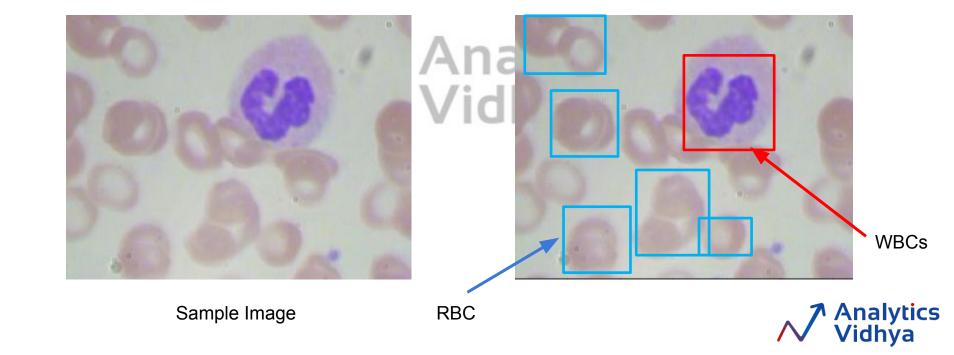


Problem Statement: Detect the RBCs and WBCs in the Images of Blood Cells



Library used - <u>ultralytics/yolov3</u>





Step 1 - Clone repo and install dependencies





- Step 1 Clone repo and install dependencies
- Step 2 Update the architecture file based on the dataset

```
[convolutional]
batch normalize=1
size=3
stride=1
pad=1
filters=256
activation=leaky
[convolutional]
size=1
stride=1
pad=1
filters=255
activation=linear
[volo]
mask = 0.1.2
anchors = 10,13, 16,30, 33,23, 30,61, 62,45, 59,119, 116,90, 156,198, 373,326
classes=80
num=9
iitter=.3
ignore_thresh = .7
truth thresh = 1
random=1
```



- Step 1 Clone repo and install dependencies
- Step 2 Update the architecture file based on the dataset
- Step 3 Load and Preprocess Data

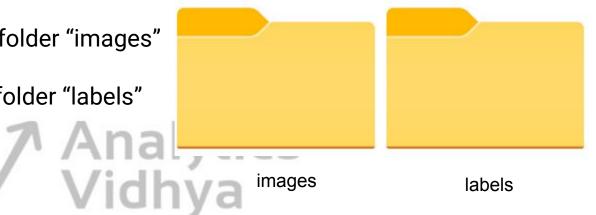


- Step 1 Clone repo and install dependencies
- Step 2 Update the architecture file based on the dataset
- Step 3 Load and Preprocess Data
- Step 4 Arrange Data in required format



All images stored in a folder "images"

All targets stored in a folder "labels"





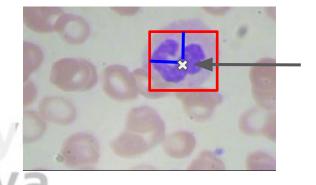
Vidhya

- All images stored in a folder "images"
- All targets stored in a folder "labels"
- Every image should have a labels file

```
/images/train2017/000000109622.jpg  # image
/labels/train2017/000000109622.txt  # label
```



- All images stored in a folder "images"
- All targets stored in a folder "labels"
- Every image should have a labels file



Bounding Box Coordinates: x-centre, y-centre, height and width

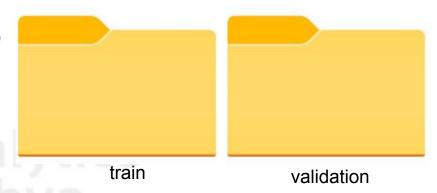


- All images stored in a folder "images"
- All targets stored in a folder "labels"
- Every image should have a labels file
- Bounding Box Coordinates: x-centre, y-centre, height and width
- Box coordinates must be in normalized xywh format (from 0 1)

```
<u>x-centre</u> <u>box_width</u> <u>y-centre</u> <u>box_height</u>
img_width img_height img_height
```



- All images stored in a folder "images"
- All targets stored in a folder "labels"
- Every image should have a labels file



- Bounding Box Coordinates x-centre, y-centre, height and width
- Box coordinates must be in normalized xywh format (from 0 1)
- Separate folders for train and validation



- All images stored in a folder "images"
- All targets stored in a folder "labels"

- classes=2
 train=/content/yolov3/bloodCellDet_train.txt
 valid=/content/yolov3/bloodCellDet_val.txt
 names=/content/yolov3/bloodCellDet.names
- Every image should have a labels file
- Bounding Box Coordinates x-centre, y-centre, height and width
- Box coordinates must be in normalized xywh format (from 0 1)
- Separate folders for train and validation
- "Data file" containing class names, path



- Step 1 Clone repo and install dependencies
- Step 2 Update the architecture file based on the dataset
- Step 3 Load and Preprocess Data
- Step 4 Arrange Data in required format
- Step 5 Train the model





