

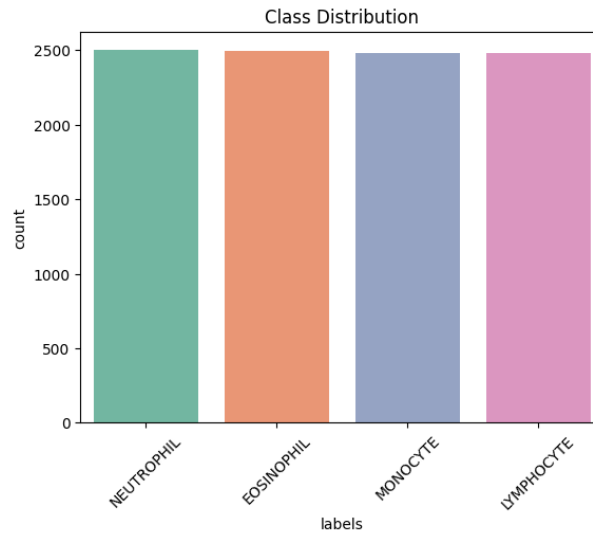
Data Collection and Preprocessing Phase

Date	05 July 2025
Team ID	SWTID1749835721
Project Title	HematoVision – Blood Cell Classification using Transfer Learning
Maximum Marks	6 Marks

Data Exploration and Preprocessing Report

In this phase, image data of blood cells are analyzed and preprocessed for use in a deep learning pipeline. The dataset comprises images from four blood cell classes: **NEUTROPHIL**, **LYMPHOCYTE**, **MONOCYTE**, and **EOSINOPHIL**. Each image is linked to a class label and stored in a structured directory format. The dataset is explored for class balance, image integrity, and shape variation, and preprocessed to support accurate training of image classification models.

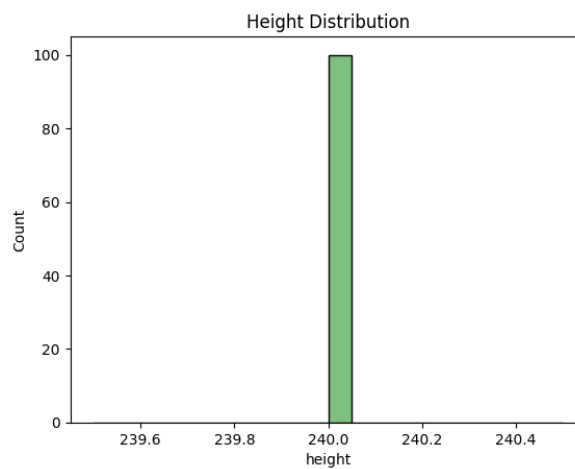
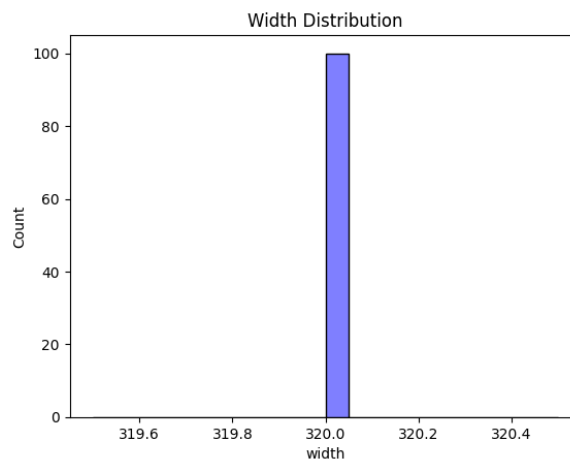
Section	Description
Data Overview	<div><div><input type="checkbox"/> Dimension:<ul style="list-style-type: none">Number of images: XXXX (replace with actual count)Number of classes: 4</div><div><input type="checkbox"/> Class Labels:<ul style="list-style-type: none">NEUTROPHILLYMPHOCYTEMONOCYTEEOSINOPHIL</div><div><input type="checkbox"/> Format:<ul style="list-style-type: none">Image formats: .jpeg, .jpg, .pngDirectory structure used to assign labels</div><div>Descriptive Statistics:<ul style="list-style-type: none">Class Distribution: The count of images per class is analyzed to detect any class imbalance.</div></div>



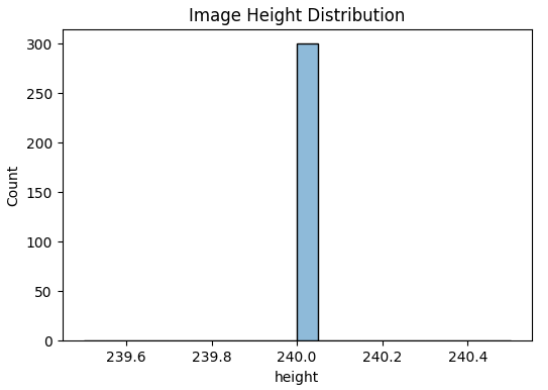
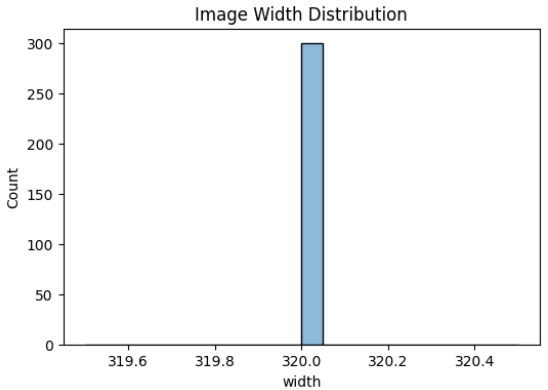
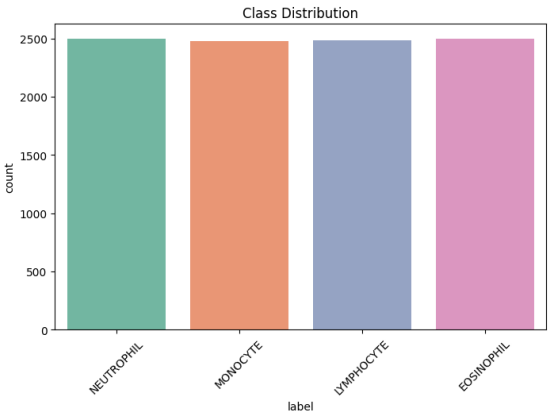
- **Image Dimensions:**

A sample of images is used to understand the variation in width and height.

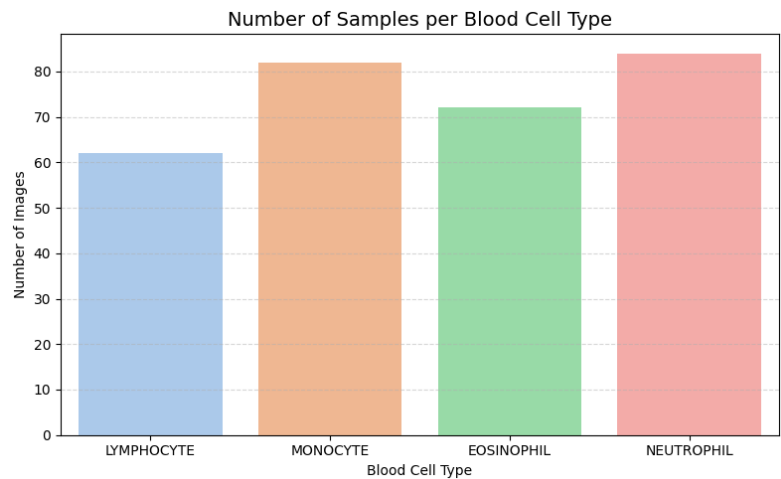
This ensures input shapes are consistent before feeding to a CNN.



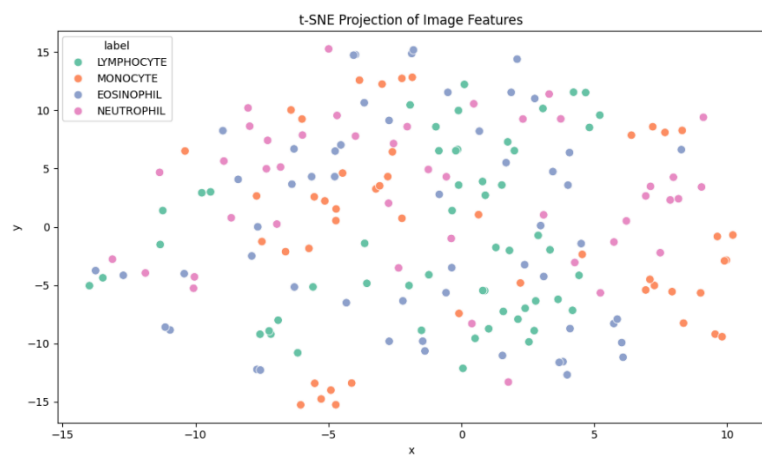
Univariate Analysis



Bivariate Analysis



Multivariate Analysis



Data Preprocessing Code Screenshots

Loading Data

Importing the libraries

```
156 import os
import pandas as pd
import tensorflow as tf
from tensorflow.keras import keras
import matplotlib.pyplot as plt
import seaborn as sns

import cv2
from tensorflow.keras.models import load_model
from tensorflow.keras.applications.mobilenet_v2 import preprocess_input
from sklearn.metrics import confusion_matrix, accuracy_score
from sklearn.metrics import classification_report
from sklearn.model_selection import train_test_split
from tensorflow.keras.preprocessing.image import ImageDataGenerator

[3] from google.colab import drive
drive.mount('/content/drive')

Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).

[6] #Define the directory path
data_dir="/content/drive/MyDrive/TRAIN"
data_dir

'/content/drive/MyDrive/TRAIN'
```

bloodCell_df.head()

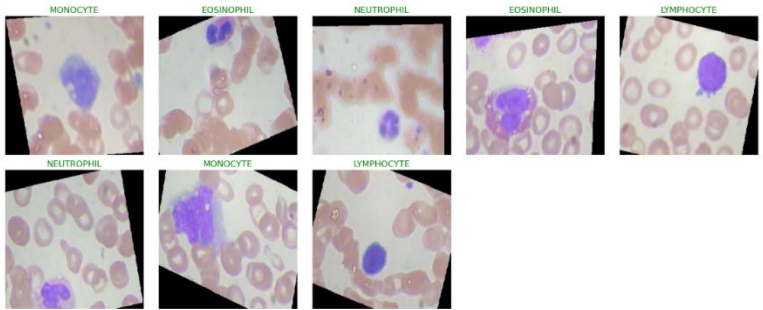
1 to 5 of 5 entries

Filter

index	filepaths	labels
0	./content/drive/MyDrive/TRAIN/EOSINOPHIL/37_5032.jpeg	EOSINOPHIL
1	./content/drive/MyDrive/TRAIN/MONOCYTE/5_1663.jpeg	MONOCYTE
2	./content/drive/MyDrive/TRAIN/MONOCYTE/8_2755.jpeg	MONOCYTE
3	./content/drive/MyDrive/TRAIN/MONOCYTE/10_7297.jpeg	MONOCYTE
4	./content/drive/MyDrive/TRAIN/LYMPHOCYTE/1_9547.jpeg	LYMPHOCYTE

Handling Missing Data	<div><div><pre>[13] from PIL import Image bad_files = [] for path in bloodCell_df['filepaths']: try: img = Image.open(path) img.verify() # Checks if it's corrupted except Exception as e: bad_files.append(path) print(f"Corrupted images found: {len(bad_files)}")</pre></div><div><div>Corrupted images found: 0</div></div></div>
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Data Transformation	<div><div><div><div><div><div></div><div></div></div></div><div><div><div></div><div></div></div></div><div><div><div></div><div></div></div></div></div></div><div><div><div>train_images, test_images=train_test_split(bloodCell_df, test_size=0.3, random_state=42)</div><div>train_set, val_set=train_test_split(bloodCell_df, test_size=0.2, random_state=42)</div></div><div><div><div>[] print(train_set.shape)</div><div>print(test_images.shape)</div><div>print(val_set.shape)</div><div>print(train_images.shape)</div></div><div><div>(7965, 2)</div><div>(2988, 2)</div><div>(1992, 2)</div><div>(6969, 2)</div></div></div><div><div><div>image_gen=ImageDataGenerator(preprocessing_function=tf.keras.applications.mobilenet_v2.preprocess_input)</div><div>train=image_gen.flow_from_dataframe(dataframe=train_set, x_col="filepaths", y_col="labels", target_size=(244, 244), color_mode="rgb", class_mode="categorical")</div><div>test=image_gen.flow_from_dataframe(dataframe=test_images, x_col="filepaths", y_col="labels", target_size=(244, 244), color_mode="rgb", class_mode="categorical")</div><div>val=image_gen.flow_from_dataframe(dataframe=val_set, x_col="filepaths", y_col="labels", target_size=(244, 244), color_mode="rgb", class_mode="categorical")</div></div><div><div>Found 7965 validated image filenames belonging to 4 classes.</div><div>Found 2988 validated image filenames belonging to 4 classes.</div><div>Found 1992 validated image filenames belonging to 4 classes.</div></div></div></div></div>
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	<pre> def show_knee_images(image_gen): test_dict = test.class_indices classes = list(test_dict.keys()) images, labels = next(image_gen) plt.figure(figsize=(20, 20)) length = len(images) r = min(25, length) for i in range(r): plt.subplot(5, 5, i + 1) image = (images[i] + 1) / 2 plt.imshow(image) if labels[i].ndim > 0: index = np.argmax(labels[i]) else: index = int(labels[i]) class_name = classes[index] plt.title(class_name, color="green", fontsize=16) plt.axis('off') plt.tight_layout() plt.show() show_knee_images(train) </pre> 
Feature Engineering	Attached the codes in final submission.
Save Processed Data	-