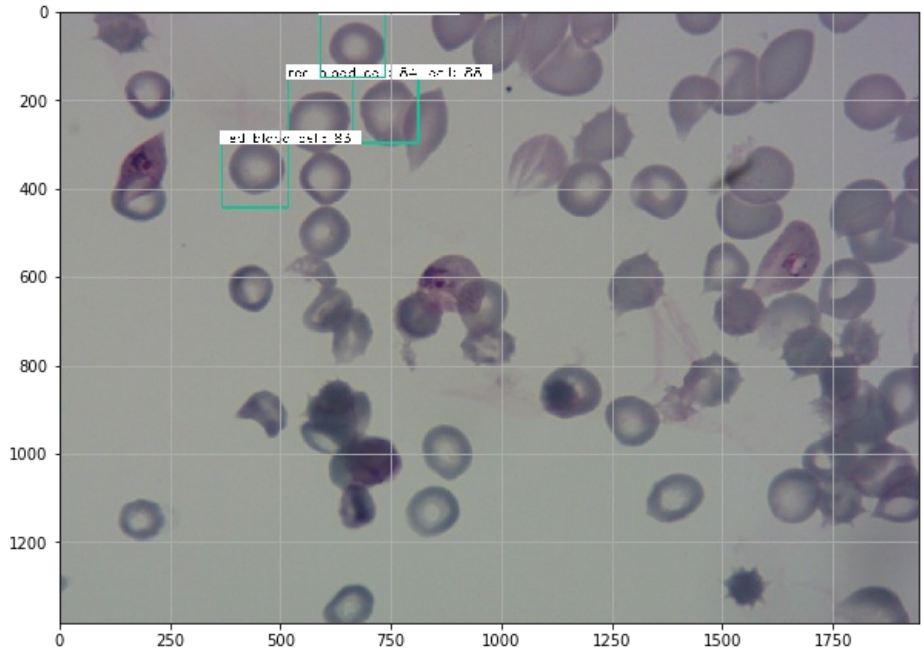
b1d312cf-1f52-4955-bf42-58d3664c254a.jpg
Elapsed time = 6.1871373653411865
[('red blood cell', 84.05143618583679), ('red blood cell', 75.05466938018799), ('red blood cell', 71.99174165725708), ('red blood cell', 71.34367227554321)]



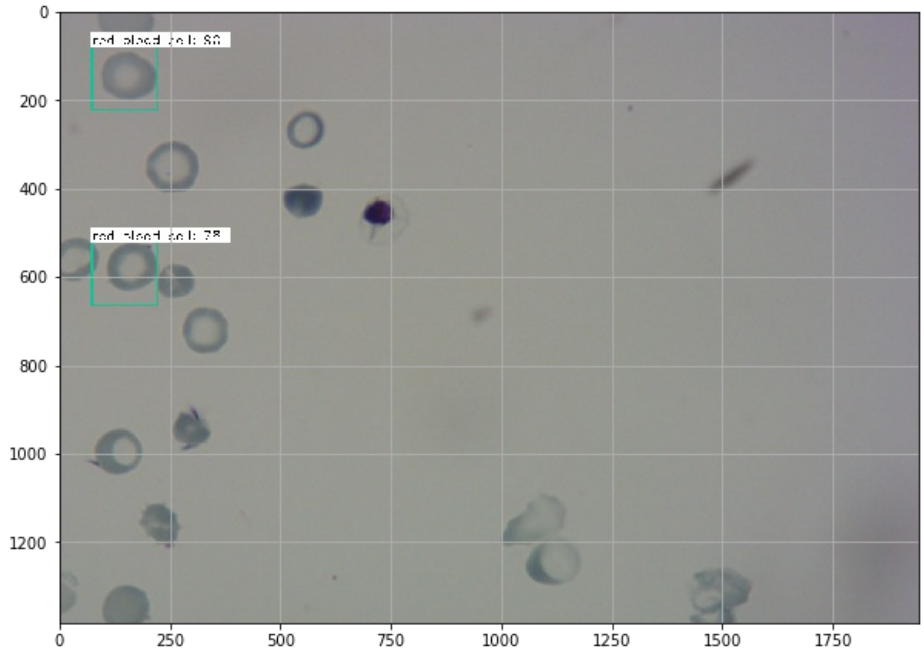
351d6536-3a5c-46eb-a6e4-d71dd999908a.jpg
Elapsed time = 6.748375415802002
[('red blood cell', 77.94932126998901), ('red blood cell', 77.71667838096619), ('red blood cell', 70
.84638476371765)]



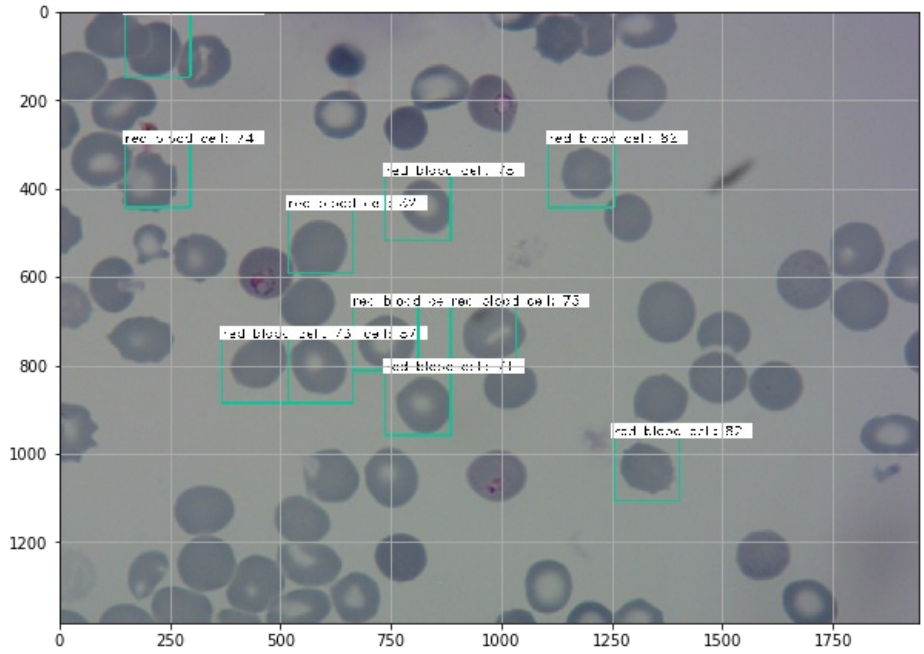
010961af-b38c-49de-aca0-e3732d73d414.jpg
Elapsed time = 7.305881977081299
[('red blood cell', 88.01528811454773), ('red blood cell', 84.13759469985962), ('red blood cell', 83
.92483592033386), ('red blood cell', 79.91409301757812)]



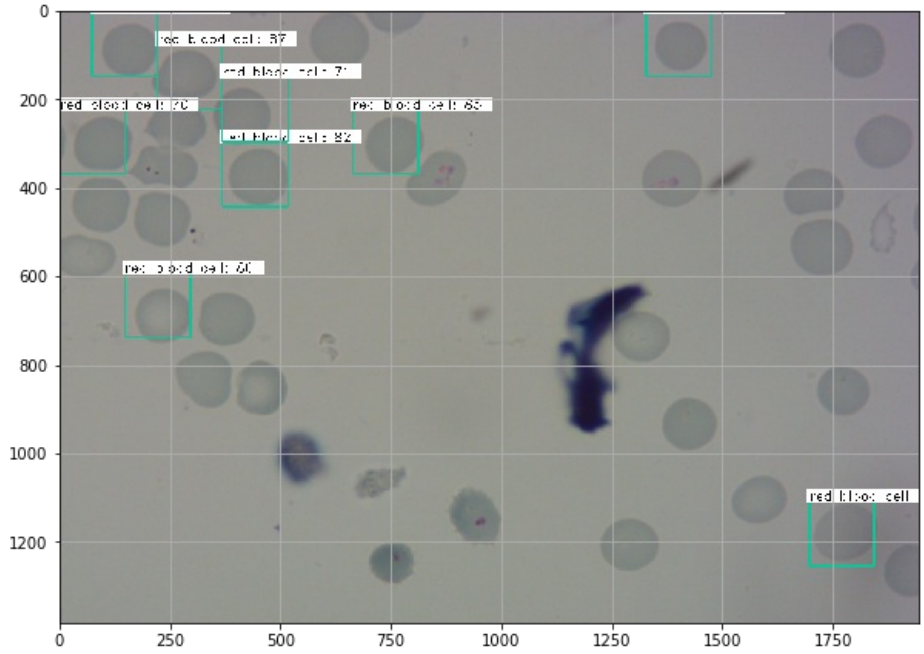
54c88d45-30c3-46f8-8fef-b3e9c07781f2.jpg
Elapsed time = 5.58755350112915
[('red blood cell', 90.44992327690125), ('red blood cell', 78.58656644821167)]



9cf0b006-cb5c-47e7-b076-1dcacf1fbfb1.jpg
Elapsed time = 7.678584814071655
[('red blood cell', 87.13012337684631), ('red blood cell', 82.90165662765503), ('red blood cell', 82
.86288380622864), ('red blood cell', 82.49022960662842), ('red blood cell', 81.29435777664185), ('re
d blood cell', 78.39835286140442), ('red blood cell', 74.62996244430542), ('red blood cell', 73.4887
182712555), ('red blood cell', 73.10177683830261), ('red blood cell', 72.62356281280518), ('red bloo
d cell', 71.26051783561707)]



47112c6b-aaf6-488d-8f3b-f9ed0cce9a95.jpg
Elapsed time = 5.477636814117432
[('red blood cell', 91.29507541656494), ('red blood cell', 87.71923780441284), ('red blood cell', 85.2257251739502), ('red blood cell', 84.69824194908142), ('red blood cell', 82.75554180145264), ('red blood cell', 80.56358695030212), ('red blood cell', 75.86962580680847), ('red blood cell', 71.07610702514648), ('red blood cell', 70.17082571983337)]



Measure mAP

In [29]:

```
def get_map(pred, gt, f):
        T = {}
        P = {}
        fx, fy = f

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

        pred_probs = np.array([s['prob'] for s in pred])
        box_idx_sorted_by_prob = np.argsort(pred_probs)[::-1]

        for box_idx in box_idx_sorted_by_prob:
                pred_box = pred[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 P:
                        P[pred_class] = []
                        T[pred_class] = []
                P[pred_class].append(pred_prob)
                found_match = False

                for gt_box in gt:
                        gt_class = gt_box['class']
                        gt_x1 = gt_box['x1']/fx
                        gt_x2 = gt_box['x2']/fx
                        gt_y1 = gt_box['y1']/fy
                        gt_y2 = gt_box['y2']/fy
                        gt_seen = gt_box['bbox_matched']
                        if gt_class != pred_class:
                                continue
                        if gt_seen:
                                continue
                        iou_map = iou((pred_x1, pred_y1, pred_x2, pred_y2), (gt_x1, gt_y1, gt_x2, gt_y2))
                        if iou_map >= 0.5:
                                found_match = True
                                gt_box['bbox_matched'] = True
                                break
                        else:
                                continue

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

        for gt_box in gt:
                if not gt_box['bbox_matched']:# and not gt_box['difficult']:
                        if gt_box['class'] not in P:
                                P[gt_box['class']] = []
                                T[gt_box['class']] = []

                        T[gt_box['class']].append(1)
                        P[gt_box['class']].append(0)

        #import pdb
        #pdb.set_trace()
        return T, P
```

In [30]:

```
def format_img_map(img, C):
        """Format image for mAP. Resize original image to C.im_size (300 in here)

        Args:
                img: cv2 image
                C: config

        Returns:
                img: Scaled and normalized image with expanding dimension
                fx: ratio for width scaling
                fy: ratio for height scaling
        """

        img_min_side = float(C.im_size)
        (height,width,_) = img.shape

        if width <= height:
                f = img_min_side/width
                new_height = int(f * height)
                new_width = int(img_min_side)
        else:
                f = img_min_side/height
                new_width = int(f * width)
                new_height = int(img_min_side)
        fx = width/float(new_width)
        fy = height/float(new_height)
        img = cv2.resize(img, (new_width, new_height), interpolation=cv2.INTER_CUBIC)
        # Change image channel from BGR to RGB
        img = img[:, :, (2, 1, 0)]
        img = img.astype(np.float32)
        img[:, :, 0] -= C.img_channel_mean[0]
        img[:, :, 1] -= C.img_channel_mean[1]
        img[:, :, 2] -= C.img_channel_mean[2]
        img /= C.img_scaling_factor
        # Change img shape from (height, width, channel) to (channel, height, width)
        img = np.transpose(img, (2, 0, 1))
        # Expand one dimension at axis 0
        # img shape becames (1, channel, height, width)
        img = np.expand_dims(img, axis=0)
        return img, fx, fy
```

In [31]:

```
print(class_mapping)
```

```
{0: 'red blood cell', 1: 'trophozoite', 2: 'schizont', 3: 'difficult', 4: 'ring', 5: 'leukocyte', 6:
'gametocyte', 7: 'bg'}
```

In [32]:

```
# This might takes a while to parser the data
test_imgs, _, _ = get_data(test_path)
```

```
Parsing annotation files
idx=5922
```

To calcualte Mean Average Precision for Test images based on the trained weights

In [33]:

```
T = {}
P = {}
mAPs = []
for idx, img_data in enumerate(test_imgs):
    print('{}/{}'.format(idx,len(test_imgs)))
    st = time.time()
    filepath = img_data['filepath']

    img = cv2.imread(filepath)

    X, fx, fy = format_img_map(img, C)

    # Change X (img) shape from (1, channel, height, width) to (1, height, width, channel)
    X = np.transpose(X, (0, 2, 3, 1))

    # get the feature maps and output from the RPN
    [Y1, Y2, F] = model_rpn.predict(X)


    R = rpn_to_roi(Y1, Y2, C, K.image_data_format(), overlap_thresh=0.7)
```

```
# convert from (x1,y1,x2,y2) to (x,y,w,h)
R[:, 2] -= R[:, 0]
R[:, 3] -= R[:, 1]

# apply the spatial pyramid pooling to the proposed regions
bboxes = {}
probs = {}

for jk in range(R.shape[0] // C.num_rois + 1):
    ROIs = np.expand_dims(R[C.num_rois * jk:C.num_rois * (jk + 1), :], axis=0)
    if ROIs.shape[1] == 0:
        break

    if jk == R.shape[0] // C.num_rois:
        # pad R
        curr_shape = ROIs.shape
        target_shape = (curr_shape[0], C.num_rois, curr_shape[2])
        ROIs_padded = np.zeros(target_shape).astype(ROIs.dtype)
        ROIs_padded[:, :curr_shape[1], :] = ROIs
        ROIs_padded[0, curr_shape[1]:, :] = ROIs[0, 0, :]
        ROIs = ROIs_padded

    [P_cls, P_regr] = model_classifier_only.predict([F, ROIs])

    # Calculate all classes' bboxes coordinates on resized image (300, 400)
    # Drop 'bg' classes bboxes
    for ii in range(P_cls.shape[1]):

        # If class name is 'bg', continue
        if np.argmax(P_cls[0, ii, :]) == (P_cls.shape[2] - 1):
            continue

        # Get class name
        cls_name = class_mapping[np.argmax(P_cls[0, ii, :])]

        if cls_name not in bboxes:
            bboxes[cls_name] = []
            probs[cls_name] = []

        (x, y, w, h) = ROIs[0, ii, :]

        cls_num = np.argmax(P_cls[0, ii, :])
        try:
            (tx, ty, tw, th) = P_regr[0, ii, 4 * cls_num:4 * (cls_num + 1)]
            tx /= C.classifier_regr_std[0]
            ty /= C.classifier_regr_std[1]
            tw /= C.classifier_regr_std[2]
            th /= C.classifier_regr_std[3]
            x, y, w, h = roi_helpers.apply_regr(x, y, w, h, tx, ty, tw, th)
        except:
            pass
        bboxes[cls_name].append([16 * x, 16 * y, 16 * (x + w), 16 * (y + h)])
        probs[cls_name].append(np.max(P_cls[0, ii, :]))

all_dets = []

for key in bboxes:
    bbox = np.array(bboxes[key])

    # Apply non-max-suppression on final bboxes to get the output bounding boxe
    new_boxes, new_probs = non_max_suppression_fast(bbox, np.array(probs[key]), overlap_thresh=0.5)
    for jk in range(new_boxes.shape[0]):
        (x1, y1, x2, y2) = new_boxes[jk, :]
        det = {'x1': x1, 'x2': x2, 'y1': y1, 'y2': y2, 'class': key, 'prob': new_probs[jk]}
        all_dets.append(det)


print('Elapsed time = {}'.format(time.time() - st))
t, p = get_map(all_dets, img_data['bboxes'], (fx, fy))
for key in t.keys():
    if key not in T:
        #print(key)
        T[key] = []
        P[key] = []
    T[key].extend(t[key])
    P[key].extend(p[key])
all_aps = []
for key in T.keys():
    if key != 'bg' and key != 'leukocyte':
        #print(key)
        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))))
    mAPs.append(np.mean(np.array(all_aps)))
    #print(T)
    #print(P)

print()
print('mean average precision:', np.mean(np.array(mAPs)))
```

```
0/120
Elapsed time = 3.8097853660583496
red blood cell AP: 0.8444833090734594
gametocyte AP: nan
trophozoite AP: 0.5
mAP = nan
1/120
Elapsed time = 3.6831552982330322
red blood cell AP: 0.8882549183112614
gametocyte AP: nan
trophozoite AP: 0.5
ring AP: 0.6388888888888888
mAP = nan
2/120
Elapsed time = 3.467728853225708
red blood cell AP: 0.8694447768770117
gametocyte AP: nan
trophozoite AP: 0.6
ring AP: 0.625
schizont AP: nan
difficult AP: nan
mAP = nan
3/120
Elapsed time = 3.410881996154785
red blood cell AP: 0.8913587383645247
gametocyte AP: nan
trophozoite AP: 0.6
ring AP: 0.5357142857142857
schizont AP: 0.3333333333333333
difficult AP: nan
mAP = nan
4/120
Elapsed time = 3.4627456665039062
red blood cell AP: 0.8994567626012081
gametocyte AP: nan
trophozoite AP: 0.5
ring AP: 0.6111111111111112
schizont AP: 0.3333333333333333
difficult AP: nan
mAP = nan
5/120
Elapsed time = 3.330098867416382
red blood cell AP: 0.8983906681342
gametocyte AP: nan
trophozoite AP: 0.42857142857142855
ring AP: 0.6111111111111112
schizont AP: 0.3333333333333333
difficult AP: 0.3333333333333333
mAP = nan
6/120
Elapsed time = 3.3610165119171143
red blood cell AP: 0.8903110050059345
gametocyte AP: nan
trophozoite AP: 0.5
ring AP: 0.6111111111111112
schizont AP: 0.3333333333333333
difficult AP: 0.25
mAP = nan
7/120
Elapsed time = 3.414872646331787
red blood cell AP: 0.9045943476890778
gametocyte AP: nan
trophozoite AP: 0.5
ring AP: 0.6428571428571428
schizont AP: 0.3333333333333333
difficult AP: 0.25
mAP = nan
8/120
Elapsed time = 3.286217212677002
red blood cell AP: 0.9083529484460158
gametocyte AP: nan
trophozoite AP: 0.5
ring AP: 0.6599999999999999
schizont AP: 0.3333333333333333
```

```
difficult AP: 0.25
mAP = nan
9/120
Elapsed time = 3.308157444000244
red blood cell AP: 0.909943041388194
gametocyte AP: nan
trophozoite AP: 0.6363636363636364
ring AP: 0.6599999999999999
schizont AP: 0.3333333333333333
difficult AP: 0.2
mAP = nan
10/120
Elapsed time = 3.304168224334717
red blood cell AP: 0.9042595792679238
gametocyte AP: nan
trophozoite AP: 0.6363636363636364
ring AP: 0.6599999999999999
schizont AP: 0.6
difficult AP: 0.2
mAP = nan
11/120
Elapsed time = 3.5245795249938965
red blood cell AP: 0.9040026865823572
gametocyte AP: nan
trophozoite AP: 0.6666666666666666
ring AP: 0.6363636363636364
schizont AP: 0.6
difficult AP: 0.2
mAP = nan
12/120
Elapsed time = 3.6213185787200928
red blood cell AP: 0.9089201446994699
gametocyte AP: 0.5
trophozoite AP: 0.7142857142857143
ring AP: 0.6363636363636364
schizont AP: 0.6
difficult AP: 0.125
mAP = 0.5807615825581368
13/120
Elapsed time = 3.5774378776550293
red blood cell AP: 0.9109646332319064
gametocyte AP: 0.5
trophozoite AP: 0.75
ring AP: 0.6363636363636364
schizont AP: 0.6
difficult AP: 0.125
mAP = 0.5870547115992572
14/120
Elapsed time = 3.6811623573303223
red blood cell AP: 0.9097297351541851
gametocyte AP: 0.5
trophozoite AP: 0.7777777777777778
ring AP: 0.6363636363636364
schizont AP: 0.6
difficult AP: 0.1111111111111111
mAP = 0.589163710067785
15/120
Elapsed time = 3.395921230316162
red blood cell AP: 0.9139865677117149
gametocyte AP: 0.5
trophozoite AP: 0.7
ring AP: 0.648529411764706
schizont AP: 0.6
difficult AP: 0.1
mAP = 0.5770859965794034
16/120
Elapsed time = 3.531559944152832
red blood cell AP: 0.9171852458721401
gametocyte AP: 0.5
trophozoite AP: 0.7142857142857143
ring AP: 0.648529411764706
schizont AP: 0.6
difficult AP: 0.09090909090909091
mAP = 0.578484910471942
17/120
Elapsed time = 3.497653007507324
red blood cell AP: 0.9182793380861106
gametocyte AP: 0.5
trophozoite AP: 0.7142857142857143
ring AP: 0.648529411764706
schizont AP: 0.6
difficult AP: 0.16666666666666666
mAP = 0.591293521800533
```

```
18/120
Elapsed time = 3.487677812576294
red blood cell AP: 0.9182709408106 12
gametocyte AP: 0.5
trophozoite AP: 0.7142857142857143
ring AP: 0.6312590187590187
schizont AP: 0.6
difficult AP: 0.16666666666666666
mAP = 0.5884137234203353
19/120
Elapsed time = 3.3400731086730957
red blood cell AP: 0.9215873252198461
gametocyte AP: 0.5
trophozoite AP: 0.6818181818181818
ring AP: 0.678900432900433
schizont AP: 0.6
difficult AP: 0.14285714285714285
mAP = 0.587527180465934
20/120
Elapsed time = 3.372986078262329
red blood cell AP: 0.9220210536500694
gametocyte AP: 0.5
trophozoite AP: 0.6818181818181818
ring AP: 0.678900432900433
schizont AP: 0.7142857142857143
difficult AP: 0.14285714285714285
mAP = 0.6066470875852569
21/120
Elapsed time = 3.3729844093322754
red blood cell AP: 0.9203439837078203
gametocyte AP: 0.5
trophozoite AP: 0.6956521739130435
ring AP: 0.678900432900433
schizont AP: 0.7142857142857143
difficult AP: 0.14285714285714285
mAP = 0.608673241277359
22/120
Elapsed time = 3.3051657676696777
red blood cell AP: 0.9187281166366613
gametocyte AP: 0.5
trophozoite AP: 0.7083333333333334
ring AP: 0.678900432900433
schizont AP: 0.625
difficult AP: 0.13333333333333333
mAP = 0.5940492027006269
23/120
Elapsed time = 3.2612826824188232
red blood cell AP: 0.916449599318705
gametocyte AP: 0.5
trophozoite AP: 0.7083333333333334
ring AP: 0.6934489348282453
schizont AP: 0.625
difficult AP: 0.13333333333333333
mAP = 0.5960942001356029
24/120
Elapsed time = 3.3939287662506104
red blood cell AP: 0.9167216147387057
gametocyte AP: 0.5
trophozoite AP: 0.7083333333333334
ring AP: 0.7071459006942877
schizont AP: 0.625
difficult AP: 0.13333333333333333
mAP = 0.5984223636832767
25/120
Elapsed time = 3.4737141132354736
red blood cell AP: 0.91370666469473
gametocyte AP: 0.5
trophozoite AP: 0.72
ring AP: 0.7071459006942877
schizont AP: 0.625
difficult AP: 0.13333333333333333
mAP = 0.5998643164537252
26/120
Elapsed time = 3.5704572200775146
red blood cell AP: 0.9166971703962008
gametocyte AP: 0.5
trophozoite AP: 0.75
ring AP: 0.6786152467604081
schizont AP: 0.625
difficult AP: 0.11764705882352941
mAP = 0.5979932459966897
27/120
Elapsed time = 3.488675117492676
```

```
red blood cell AP: 0.9179179577080445
gametocyte AP: 0.5
trophozoite AP: 0.7241379310344828
ring AP: 0.6856280722152411
schizont AP: 0.625
difficult AP: 0.11764705882352941
mAP = 0.5950551699635497
28/120
Elapsed time = 3.3979172706604004
red blood cell AP: 0.9201710251653233
gametocyte AP: 0.5
trophozoite AP: 0.7333333333333333
ring AP: 0.6856280722152411
schizont AP: 0.625
difficult AP: 0.11764705882352941
mAP = 0.5969632482562379
29/120
Elapsed time = 3.6273045539855957
red blood cell AP: 0.9145715594771033
gametocyte AP: 0.5
trophozoite AP: 0.7575757575757576
ring AP: 0.6856280722152411
schizont AP: 0.625
difficult AP: 0.1111111111111111
mAP = 0.5989810833965356
30/120
Elapsed time = 3.9324870109558105
red blood cell AP: 0.9132592759403202
gametocyte AP: 0.5
trophozoite AP: 0.7575757575757576
ring AP: 0.7093446099403381
schizont AP: 0.625
difficult AP: 0.1111111111111111
mAP = 0.6027151257612545
31/120
Elapsed time = 3.7390074729919434
red blood cell AP: 0.9138303734089712
gametocyte AP: 0.5
trophozoite AP: 0.7575757575757576
ring AP: 0.7285916950307707
schizont AP: 0.625
difficult AP: 0.1111111111111111
mAP = 0.6060181561877684
32/120
Elapsed time = 3.51360821723938
red blood cell AP: 0.9141469402126476
gametocyte AP: 0.5
trophozoite AP: 0.7571428571428571
ring AP: 0.7285916950307707
schizont AP: 0.625
difficult AP: 0.1111111111111111
mAP = 0.6059987672495645
33/120
Elapsed time = 3.7689266204833984
red blood cell AP: 0.9134764237816018
gametocyte AP: 0.5
trophozoite AP: 0.7571428571428571
ring AP: 0.7206668022268831
schizont AP: 0.625
difficult AP: 0.09523809523809523
mAP = 0.6019206963982396
34/120
Elapsed time = 3.6592180728912354
red blood cell AP: 0.9119682499081465
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7698245614035089
ring AP: 0.7206668022268831
schizont AP: 0.5555555555555556
difficult AP: 0.09090909090909091
mAP = 0.6192651544449753
35/120
Elapsed time = 3.5953919887542725
red blood cell AP: 0.91163500331195
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7613058943089431
ring AP: 0.7071374860187101
schizont AP: 0.5555555555555556
difficult AP: 0.08695652173913043
mAP = 0.6148761879334926
36/120
Elapsed time = 3.844724416732788
red blood cell AP: 0.9126021666236805
gametocyte AP: 0.6666666666666666
```

trophozoite AP: 0.7613058943089431
ring AP: 0.7115645725351476
schizont AP: 0.5555555555555556
difficult AP: 0.08333333333333333
mAP = 0.6151713648372211
37/120
Elapsed time = 3.834747791290283
red blood cell AP: 0.911960813510497
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7253945182724252
ring AP: 0.7232824644065416
schizont AP: 0.5555555555555556
difficult AP: 0.08333333333333333
mAP = 0.6110322252908366
38/120
Elapsed time = 3.579432487487793
red blood cell AP: 0.9128304846102127
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7253945182724252
ring AP: 0.7232824644065416
schizont AP: 0.6
difficult AP: 0.08
mAP = 0.6180290223259745
39/120
Elapsed time = 3.6562275886535645
red blood cell AP: 0.9122120130459054
gametocyte AP: 0.6
trophozoite AP: 0.7253945182724252
ring AP: 0.7232824644065416
schizont AP: 0.5
difficult AP: 0.10344827586206896
mAP = 0.5940562119311569
40/120
Elapsed time = 3.6283020973205566
red blood cell AP: 0.9125833406771218
gametocyte AP: 0.6
trophozoite AP: 0.7375350140056022
ring AP: 0.7232824644065416
schizont AP: 0.5
difficult AP: 0.09375
mAP = 0.5945251365148776
41/120
Elapsed time = 3.598381280899048
red blood cell AP: 0.9126068368755298
gametocyte AP: 0.6
trophozoite AP: 0.7486491050320837
ring AP: 0.7128640953824033
schizont AP: 0.5
difficult AP: 0.09375
mAP = 0.5946450062150027
42/120
Elapsed time = 3.833751916885376
red blood cell AP: 0.9129279890227515
gametocyte AP: 0.6
trophozoite AP: 0.7486491050320837
ring AP: 0.7218513102819838
schizont AP: 0.5
difficult AP: 0.09375
mAP = 0.5961964007228032
43/120
Elapsed time = 3.7529687881469727
red blood cell AP: 0.9111637519390888
gametocyte AP: 0.6
trophozoite AP: 0.7486491050320837
ring AP: 0.7205847811336972
schizont AP: 0.5
difficult AP: 0.09375
mAP = 0.5956912730174783
44/120
Elapsed time = 3.3211231231689453
red blood cell AP: 0.91104867462261
gametocyte AP: 0.6
trophozoite AP: 0.7326388888888888
ring AP: 0.7060489982666778
schizont AP: 0.5
difficult AP: 0.08823529411764706
mAP = 0.5896619759826373
45/120
Elapsed time = 3.3759772777557373
red blood cell AP: 0.9103244706942726
gametocyte AP: 0.6
trophozoite AP: 0.7195156695156695
ring AP: 0.7001115402738327

schizont AP: 0.5
difficult AP: 0.08571428571428572
mAP = 0.5859443276996769
46/120
Elapsed time = 3.431828260421753
red blood cell AP: 0.9106173739247906
gametocyte AP: 0.6
trophozoite AP: 0.7247589098532495
ring AP: 0.7001115402738327
schizont AP: 0.5
difficult AP: 0.08571428571428572
mAP = 0.5868670182943598
47/120
Elapsed time = 3.3889424800872803
red blood cell AP: 0.911050442990725
gametocyte AP: 0.6
trophozoite AP: 0.729810298102981
ring AP: 0.7001115402738327
schizont AP: 0.5
difficult AP: 0.08571428571428572
mAP = 0.5877810945136374
48/120
Elapsed time = 3.493661880493164
red blood cell AP: 0.9120007966020773
gametocyte AP: 0.6
trophozoite AP: 0.729810298102981
ring AP: 0.716045663457563
schizont AP: 0.5
difficult AP: 0.08333333333333333
mAP = 0.5901983485826591
49/120
Elapsed time = 3.6482489109039307
red blood cell AP: 0.9136636937247562
gametocyte AP: 0.6
trophozoite AP: 0.729810298102981
ring AP: 0.7217305451725476
schizont AP: 0.5
difficult AP: 0.08108108108108109
mAP = 0.591047603013561
50/120
Elapsed time = 3.3739819526672363
red blood cell AP: 0.9111395020916924
gametocyte AP: 0.6
trophozoite AP: 0.7305428897121687
ring AP: 0.7217305451725476
schizont AP: 0.5
difficult AP: 0.07692307692307693
mAP = 0.590056002316581
51/120
Elapsed time = 3.7070913314819336
red blood cell AP: 0.9113195379069288
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7394598155467721
ring AP: 0.714621805663024
schizont AP: 0.46153846153846156
difficult AP: 0.075
mAP = 0.5947677145536422
52/120
Elapsed time = 3.591400384902954
red blood cell AP: 0.9102700612680398
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7394598155467721
ring AP: 0.714621805663024
schizont AP: 0.5
difficult AP: 0.075
mAP = 0.6010030581907505
53/120
Elapsed time = 3.706094980239868
red blood cell AP: 0.9094457025650007
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7394598155467721
ring AP: 0.7161668690972559
schizont AP: 0.5
difficult AP: 0.075
mAP = 0.6011231756459492
54/120
Elapsed time = 3.7639400959014893
red blood cell AP: 0.9086583582387497
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7394598155467721
ring AP: 0.7188954102215078
schizont AP: 0.5
difficult AP: 0.075

```
mAP = 0.6014467084456l6
55/120
Elapsed time = 3.5495145320892334
red blood cell AP: 0.909269764565954
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7394598155467721
ring AP: 0.723108118271937
schizont AP: 0.5
difficult AP: 0.07317073170731707
mAP = 0.6019458494597745
56/120
Elapsed time = 3.5784356594085693
red blood cell AP: 0.9097848849214794
gametocyte AP: 0.6666666666666666
trophozoite AP: 0.7478066959921799
ring AP: 0.723108118271937
schizont AP: 0.5
difficult AP: 0.06818181818181818
mAP = 0.6025913640056801
57/120
Elapsed time = 3.600375175476074
red blood cell AP: 0.9096919085785683
gametocyte AP: 0.7142857142857143
trophozoite AP: 0.7478066959921799
ring AP: 0.723108118271937
schizont AP: 0.5
difficult AP: 0.06521739130434782
mAP = 0.6100183047387912
58/120
Elapsed time = 3.586414098739624
red blood cell AP: 0.9083600698800046
gametocyte AP: 0.7142857142857143
trophozoite AP: 0.762995337995338
ring AP: 0.7268689623996292
schizont AP: 0.4666666666666667
difficult AP: 0.06521739130434782
mAP = 0.6073990237552834
59/120
Elapsed time = 3.528566598892212
red blood cell AP: 0.9090874318561564
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7665113540359949
ring AP: 0.7189087751338623
schizont AP: 0.4666666666666667
difficult AP: 0.0625
mAP = 0.6169086675784097
60/120
Elapsed time = 3.822782278060913
red blood cell AP: 0.9083126921317769
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7553173241852487
ring AP: 0.7172584021430634
schizont AP: 0.4666666666666667
difficult AP: 0.0625
mAP = 0.6146388104840889
61/120
Elapsed time = 3.5884077548980713
red blood cell AP: 0.9095035224460399
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7553173241852487
ring AP: 0.7340594221377492
schizont AP: 0.4666666666666667
difficult AP: 0.061224489795918366
mAP = 0.6174248671682335
62/120
Elapsed time = 3.3181309700012207
red blood cell AP: 0.9090343832211973
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7655958478141577
ring AP: 0.7325124247110079
schizont AP: 0.4666666666666667
difficult AP: 0.06
mAP = 0.6185978500318013
63/120
Elapsed time = 3.501640558242798
red blood cell AP: 0.9080881412852019
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.768833067517278
ring AP: 0.7325124247110079
schizont AP: 0.4666666666666667
difficult AP: 0.058823529411764705
mAP = 0.6187836012282828
64/120
```

```
Elapsed time = 3.6871445178985596
red blood cell AP: 0.9073923233526374
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7719822218405118
ring AP: 0.7344408077378451
schizont AP: 0.4666666666666667
difficult AP: 0.058823529411764705
mAP = 0.6195138877978673
65/120
Elapsed time = 3.4886744022369385
red blood cell AP: 0.9072677634741245
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7780303030303032
ring AP: 0.7189537925493434
schizont AP: 0.4666666666666667
difficult AP: 0.058823529411764705
mAP = 0.6179199721516634
66/120
Elapsed time = 3.3929309844970703
red blood cell AP: 0.9075747797581813
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7708516354223861
ring AP: 0.7189537925493434
schizont AP: 0.4666666666666667
difficult AP: 0.057692307692307696
mAP = 0.6165861599777772
67/120
Elapsed time = 3.488675355911255
red blood cell AP: 0.9074835284275515
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7738034143276079
ring AP: 0.7189537925493434
schizont AP: 0.5
difficult AP: 0.05454545454545454
mAP = 0.6220939946046226
68/120
Elapsed time = 3.436814308166504
red blood cell AP: 0.9083211258764201
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7785701639088448
ring AP: 0.7087875023129603
schizont AP: 0.5
difficult AP: 0.05357142857142857
mAP = 0.621171333074572
69/120
Elapsed time = 3.383953094482422
red blood cell AP: 0.9083953832839139
gametocyte AP: 0.7777777777777778
trophozoite AP: 0.7863763687293098
ring AP: 0.6991540721059544
schizont AP: 0.5
difficult AP: 0.05263157894736842
mAP = 0.6207225301407208
70/120
Elapsed time = 3.5574910640716553
red blood cell AP: 0.9083716719442059
gametocyte AP: 0.7
trophozoite AP: 0.7936524217837604
ring AP: 0.6929210647063648
schizont AP: 0.5
difficult AP: 0.05263157894736842
mAP = 0.6079294562302833
71/120
Elapsed time = 3.6622116565704346
red blood cell AP: 0.9093239786415936
gametocyte AP: 0.7
trophozoite AP: 0.7936524217837604
ring AP: 0.6874657972441267
schizont AP: 0.5
difficult AP: 0.05263157894736842
mAP = 0.6071789627694749
72/120
Elapsed time = 3.754969835281372
red blood cell AP: 0.908885476001984
gametocyte AP: 0.7
trophozoite AP: 0.7959691597685152
ring AP: 0.6874657972441267
schizont AP: 0.5
difficult AP: 0.06896551724137931
mAP = 0.6102143250426676
73/120
Elapsed time = 3.611346960067749
red blood cell AP: 0.9090613783079373
```

gametocyte AP: 0.7
trophozoite AP: 0.7982345877091416
ring AP: 0.6874657972441267
schizont AP: 0.5
difficult AP: 0.06896551724137931
mAP = 0.6106212134170975
74/120
Elapsed time = 3.70110821723938
red blood cell AP: 0.9086254440300636
gametocyte AP: 0.7
trophozoite AP: 0.7982345877091416
ring AP: 0.6849711852161038
schizont AP: 0.5
difficult AP: 0.06896551724137931
mAP = 0.6101327890327813
75/120
Elapsed time = 3.8546977043151855
red blood cell AP: 0.9066388860864173
gametocyte AP: 0.7
trophozoite AP: 0.804739459563919
ring AP: 0.6890537145365961
schizont AP: 0.5
difficult AP: 0.06779661016949153
mAP = 0.611371445059404
76/120
Elapsed time = 3.7968504428863525
red blood cell AP: 0.9070127735281418
gametocyte AP: 0.7
trophozoite AP: 0.8146872503861461
ring AP: 0.6829462183081243
schizont AP: 0.5
difficult AP: 0.06666666666666667
mAP = 0.6118854848148465
77/120
Elapsed time = 3.737011194229126
red blood cell AP: 0.9074621747507261
gametocyte AP: 0.7
trophozoite AP: 0.8184420175160916
ring AP: 0.6849751132873813
schizont AP: 0.5
difficult AP: 0.06451612903225806
mAP = 0.6125659057644095
78/120
Elapsed time = 3.7659339904785156
red blood cell AP: 0.9077671552459756
gametocyte AP: 0.7
trophozoite AP: 0.7928090428090429
ring AP: 0.69285728096167
schizont AP: 0.5
difficult AP: 0.06451612903225806
mAP = 0.6096582680081578
79/120
Elapsed time = 3.3580257892608643
red blood cell AP: 0.9072549391636651
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7948257839721253
ring AP: 0.69285728096167
schizont AP: 0.47058823529411764
difficult AP: 0.06451612903225806
mAP = 0.6095525159494272
80/120
Elapsed time = 3.329101085662842
red blood cell AP: 0.9071875223796018
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7948257839721253
ring AP: 0.69285728096167
schizont AP: 0.47368421052631576
difficult AP: 0.06349206349206349
mAP = 0.6098865981007506
81/120
Elapsed time = 3.5285685062408447
red blood cell AP: 0.9079754794921602
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7948257839721253
ring AP: 0.6888715827879801
schizont AP: 0.47368421052631576
difficult AP: 0.06349206349206349
mAP = 0.6093536412572287
82/120
Elapsed time = 3.3580245971679688
red blood cell AP: 0.9081326205455976
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7948257839721253

ring AP: 0.693859968967351
schizont AP: 0.47368421052631576
difficult AP: 0.0625
mAP = 0.6100458852140195
83/120
Elapsed time = 3.7021055221557617
red blood cell AP: 0.9078764644268565
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7968039058639084
ring AP: 0.693859968967351
schizont AP: 0.47368421052631576
difficult AP: 0.0625
mAP = 0.6103328795095265
84/120
Elapsed time = 3.670189142227173
red blood cell AP: 0.9073722227978849
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7931803490627019
ring AP: 0.693859968967351
schizont AP: 0.47368421052631576
difficult AP: 0.06153846153846154
mAP = 0.6094846566942405
85/120
Elapsed time = 3.4298336505889893
red blood cell AP: 0.9076704983045725
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7931803490627019
ring AP: 0.7069250874416595
schizont AP: 0.47368421052631576
difficult AP: 0.06153846153846154
mAP = 0.6117118890244063
86/120
Elapsed time = 3.476708173751831
red blood cell AP: 0.9075638851099661
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7931803490627019
ring AP: 0.7031901003447794
schizont AP: 0.47368421052631576
difficult AP: 0.06060606060606061
mAP = 0.6109162221537585
87/120
Elapsed time = 3.447784423828125
red blood cell AP: 0.9077917580084747
gametocyte AP: 0.7272727272727273
trophozoite AP: 0.7931803490627019
ring AP: 0.6995781387044343
schizont AP: 0.47368421052631576
difficult AP: 0.06060606060606061
mAP = 0.6103522073634524
88/120
Elapsed time = 3.5644724369049072
red blood cell AP: 0.9087201823876387
gametocyte AP: 0.75
trophozoite AP: 0.7950996677740865
ring AP: 0.6995781387044343
schizont AP: 0.45
difficult AP: 0.06060606060606061
mAP = 0.6106673415787034
89/120
Elapsed time = 3.3919341564178467
red blood cell AP: 0.908737779293713
gametocyte AP: 0.75
trophozoite AP: 0.7950996677740865
ring AP: 0.699240440081749
schizont AP: 0.45
difficult AP: 0.06060606060606061
mAP = 0.6106139912926015
90/120
Elapsed time = 3.3849525451660156
red blood cell AP: 0.9084811419854114
gametocyte AP: 0.75
trophozoite AP: 0.798834051462556
ring AP: 0.699240440081749
schizont AP: 0.42857142857142855
difficult AP: 0.058823529411764705
mAP = 0.6073250985854849
91/120
Elapsed time = 3.3779704570770264
red blood cell AP: 0.9085011943672971
gametocyte AP: 0.75
trophozoite AP: 0.8024355613805155
ring AP: 0.7070361441357449
schizont AP: 0.42857142857142855

```
difficult AP: 0.05714285714285714
mAP = 0.6089478642663072
92/120
Elapsed time = 3.461747169494629
red blood cell AP: 0.9082915288252715
gametocyte AP: 0.75
trophozoite AP: 0.8024355613805155
ring AP: 0.7058118041069127
schizont AP: 0.42857142857142855
difficult AP: 0.05714285714285714
mAP = 0.6087088633378309
93/120
Elapsed time = 3.448782444000244
red blood cell AP: 0.9082893631914548
gametocyte AP: 0.75
trophozoite AP: 0.7953463203463202
ring AP: 0.713524292405554
schizont AP: 0.42857142857142855
difficult AP: 0.05714285714285714
mAP = 0.6088123769429358
94/120
Elapsed time = 3.3719873428344727
red blood cell AP: 0.9078142107645539
gametocyte AP: 0.75
trophozoite AP: 0.7919211976301241
ring AP: 0.7117242505365547
schizont AP: 0.42857142857142855
difficult AP: 0.056338028169014086
mAP = 0.6077281859452792
95/120
Elapsed time = 3.5335566997528076
red blood cell AP: 0.9079355867347869
gametocyte AP: 0.75
trophozoite AP: 0.7919211976301241
ring AP: 0.71592504908403
schizont AP: 0.42857142857142855
difficult AP: 0.056338028169014086
mAP = 0.6084485483648973
96/120
Elapsed time = 3.8596856594085693
red blood cell AP: 0.9078565766354725
gametocyte AP: 0.6923076923076923
trophozoite AP: 0.7919211976301241
ring AP: 0.71592504908403
schizont AP: 0.45454545454545453
difficult AP: 0.05555555555555555
mAP = 0.6030185876263882
97/120
Elapsed time = 3.6731808185577393
red blood cell AP: 0.9081569605939352
gametocyte AP: 0.6923076923076923
trophozoite AP: 0.7937028543989495
ring AP: 0.71592504908403
schizont AP: 0.45454545454545453
difficult AP: 0.05405405405405406
mAP = 0.6031153441640192
98/120
Elapsed time = 3.4757113456726074
red blood cell AP: 0.9078342770419319
gametocyte AP: 0.7142857142857143
trophozoite AP: 0.7937028543989495
ring AP: 0.71592504908403
schizont AP: 0.45454545454545453
difficult AP: 0.06493506493506493
mAP = 0.6085380690485243
99/120
Elapsed time = 3.5295684337615967
red blood cell AP: 0.9075832283002878
gametocyte AP: 0.7142857142857143
trophozoite AP: 0.7937028543989495
ring AP: 0.721357241882777
schizont AP: 0.45454545454545453
difficult AP: 0.06493506493506493
mAP = 0.6094015930580414
100/120
Elapsed time = 3.5435292720794678
red blood cell AP: 0.9077894559648447
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7887827811708955
ring AP: 0.7177747871477758
schizont AP: 0.45454545454545453
difficult AP: 0.0625
mAP = 0.6107876353603839
```

```
101/120
Elapsed time = 3.415870189666748
red blood cell AP: 0.9080185253580227
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.790545419492788
ring AP: 0.7138650470836064
schizont AP: 0.4166666666666667
difficult AP: 0.0625
mAP = 0.6041548319890695
102/120
Elapsed time = 3.47271990776062
red blood cell AP: 0.9077182764616627
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.790545419492788
ring AP: 0.7179173907374058
schizont AP: 0.4166666666666667
difficult AP: 0.0625
mAP = 0.6047801811153094
103/120
Elapsed time = 3.4328250885009766
red blood cell AP: 0.9076038057559701
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.790545419492788
ring AP: 0.7179173907374058
schizont AP: 0.4166666666666667
difficult AP: 0.0625
mAP = 0.6047611026643606
104/120
Elapsed time = 3.543527364730835
red blood cell AP: 0.9080898890965634
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.790545419492788
ring AP: 0.7179173907374058
schizont AP: 0.44
difficult AP: 0.0625
mAP = 0.6087310054433485
105/120
Elapsed time = 3.3789687156677246
red blood cell AP: 0.9083507988252493
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7874399692642632
ring AP: 0.7179173907374058
schizont AP: 0.44
difficult AP: 0.0625
mAP = 0.6082569153600419
106/120
Elapsed time = 3.332092761993408
red blood cell AP: 0.9086068398044301
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7811038811099932
ring AP: 0.7081487269495074
schizont AP: 0.44
difficult AP: 0.06097560975609756
mAP = 0.6053613984922269
107/120
Elapsed time = 3.365006446838379
red blood cell AP: 0.9088593120224185
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7862791357777331
ring AP: 0.7081487269495074
schizont AP: 0.44
difficult AP: 0.05813953488372093
mAP = 0.6057933404944522
108/120
Elapsed time = 3.4048995971679688
red blood cell AP: 0.9094278495632422
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7867298641281198
ring AP: 0.7007321837647907
schizont AP: 0.44
difficult AP: 0.05813953488372093
mAP = 0.6047271276122012
109/120
Elapsed time = 3.6093521118164062
red blood cell AP: 0.9089417079401902
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7804675716440421
ring AP: 0.711622933550756
schizont AP: 0.44
difficult AP: 0.05813953488372093
mAP = 0.6054175135586738
110/120
Elapsed time = 3.4946579933166504
```

```
red blood cell AP: 0.9093801886066396
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7837234722362358
ring AP: 0.7067645631985475
schizont AP: 0.44
difficult AP: 0.056179775280898875
mAP = 0.6048968887759425
111/120
Elapsed time = 3.3739821910858154
red blood cell AP: 0.9098086551867395
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7837234722362358
ring AP: 0.7036900726267535
schizont AP: 0.44
difficult AP: 0.056179775280898875
mAP = 0.6044558847773268
112/120
Elapsed time = 3.3699944019317627
red blood cell AP: 0.9095687056598919
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7884311726729429
ring AP: 0.7036900726267535
schizont AP: 0.4230769230769231
difficult AP: 0.053763440860215055
mAP = 0.60197727470501
113/120
Elapsed time = 3.3679988384246826
red blood cell AP: 0.9098503831773301
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7884311726729429
ring AP: 0.7068164731280739
schizont AP: 0.4230769230769231
difficult AP: 0.053763440860215055
mAP = 0.6025452877081364
114/120
Elapsed time = 3.742985725402832
red blood cell AP: 0.9101059579135993
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7884311726729429
ring AP: 0.7135207354597167
schizont AP: 0.4230769230769231
difficult AP: 0.053763440860215055
mAP = 0.6037052605527884
115/120
Elapsed time = 3.854698419570923
red blood cell AP: 0.9101823806717539
gametocyte AP: 0.7333333333333333
trophozoite AP: 0.7884311726729429
ring AP: 0.7146642333156751
schizont AP: 0.4230769230769231
difficult AP: 0.053763440860215055
mAP = 0.6039085806551406
116/120
Elapsed time = 3.3181307315826416
red blood cell AP: 0.9095249366698459
gametocyte AP: 0.75
trophozoite AP: 0.7899554367201427
ring AP: 0.7146642333156751
schizont AP: 0.4230769230769231
difficult AP: 0.05319148936170213
mAP = 0.6067355031907148
117/120
Elapsed time = 3.3460564613342285
red blood cell AP: 0.9097258074309477
gametocyte AP: 0.7058823529411765
trophozoite AP: 0.7914580101784912
ring AP: 0.7169115123945246
schizont AP: 0.4230769230769231
difficult AP: 0.05319148936170213
mAP = 0.6000410158972942
118/120
Elapsed time = 3.3121471405029297
red blood cell AP: 0.9099155549306795
gametocyte AP: 0.7058823529411765
trophozoite AP: 0.7914580101784912
ring AP: 0.7186625010102929
schizont AP: 0.4230769230769231
difficult AP: 0.05263157894736842
mAP = 0.6002711535141553
119/120
Elapsed time = 3.4268405437469482
red blood cell AP: 0.9094612324851495
gametocyte AP: 0.7058823529411765
```

```
trophozoite AP: 0.7858513244702504
ring AP: 0.7220951977234226
schizont AP: 0.4230769230769231
difficult AP: 0.05263157894736842
mAP = 0.5998331016073818

mean average precision: nan
```

In [34]:

```
mAP = [mAP for mAP in mAPs if str(mAP)!='nan']
mean_average_prec = round(np.mean(np.array(mAP)), 3)
print('After training %dk batches, the mean average precision is %0.3f'%(len(record_df), mean_average_prec))

# record_df.loc[len(record_df)-1, 'mAP'] = mean_average_prec
# record_df.to_csv(C.record_path, index=0)
# print('Save mAP to {}'.format(C.record_path))
```

```
After training 61k batches, the mean average precision is 0.604
```

SUMMARY

1. Using the trained model weights that was shown in srilaxmik15@gmail.com_FRCNN_train, bounding boxes were drawn with classification label and probability of classification for each label on the test data.
2. For evaluating the model, Mean Average precision score at an IOU threshold > 0.5 is used as a metric. The MAP for train data is 60%.

In [ ]:

```
```