WHITE BLOOD CELL IMAGE CLASSIFICATION
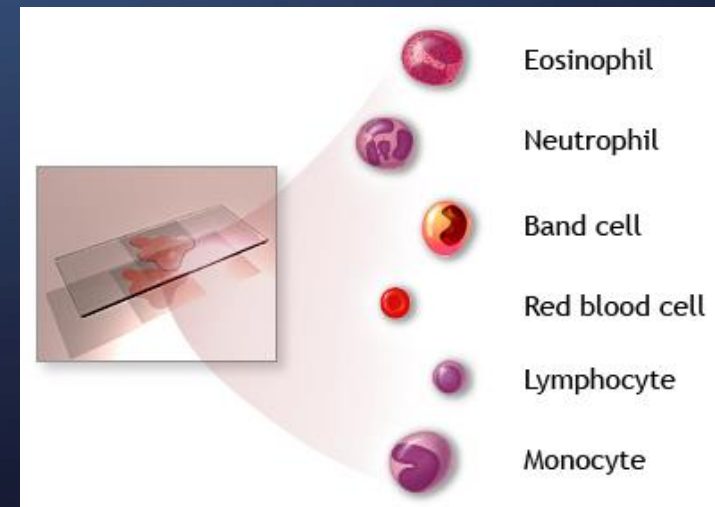
IMAGE CLASSIFICATION NEURAL NETWORK – TRANSFER LEARNING BASED

BY EDWARD SUNG

DATE: 2/14/22

COMPLETE BLOOD COUNT (CBC)

- Health related illness and diseases can be diagnosed through blood cell counting called complete blood count (CBC).

- Part of CBC is counting and identifying the types of white blood cells present and their respective levels in the sample.

WHAT ARE WHITE BLOOD CELLS?

- Eosinophils: bi-lobed, sausage-shaped nucleus; fights against parasites.

- Neutrophils: multi-lobed nucleus; fights against bacterial infections.

- Lymphocytes: single large and round nucleus: fights against viral infections.

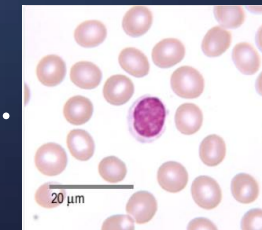- Monocytes: single large and kidney shaped nucleus; cleans up dead/damaged cells.
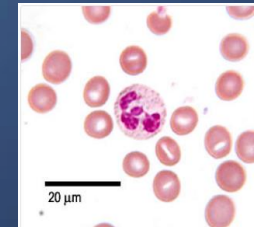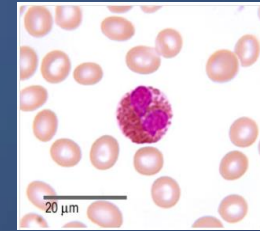
IMAGE DATABASE

- Data comes from Kaggle and is provided by Paul Mooney.

  - Augmented from 410 images from Shenggan github.

- Images are jpegs with image size of 240 x 320

- Training Set Folder:

  - Eosinophil Folder: 2497 images

  - Lymphocyte Folder: 2483 images

  - Monocyte Folder: 2478 images

  - Neutrophil Folder: 2499 images

- Testing Set Folder:

  - Eosinophil Folder: 623 images

  - Lymphocyte Folder: 620 images

  - Monocyte Folder: 620 images

  - Neutrophil Folder: 624 images

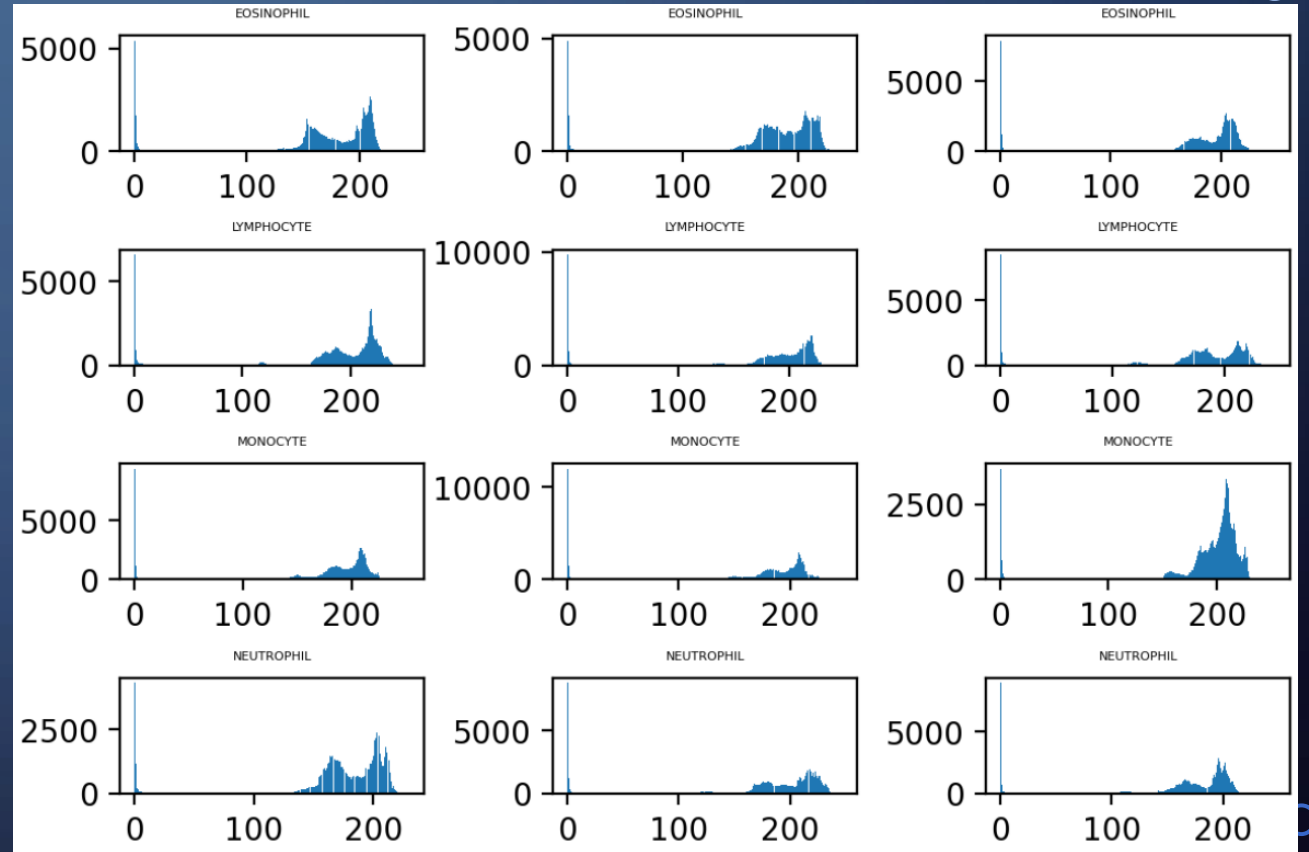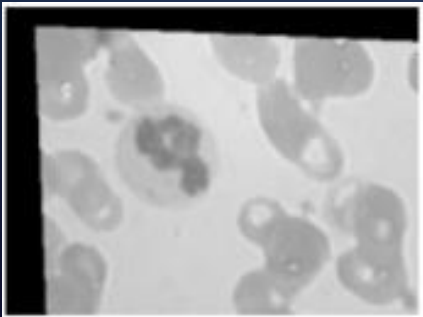# Train Data Randomly Selected Subset Images
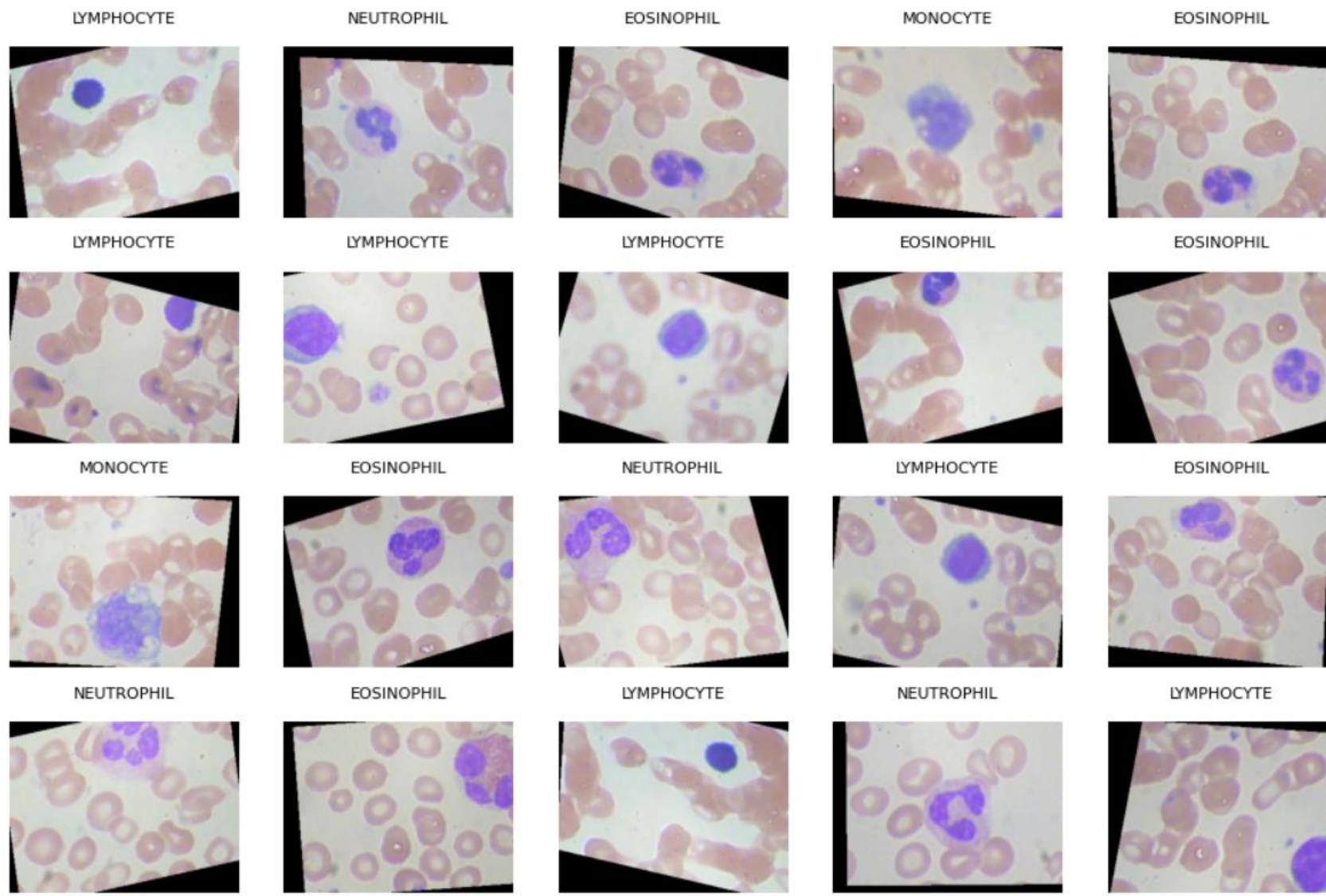
GrayScaled Train Data from Randomly Selected Subset Images
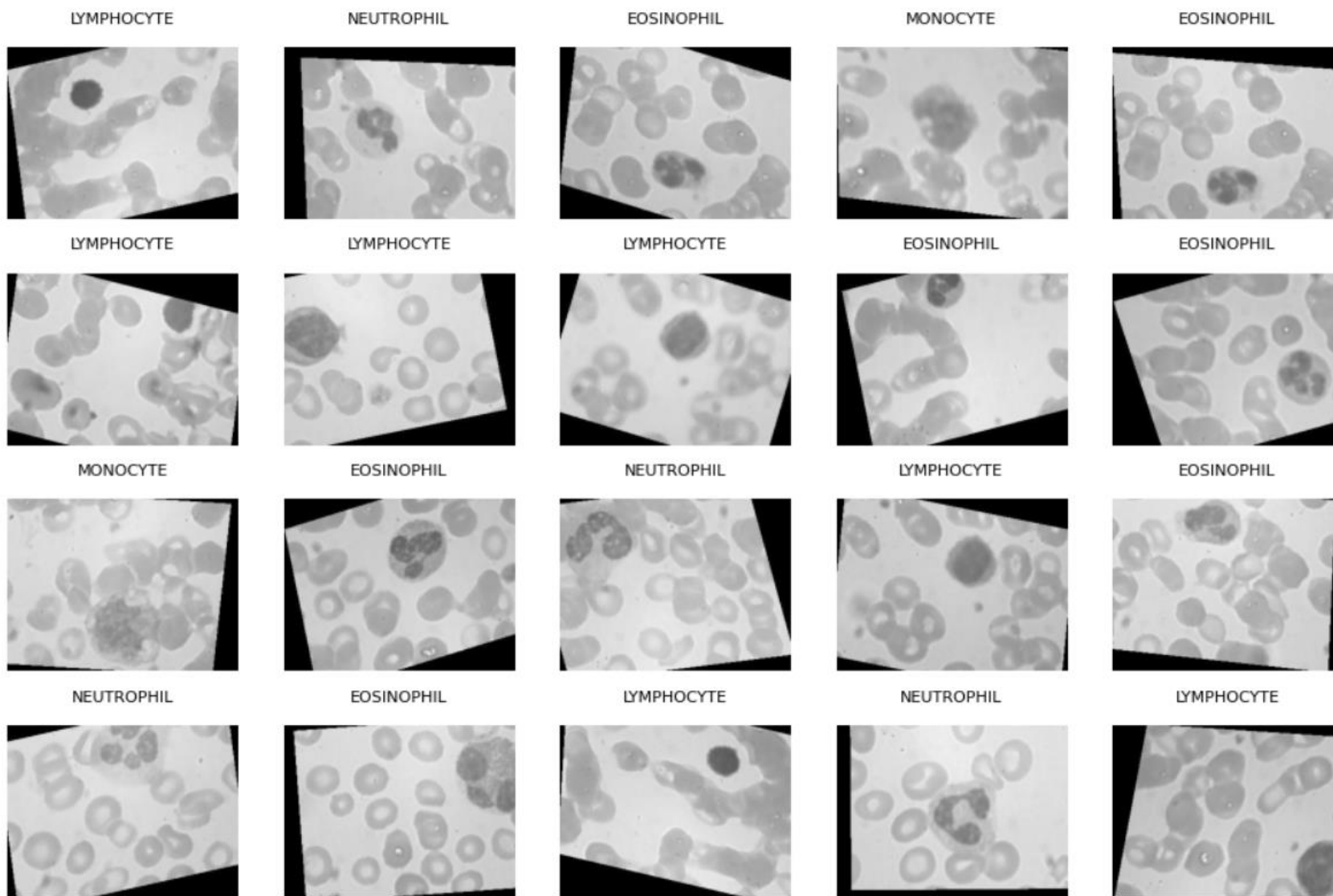
GRAY SCALE EXPLORATION

- Histogram distribution of the pixel intensities show a grouping at 0 and towards 200.

- 0 intensity pixel group are the black border caused by rotational augmentation of the image.

COMBINED AVERAGE HISTOGRAM DISTRIBUTION

- 0 pixel grouping is insignificant compared to rest of image.

- Similar bi-modal peaks for all four types of cells.

- Threshold: 200 – empty spaces between the cells.

- Threshold:180 – cells/including target cell.

- Threshold: 150 – target cell, identifiable shape.
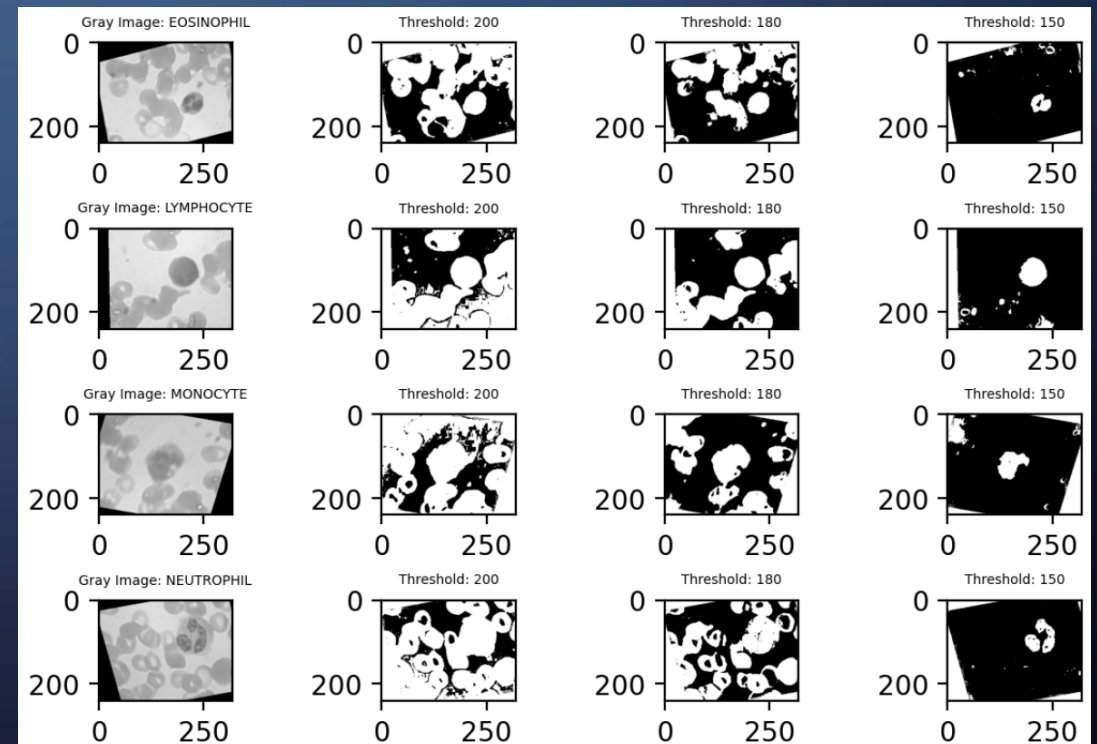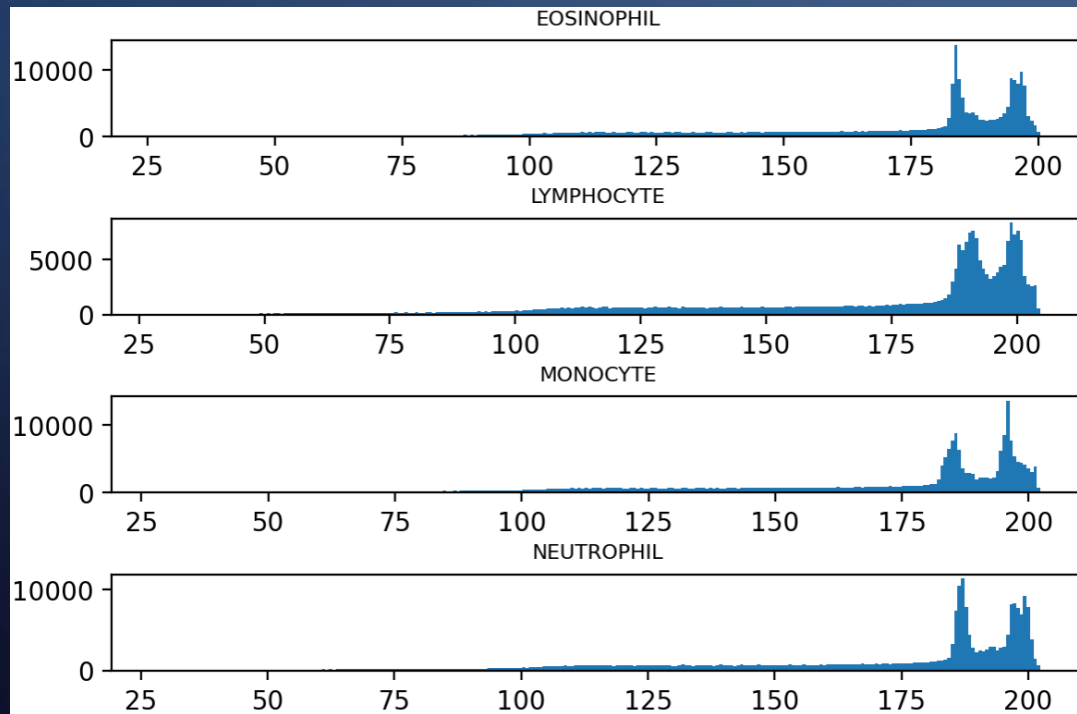
PREPROCESSING

- Augmentation process not provided by author.
  - Potential bias or separate augmentation process done to training and test set separately.
- Combined and created own training, validation, and testing sets.
  - Ensures testing sets will be representative of the training data.
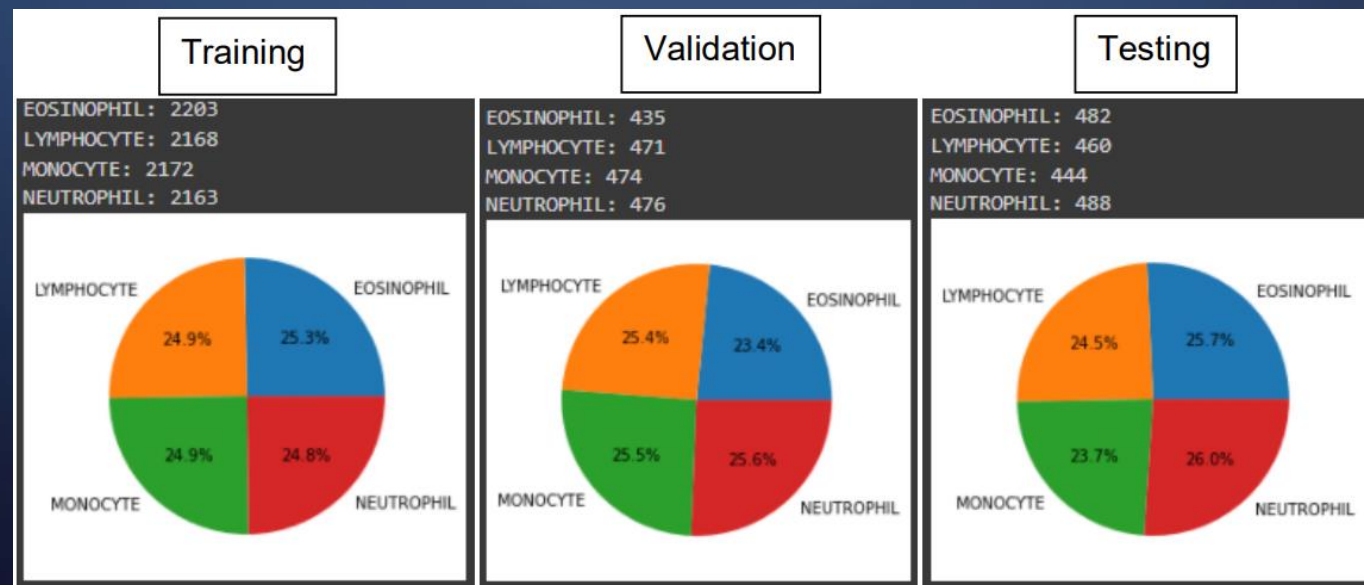
MODELING 1

- Model choice: Xception
  - Best accuracy and speed for its size
- Preprocessing Layer
  - Xception requires image array values to be -1 and 1
  - Preprocessing method included in Keras

| Model	Size (MB)	Top-1 Accuracy	Top-5 Accuracy	Parameters	Depth	Time (ms) per inference step (CPU)	Time (ms) per inference step (GPU)
Xception	88	0.790	0.945	22,910,480	126	109.42	8.06
VGG16	528	0.713	0.901	138,357,544	23	69.50	4.16
VGG19	549	0.713	0.900	143,667,240	26	84.75	4.38
ResNet50	98	0.749	0.921	25,636,712	-	58.20	4.55
ResNet101	171	0.764	0.928	44,707,176	-	89.59	5.19
ResNet152	232	0.766	0.931	60,419,944	-	127.43	6.54
ResNet50V2	98	0.760	0.930	25,613,800	-	45.63	4.42
ResNet101V2	171	0.772	0.938	44,675,560	-	72.73	5.43
ResNet152V2	232	0.780	0.942	60,380,648	-	107.50	6.64
InceptionV3	92	0.779	0.937	23,851,784	159	42.25	6.86
InceptionResNetV2	215	0.803	0.953	55,873,736	572	130.19	10.02
MobileNet	16	0.704	0.895	4,253,864	88	22.60	3.44

MODELING II

- Preprocessing layer

- Xception base model layer

- Top layer classifier, dense layers
  - Exponentially reduction in nodes to match number of class to identify

- Dropout layer in-between dense layers
  - Reduce overfitting

Layer (type)	Output Shape	Param #
input_2 (InputLayer)	[(None, 240, 320, 3)]	0
tf.math.truediv (TFOpLambda)	(None, 240, 320, 3)	0
tf.math.subtract (TFOpLambd a)	(None, 240, 320, 3)	0
xception (Functional)	(None, 8, 10, 2048)	20861480
global_average_pooling2d (G lobalAveragePooling2D)	(None, 2048)	0
dropout (Dropout)	(None, 2048)	0
dense (Dense)	(None, 1024)	2098176
dropout_1 (Dropout)	(None, 1024)	0
dense_1 (Dense)	(None, 512)	524800
dropout_2 (Dropout)	(None, 512)	0
dense_2 (Dense)	(None, 128)	65664
dropout_3 (Dropout)	(None, 128)	0
dense_3 (Dense)	(None, 64)	8256
dropout_4 (Dropout)	(None, 64)	0
dense_4 (Dense)	(None, 8)	520
dropout_5 (Dropout)	(None, 8)	0
dense_5 (Dense)	(None, 4)	36

TRAINING AND RESULTS

- 2 Rounds of training was done with the model
  - 1st round: base model Xception is frozen, training just the top layer classifier
 - 2nd round: base model Xception is unfrozen and the learning rate is set to very low.

Model	Validation Accuracy	Test Set Accuracy
Untrained Base Model	-	26%
Trained Base Model	82%	82%
Fine Tuned Entire Model	97%	96%
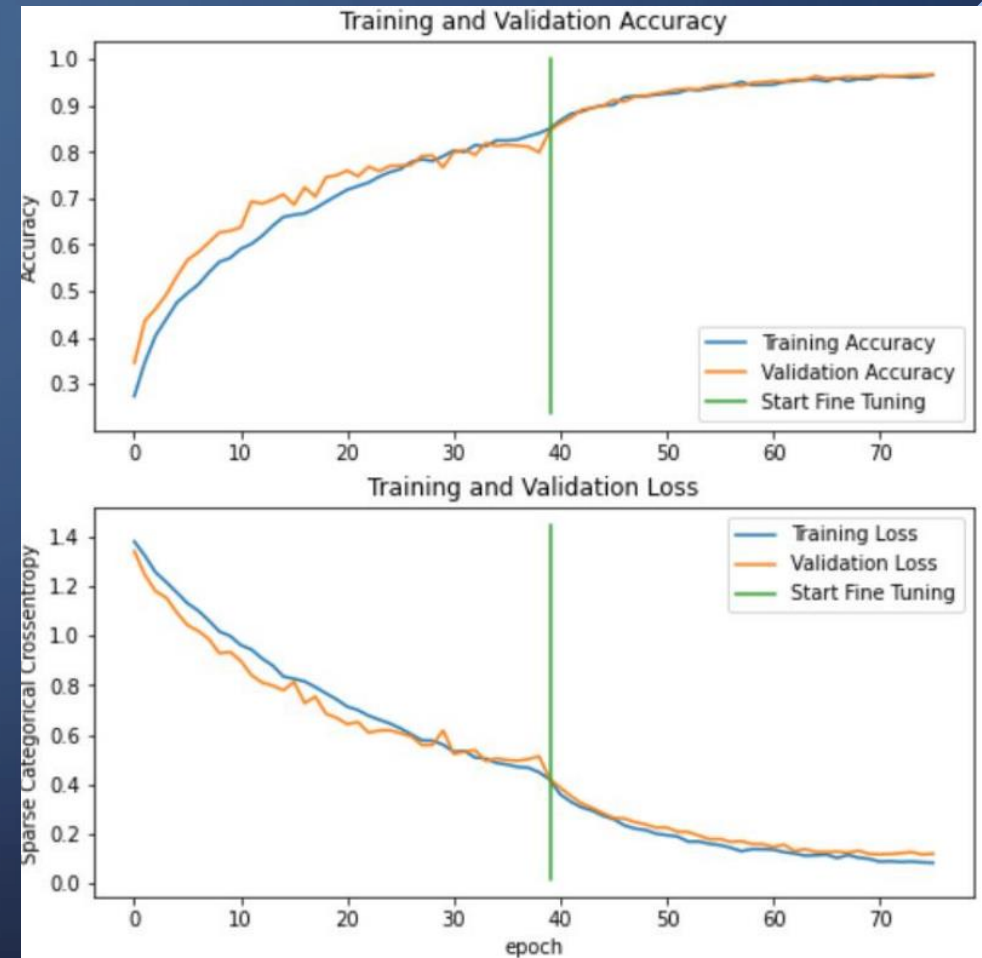
MODEL EVALUATION I

- Strong model with high classifying accuracy.

- May have underlying issue of small original training data
  - Model may be memorizing the images well rather then learning since the images are multiple augmentations of a small set of images.

|	precision	recall	f1-score	support
EOSINOPHIL	0.94	0.94	0.94	471
LYMPHOCYTE	0.99	0.98	0.99	481
MONOCYTE	1.00	0.99	0.99	447
NEUTROPHIL	0.93	0.95	0.94	475
accuracy			0.97	1874
macro avg	0.97	0.97	0.97	1874
weighted avg	0.97	0.97	0.97	1874
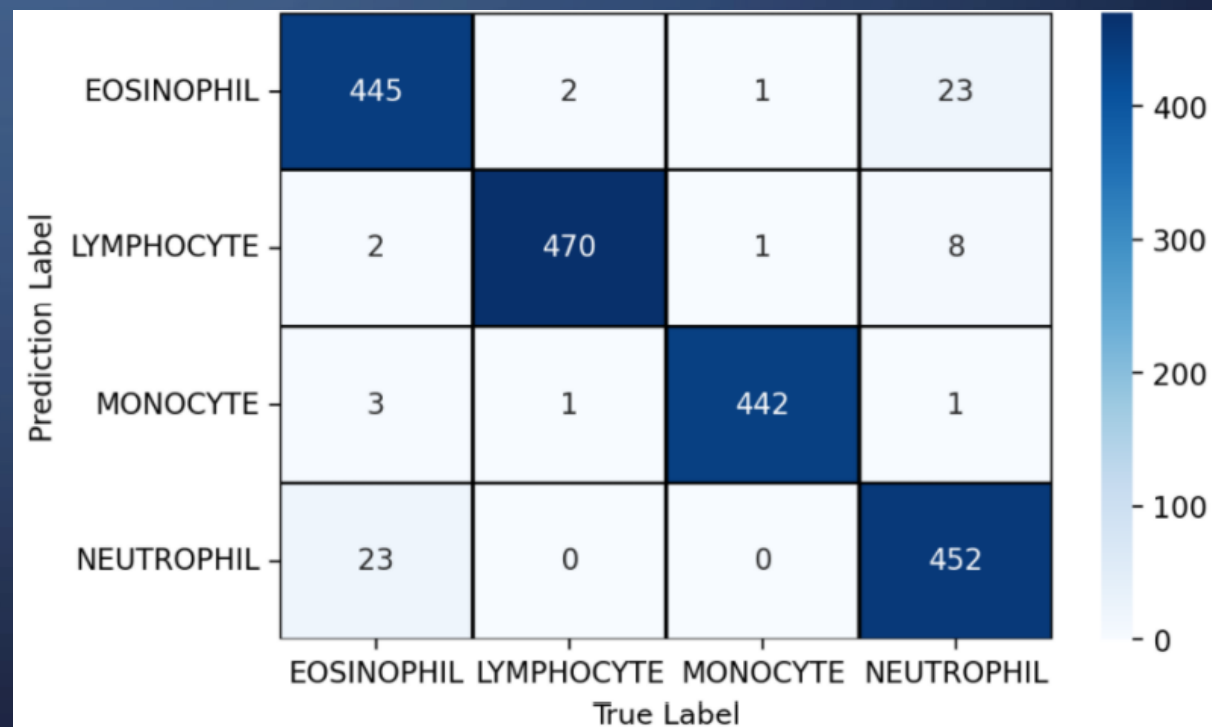
MODEL EVALUATION II

- Where the model failed to predict:
  - Eosinophils / Neutrophils: may be due to staining residues being included in the evaluation.

  - Lymphocyte / Monocyte: may be due to poor image quality / not distinct enough staining or shape.

Predicted: EOSINOPHIL, Label: NEUTROPHIL
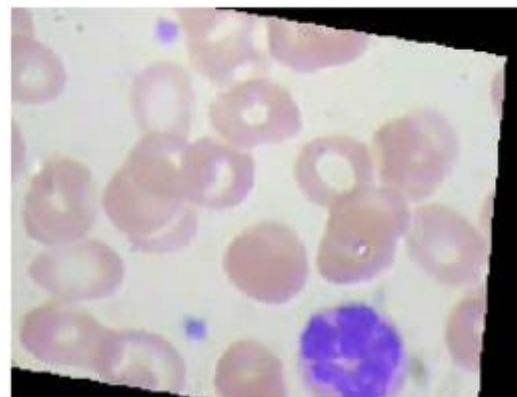
Predicted: LYMPHOCYTE, Label: MONOCYTE
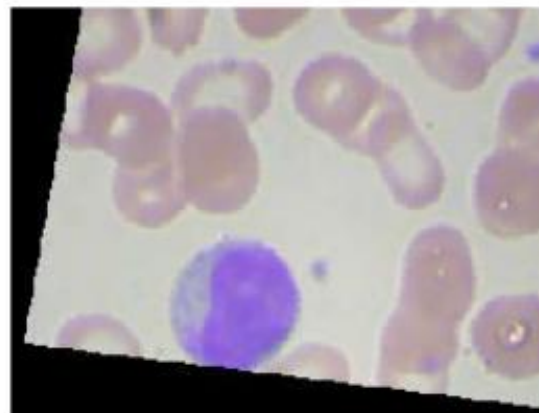
FOLLOW-UP AND FURTHER PROJECTS

- Collecting new images for the model to train on.

- Use own data augmentation generator rather than the provided image set.

- Increase model's capabilities by allowing it to classify and count multiple target cells in an image.

- Increase model's capabilities by expanding the classification nodes to different types of cells.
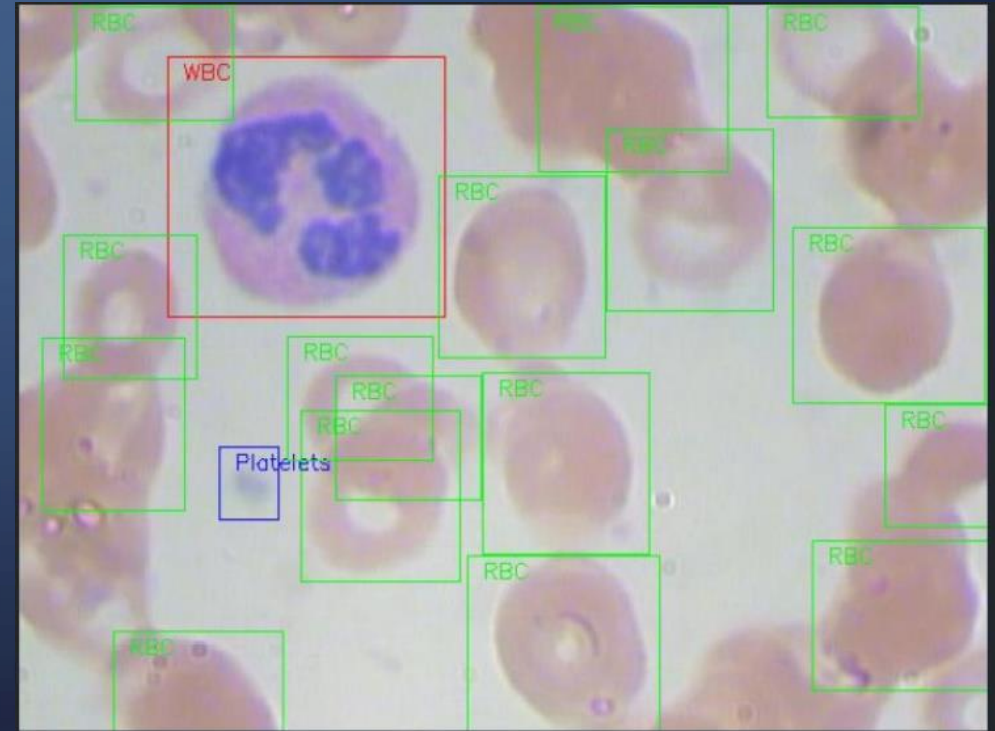 - Uses for cancer cell identification or drug discovery.

Image from Shenggan Github BCCD Project with label boxes around cells.

THANK YOU

SPRINGBOARD DATA SCIENCE TRACK

IMAGE CLASSIFICATION CAPSTONE PROJECT

MENTOR: LUCAS ALLEN