



# TensorFlow

ROADSHOW **BENGALURU**



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PyImageSearch

# Blood Cell Detection using TF Object Detection API



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The project demonstrates the use of TFOD API automatically to detect all the Red Blood Cells (RBCs), White Blood Cells (WBCs), and Platelets in each image taken via microscopic image readings.



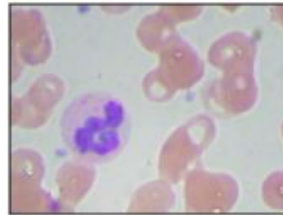
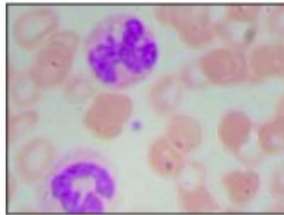
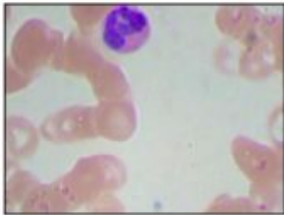
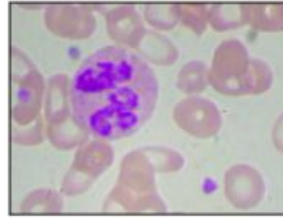
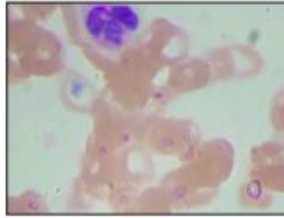
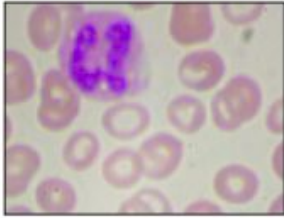
# Data

How does it look like?



# Data

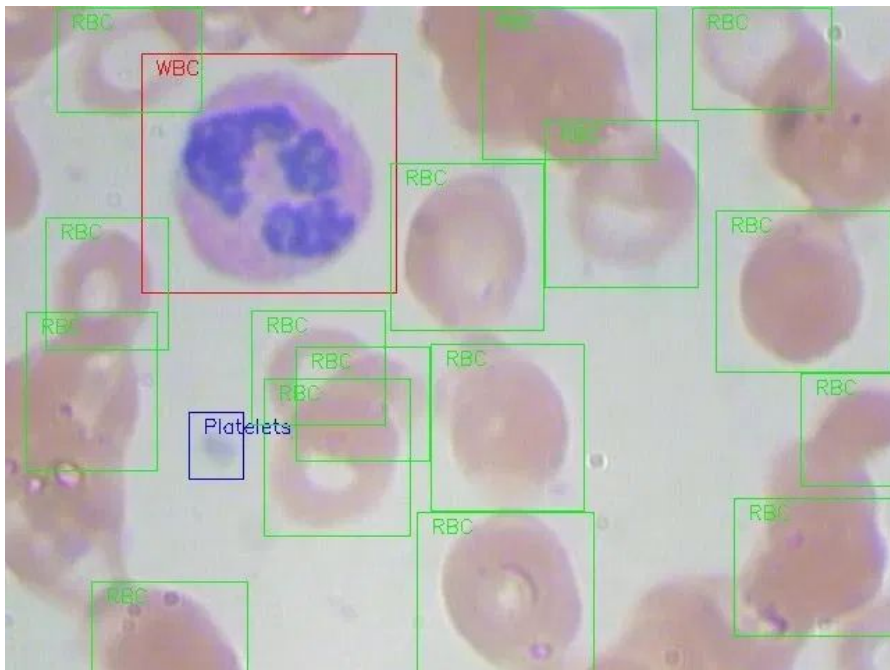
How does it look like?





# Data

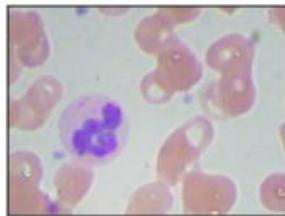
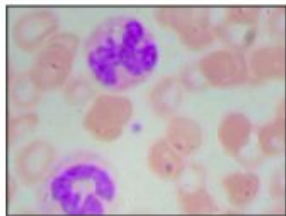
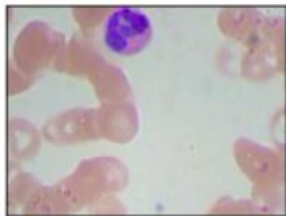
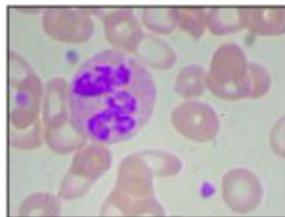
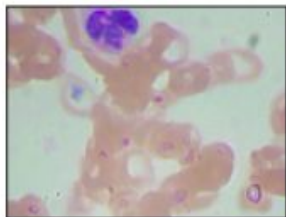
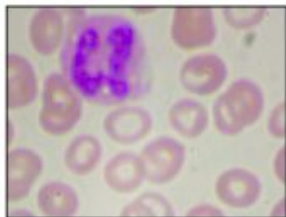
## Goal prediction





# Data

How does it look like?



Comes in **PASCAL-VOC** format!



# Data

## Sneaking into the data folders

```
BCCD_Dataset/BCCD$ ls
Annotations  ImageSets  JPEGImages

BCCD_Dataset/BCCD$ ls Annotations | head -5
BloodImage_00000.xml
BloodImage_00001.xml
BloodImage_00002.xml
BloodImage_00003.xml
BloodImage_00004.xml

BCCD_Dataset/BCCD$ ls JPEGImages | head -5
BloodImage_00000.jpg
BloodImage_00001.jpg
BloodImage_00002.jpg
BloodImage_00003.jpg
BloodImage_00004.jpg
```





# Data

## A sample XML file

```
BCCD_Dataset/BCCD$ cat Annotations/BloodImage_00000.xml
<annotation>
  <folder>JPEGImages</folder>
  <filename>BloodImage_00000.jpg</filename>
  <path>/home/pi/detection_dataset/JPEGImages/BloodImage_00000.jpg</path>
  <source>
    <database>Unknown</database>
  </source>
  <size>
    <width>640</width>
    <height>480</height>
    <depth>3</depth>
  </size>
  <segmented>0</segmented>
  <object>
    <name>WBC</name>
    <pose>Unspecified</pose>
    <truncated>0</truncated>
```



# Data

## Sneaking into the data folders

- **205** training images
- **87** evaluation images



# Data

## Sneaking into the data folders

- **205** training images
- **87** evaluation images

Seems like a **small** dataset!



# Data

## Preparation

- **TFOD API** needs the data to be in **TFRecords** format
- It provides a utility script “**generate\_tfrecord.py**”
  - Needs **.csv** files as inputs
  - XML annotations should be put together in **.csv** files (train and evaluation)
    - Another utility script “**xml\_to\_csv.py**”



# Model

**Which one?**



# Model

**Which one?**

- Faster R-CNN



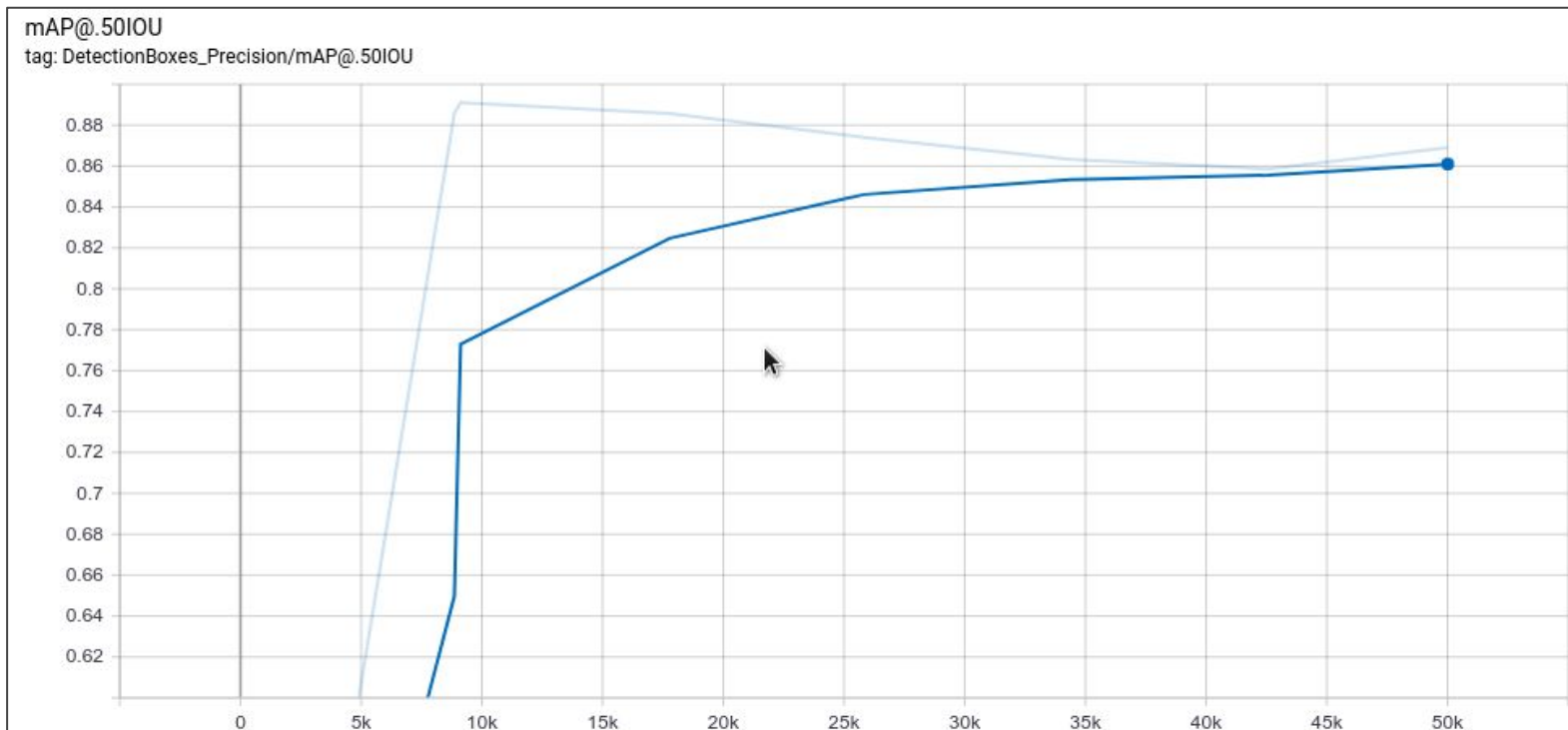
# Model

## Why Faster R-CNN?

- Solves the problem of *selective search*
  - Region Proposal Networks
- Much faster compared to other networks of R-CNN family and SSDs
- Layers easily portable to TPUs



# Results

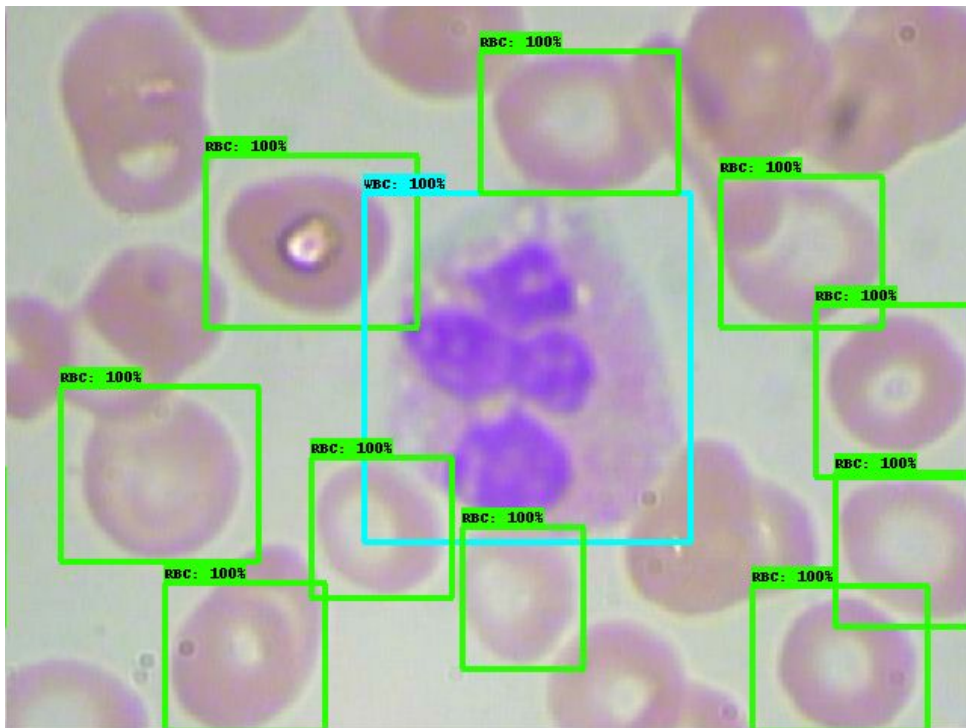


mAP@.50IOU: 86.9%



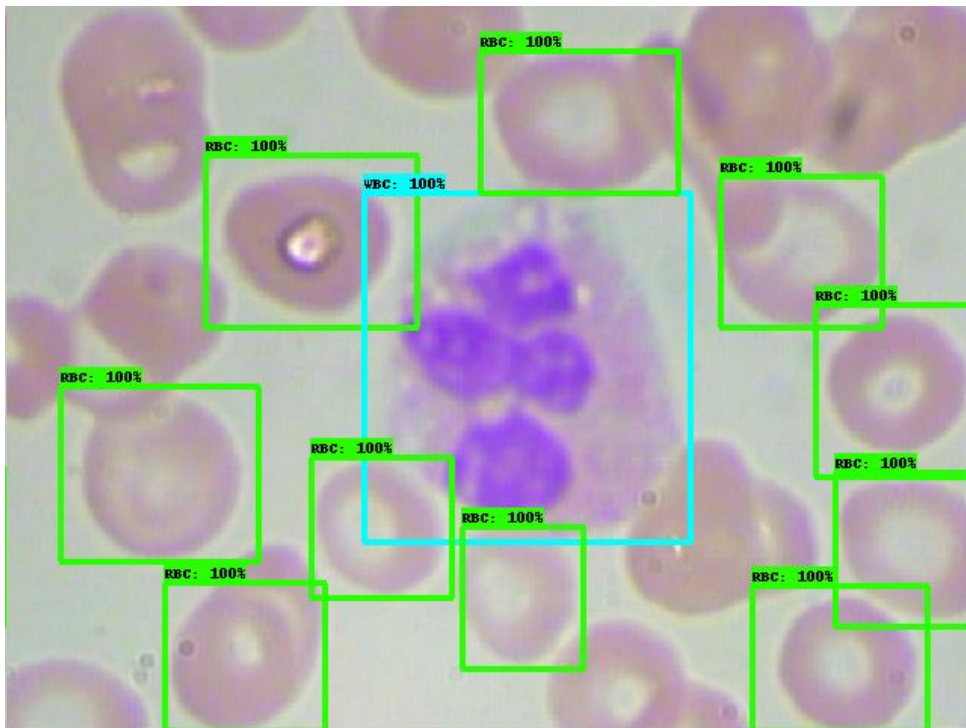


# Results





# Results



Repo available at: <http://bit.ly/BloodCell>



## Further undertakings

- Quantization aware training
- Conversion to .tflite
- Deployment to Raspberry Pi with a TPU USB Accelerator
- To be paired with microscopes used by pathologists



# Acknowledgements

- The entire team at PyImageSearch
- The entire **GDE** team
  - GCP credits
  - Qwiklabs credits
  - And many things more
- TensorFlow Research Cloud team



Thank you :)

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