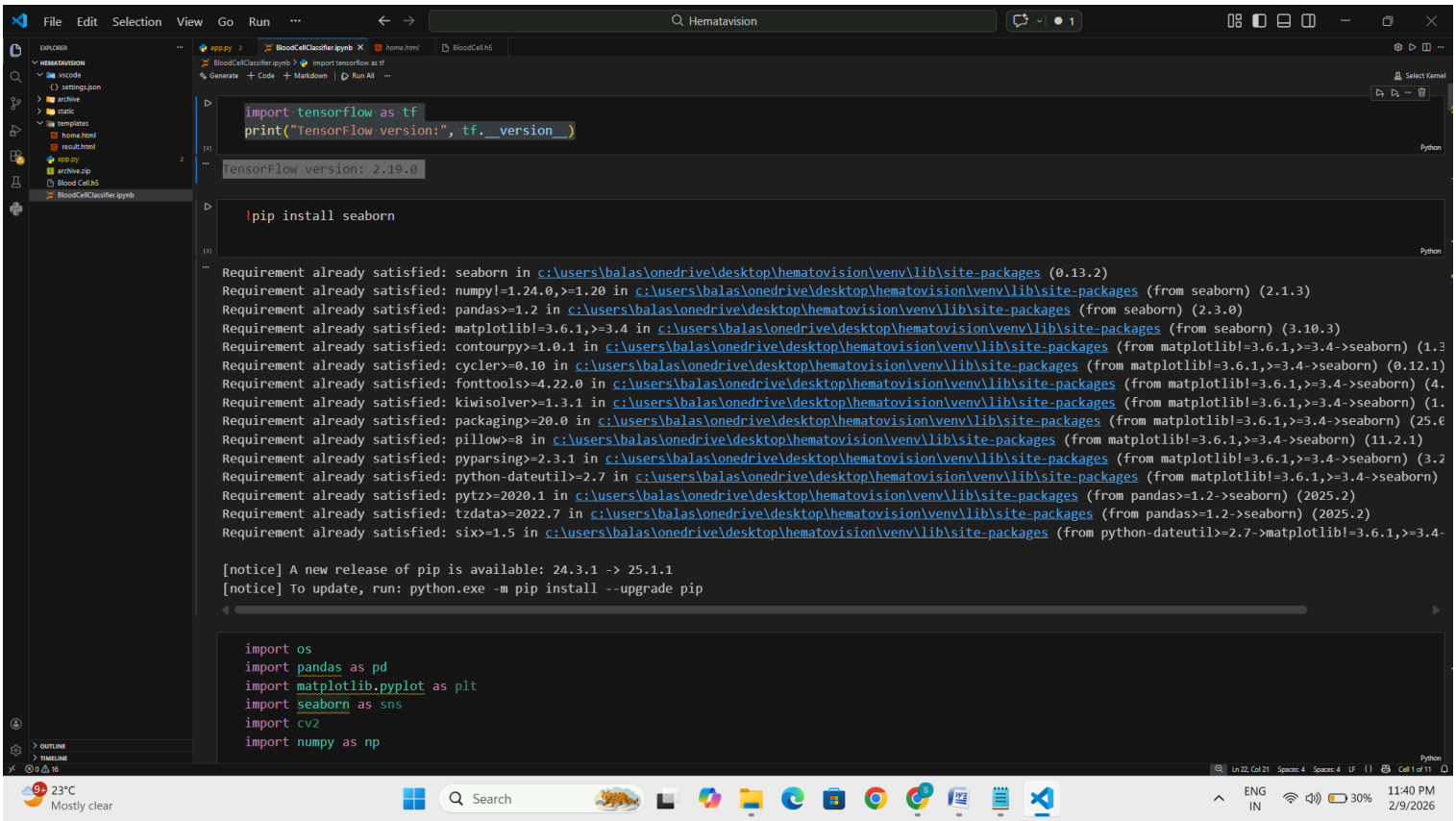
File Edit Selection View Go Run
Hematavision
EXPLORER
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vscode
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Blood Cell.h5
BloodCellClassifier.ipynb
app.py
BloodCellClassifier.ipynb
home.html
BloodCell.h5
BloodCellClassifier.ipynb > import tensorflow as tf
Generate + Code + Markdown | Run All
Select Kernel
import tensorflow as tf
print("TensorFlow version:", tf.__version__)
Python
TensorFlow version: 2.19.0
!pip install seaborn
Python
Requirement already satisfied: seaborn in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (0.13.2)
Requirement already satisfied: numpy!=1.24.0,>=1.20 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from seaborn) (2.1.3)
Requirement already satisfied: pandas>=1.2 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from seaborn) (2.3.0)
Requirement already satisfied: matplotlib!=3.6.1,>=3.4 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from seaborn) (3.10.3)
Requirement already satisfied: contourpy>=1.0.1 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.3
Requirement already satisfied: cycler>=0.10 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (4.
Requirement already satisfied: kiwisolver>=1.3.1 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.
Requirement already satisfied: packaging>=20.0 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (25.0
Requirement already satisfied: pillow>=8 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (11.2.1)
Requirement already satisfied: pyparsing>=2.3.1 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (3.2
Requirement already satisfied: python-dateutil>=2.7 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from matplotlib!=3.6.1,>=3.4->seaborn)
Requirement already satisfied: pytz>=2020.1 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from pandas>=1.2->seaborn) (2025.2)
Requirement already satisfied: tzdata>=2022.7 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from pandas>=1.2->seaborn) (2025.2)
Requirement already satisfied: six>=1.5 in c:\users\balas\onedrive\desktop\hematovision\venv\lib\site-packages (from python-dateutil>=2.7->matplotlib!=3.6.1,>=3.4-
[notice] A new release of pip is available: 24.3.1 -> 25.1.1
[notice] To update, run: python.exe -m pip install --upgrade pip
import os
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import cv2
import numpy as np
Python
OUTLINE
TIMELINE
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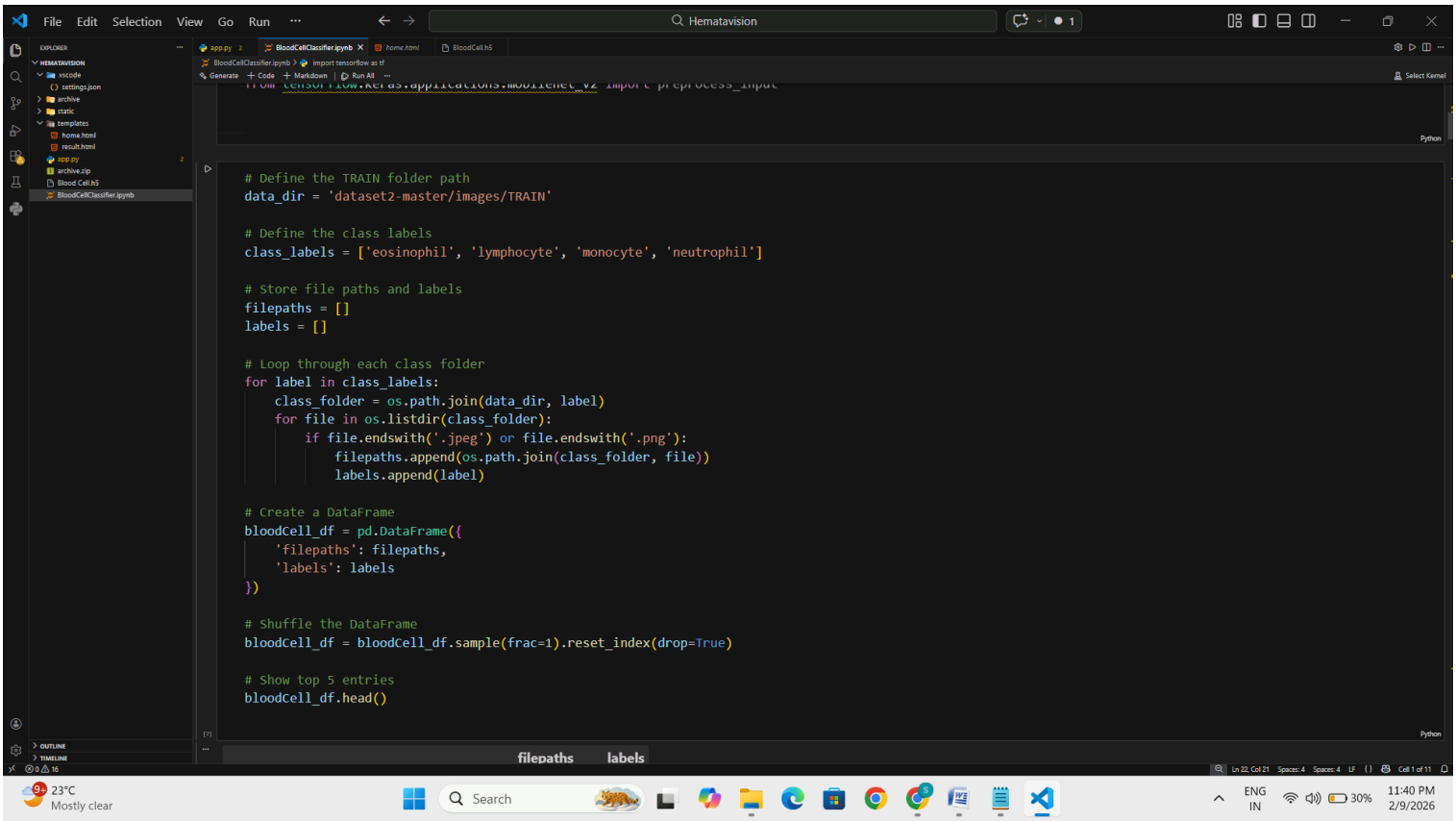
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Blood Cell.h5
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Select Kernel
Python
# Define the TRAIN folder path
data_dir = 'dataset2-master/images/TRAIN'
# Define the class labels
class_labels = ['eosinophil', 'lymphocyte', 'monocyte', 'neutrophil']
# Store file paths and labels
filepaths = []
labels = []
# Loop through each class folder
for label in class_labels:
class_folder = os.path.join(data_dir, label)
for file in os.listdir(class_folder):
if file.endswith('.jpeg') or file.endswith('.png'):
filepaths.append(os.path.join(class_folder, file))
labels.append(label)
# Create a DataFrame
bloodCell_df = pd.DataFrame({
'filepaths': filepaths,
'labels': labels
})
# Shuffle the DataFrame
bloodCell_df = bloodCell_df.sample(frac=1).reset_index(drop=True)
# Show top 5 entries
bloodCell_df.head()
Python
filepaths
labels
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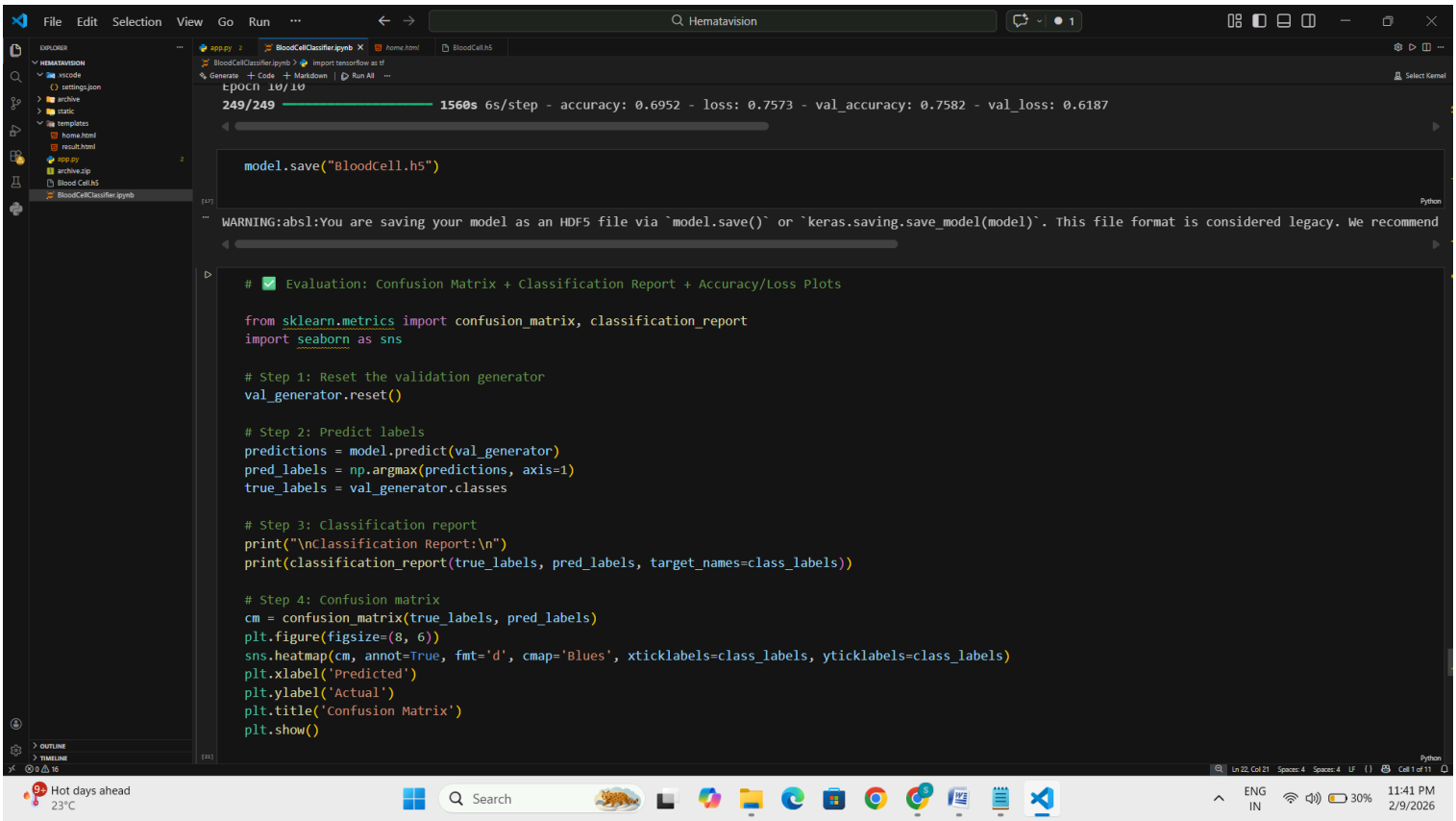
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BloodCellClassifier.ipynb
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BloodCell.h5
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Run All
Select Kernel
Epoch 10/10
249/249 1560s 6s/step - accuracy: 0.6952 - loss: 0.7573 - val_accuracy: 0.7582 - val_loss: 0.6187
model.save("BloodCell.h5")
Python
WARNING:absl:You are saving your model as an HDF5 file via `model.save()` or `keras.saving.save_model(model)`. This file format is considered legacy. We recommend
# ✅ Evaluation: Confusion Matrix + Classification Report + Accuracy/Loss Plots
from sklearn.metrics import confusion_matrix, classification_report
import seaborn as sns
# Step 1: Reset the validation generator
val_generator.reset()
# Step 2: Predict labels
predictions = model.predict(val_generator)
pred_labels = np.argmax(predictions, axis=1)
true_labels = val_generator.classes
# Step 3: Classification report
print("\nClassification Report:\n")
print(classification_report(true_labels, pred_labels, target_names=class_labels))
# Step 4: Confusion matrix
cm = confusion_matrix(true_labels, pred_labels)
plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=class_labels, yticklabels=class_labels)
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix')
plt.show()
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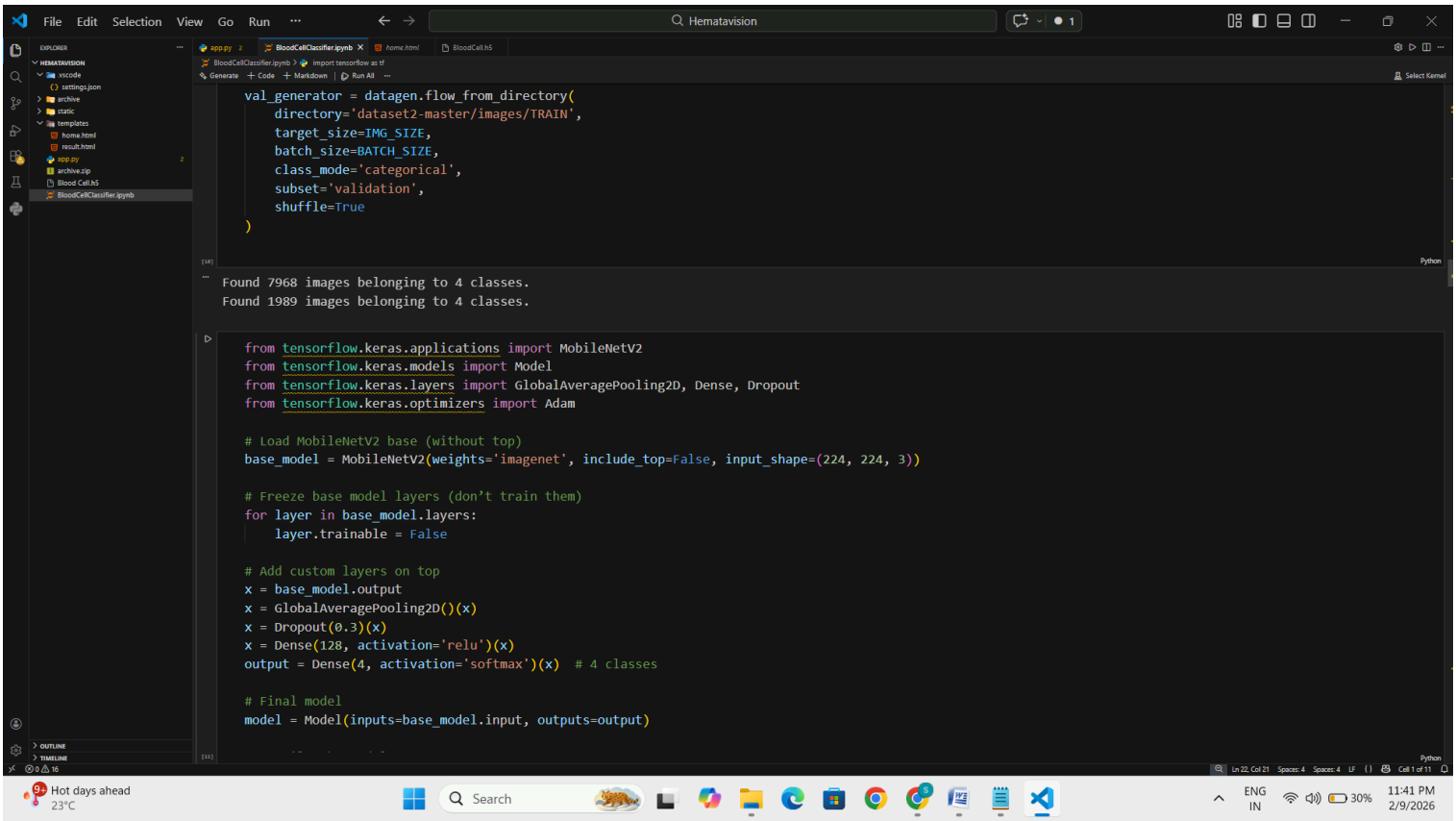
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BloodCell.h5
BloodCellClassifier.ipynb > import tensorflow as tf
Generate + Code + Markdown | Run All
Select Kernel
val_generator = datagen.flow_from_directory(
directory='dataset2-master/images/TRAIN',
target_size=IMG_SIZE,
batch_size=BATCH_SIZE,
class_mode='categorical',
subset='validation',
shuffle=True
)
Python
Found 7968 images belonging to 4 classes.
Found 1989 images belonging to 4 classes.
from tensorflow.keras.applications import MobileNetV2
from tensorflow.keras.models import Model
from tensorflow.keras.layers import GlobalAveragePooling2D, Dense, Dropout
from tensorflow.keras.optimizers import Adam
# Load MobileNetV2 base (without top)
base_model = MobileNetV2(weights='imagenet', include_top=False, input_shape=(224, 224, 3))
# Freeze base model layers (don't train them)
for layer in base_model.layers:
layer.trainable = False
# Add custom layers on top
x = base_model.output
x = GlobalAveragePooling2D()(x)
x = Dropout(0.3)(x)
x = Dense(128, activation='relu')(x)
output = Dense(4, activation='softmax')(x) # 4 classes
# Final model
model = Model(inputs=base_model.input, outputs=output)
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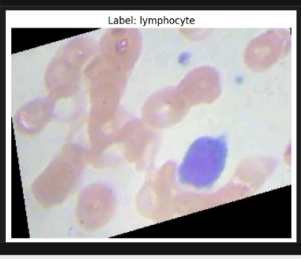
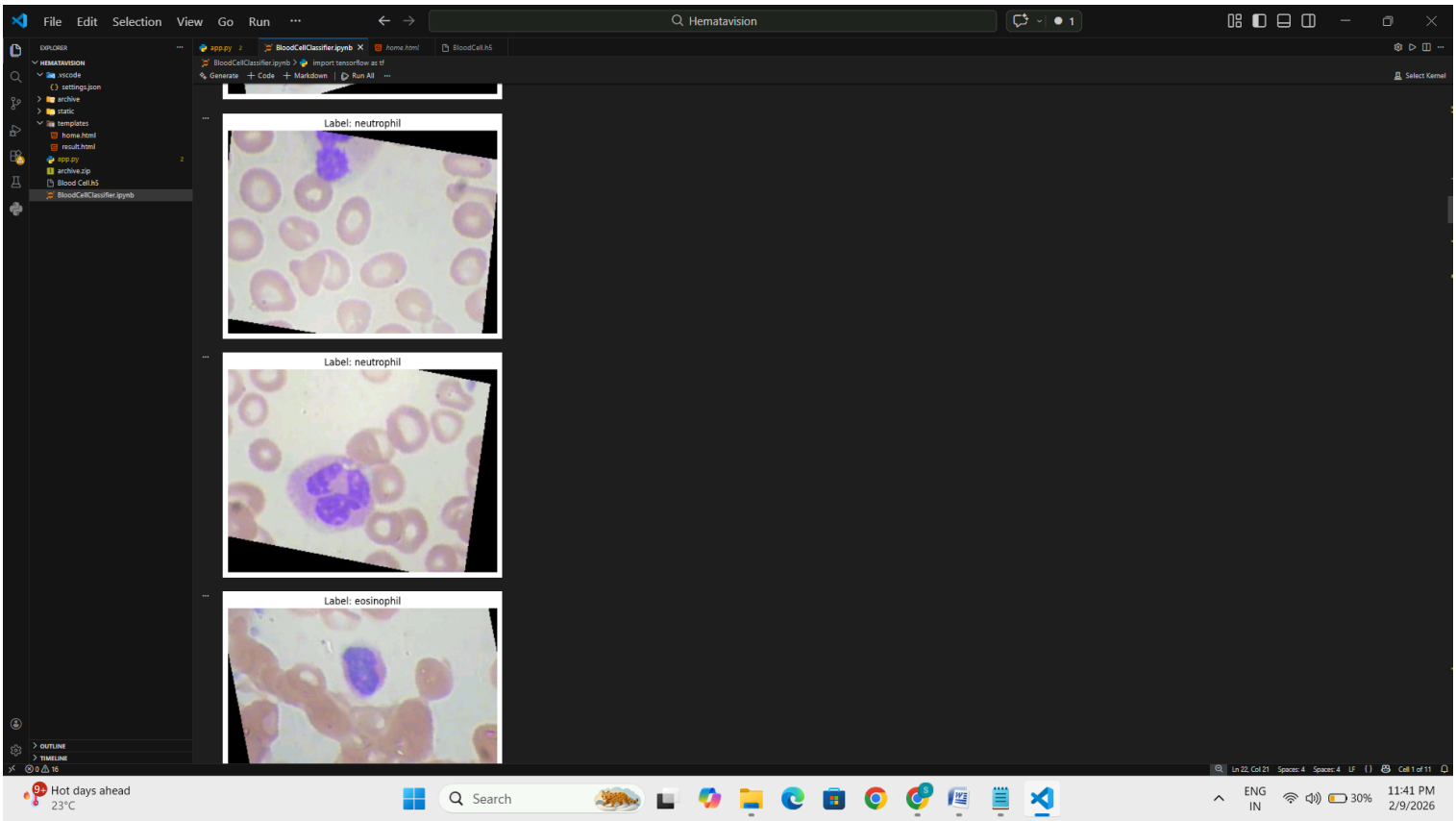
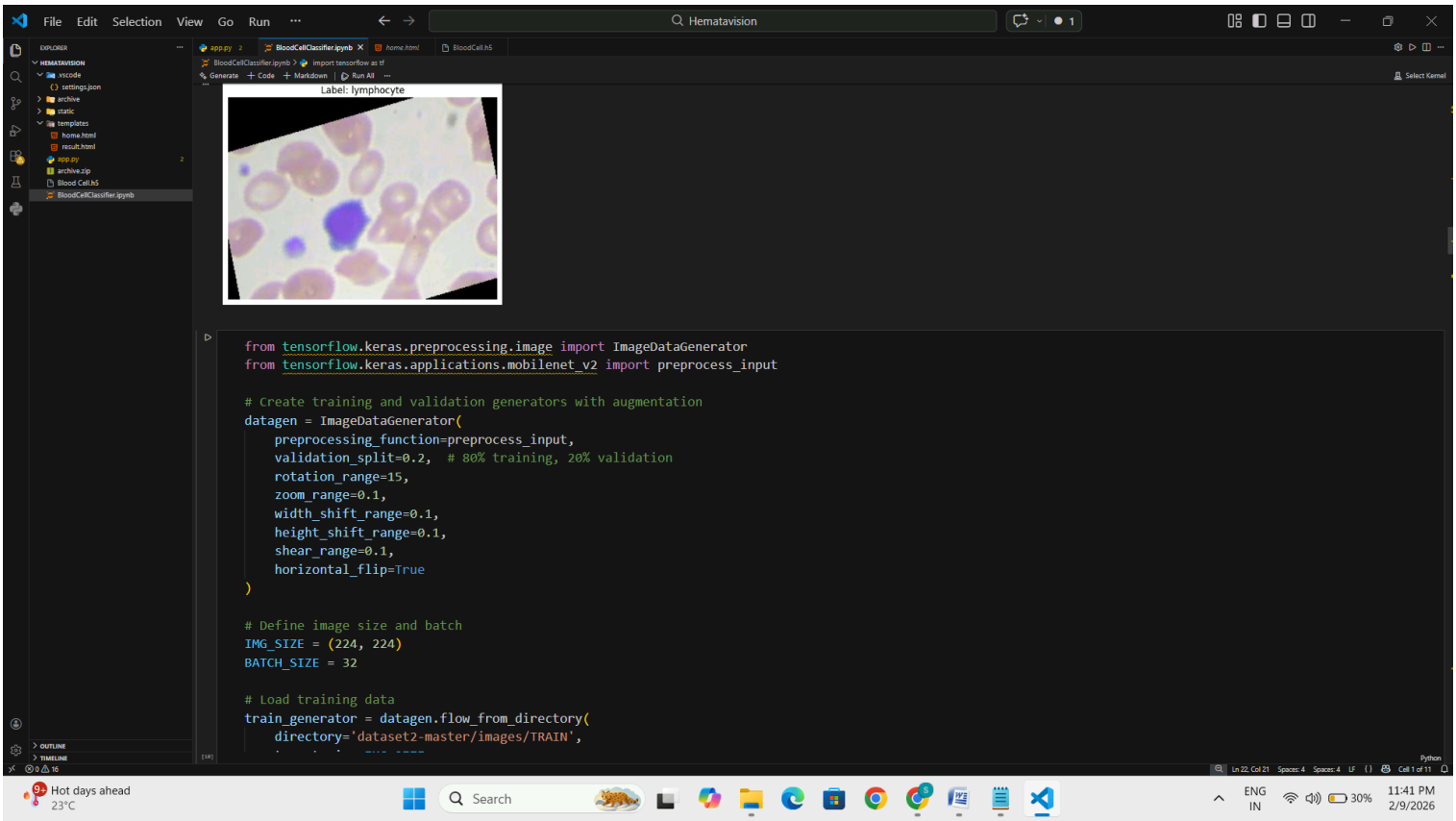
	filepaths	labels
0	dataset2-master/images/TRAIN\lymphocyte_1_59....	lymphocyte
1	dataset2-master/images/TRAIN\neutrophil_37_68...	neutrophil
2	dataset2-master/images/TRAIN\lymphocyte_15_69...	lymphocyte
3	dataset2-master/images/TRAIN\eosinophil_36_46...	eosinophil
4	dataset2-master/images/TRAIN\lymphocyte_18_17...	lymphocyte

```
import matplotlib.pyplot as plt
import random
from PIL import Image

# Show 5 random images
for i in range(5):
    img_path = random.choice(bloodCell_df['filepaths'])
    img = Image.open(img_path)
    plt.imshow(img)
    plt.title(f"Label: {bloodCell_df[bloodCell_df['filepaths'] == img_path]['labels'].values[0]}")
    plt.axis('off')
    plt.show()
```




File Edit Selection View Go Run
Hematavision
Label: neutrophil
Label: neutrophil
Label: eosinophil


File Edit Selection View Go Run
Hematavision
Label: lymphocyte
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.applications.mobilenet_v2 import preprocess_input
# Create training and validation generators with augmentation
datagen = ImageDataGenerator(
preprocessing_function=preprocess_input,
validation_split=0.2, # 80% training, 20% validation
rotation_range=15,
zoom_range=0.1,
width_shift_range=0.1,
height_shift_range=0.1,
shear_range=0.1,
horizontal_flip=True
)
# Define image size and batch
IMG_SIZE = (224, 224)
BATCH_SIZE = 32
# Load training data
train_generator = datagen.flow_from_directory(
directory='dataset2-master/images/TRAIN',
Hot days ahead
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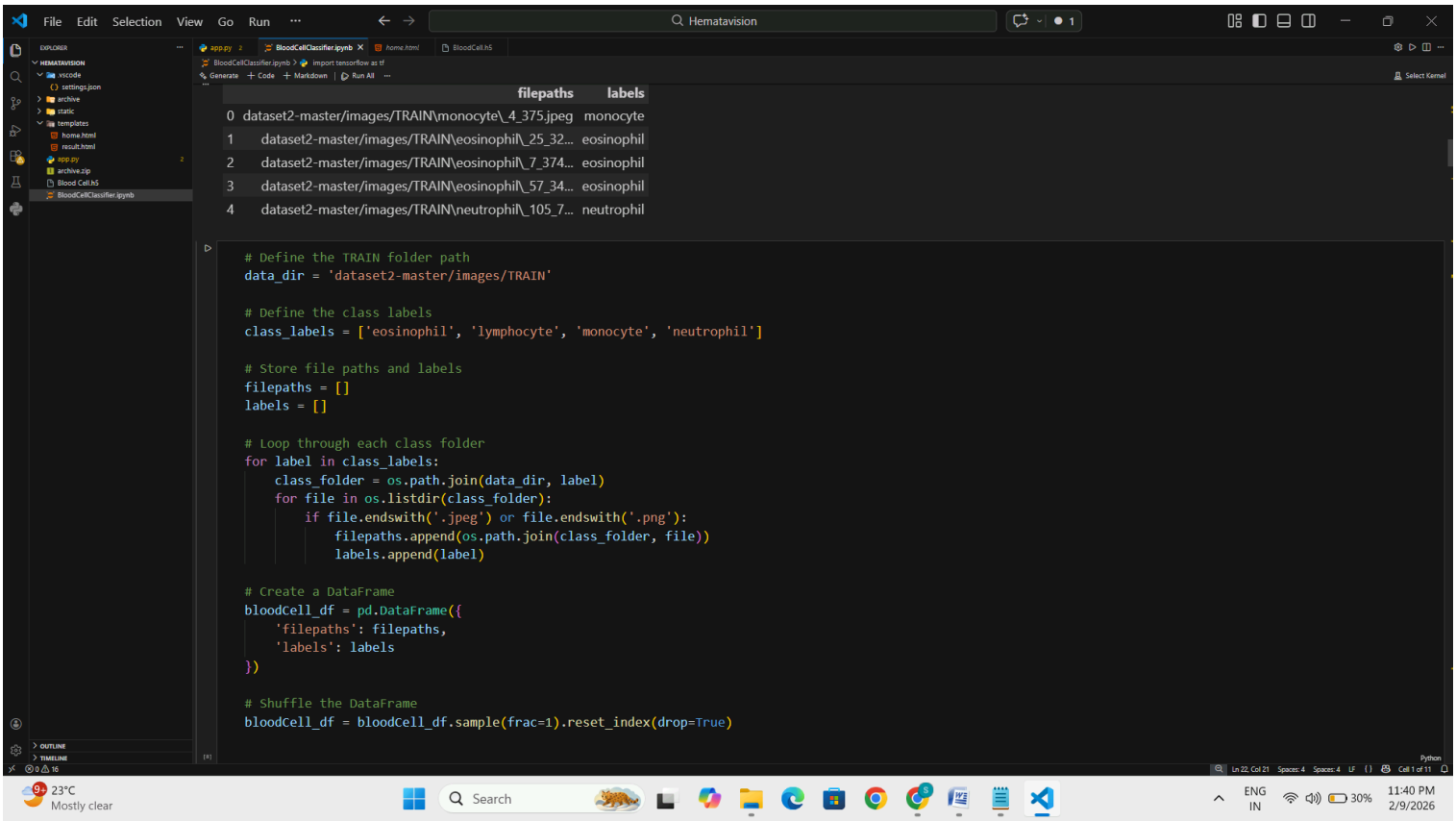
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app.py
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Blood Cell.h5
BloodCellClassifier.ipynb
app.py
BloodCellClassifier.ipynb
home.html
BloodCell.h5
BloodCellClassifier.ipynb > import tensorflow as tf
Generate + Code + Markdown | Run All
Select Kernel
filepaths labels
0 dataset2-master/images/TRAIN\monocyte_4_375.jpeg monocyte
1 dataset2-master/images/TRAIN\eosinophil_25_32... eosinophil
2 dataset2-master/images/TRAIN\eosinophil_7_374... eosinophil
3 dataset2-master/images/TRAIN\eosinophil_57_34... eosinophil
4 dataset2-master/images/TRAIN\neutrophil_105_7... neutrophil
# Define the TRAIN folder path
data_dir = 'dataset2-master/images/TRAIN'
# Define the class labels
class_labels = ['eosinophil', 'lymphocyte', 'monocyte', 'neutrophil']
# Store file paths and labels
filepaths = []
labels = []
# Loop through each class folder
for label in class_labels:
class_folder = os.path.join(data_dir, label)
for file in os.listdir(class_folder):
if file.endswith('.jpeg') or file.endswith('.png'):
filepaths.append(os.path.join(class_folder, file))
labels.append(label)
# Create a DataFrame
bloodCell_df = pd.DataFrame({
'filepaths': filepaths,
'labels': labels
})
# Shuffle the DataFrame
bloodCell_df = bloodCell_df.sample(frac=1).reset_index(drop=True)
OUTLINE
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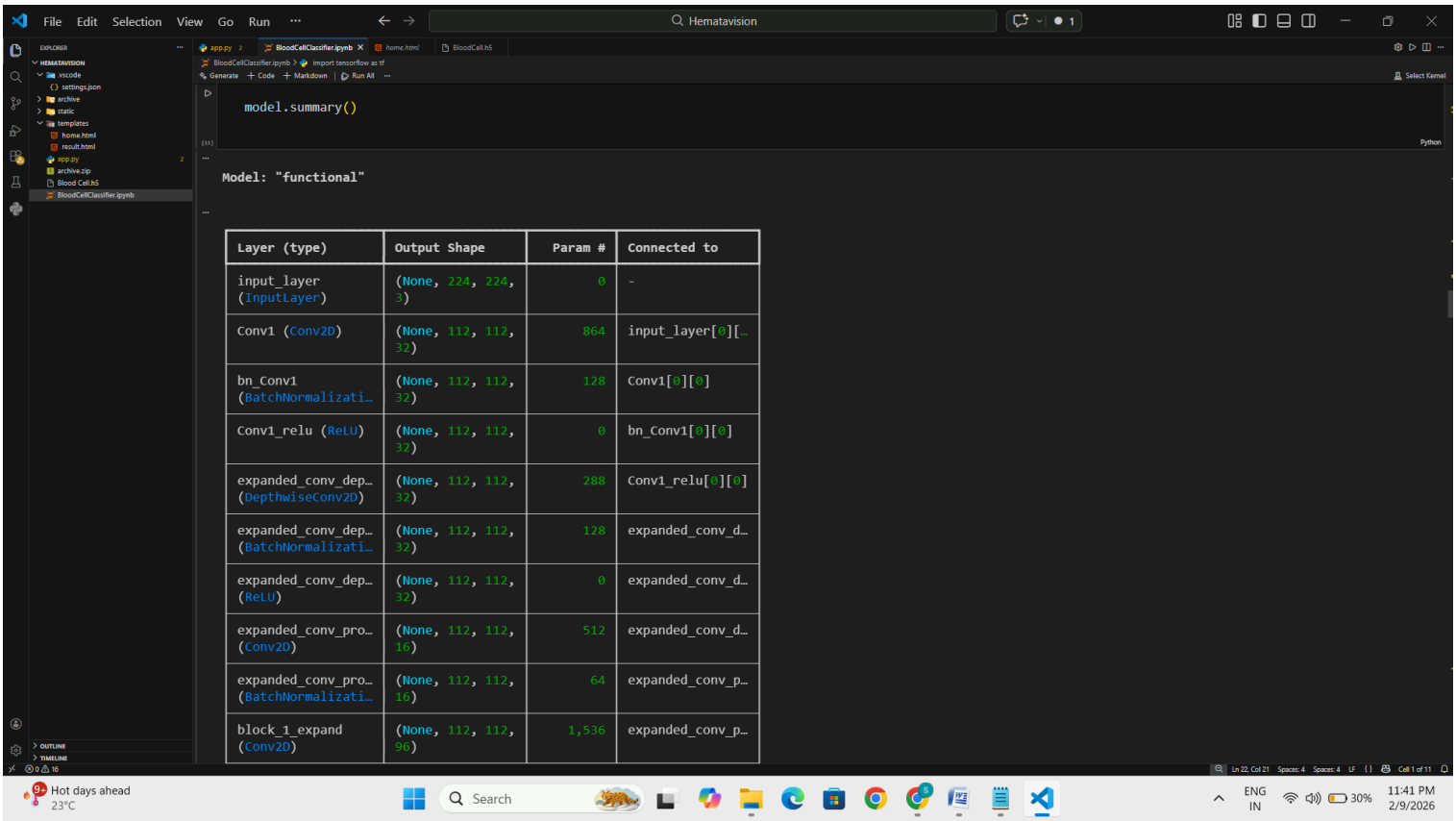
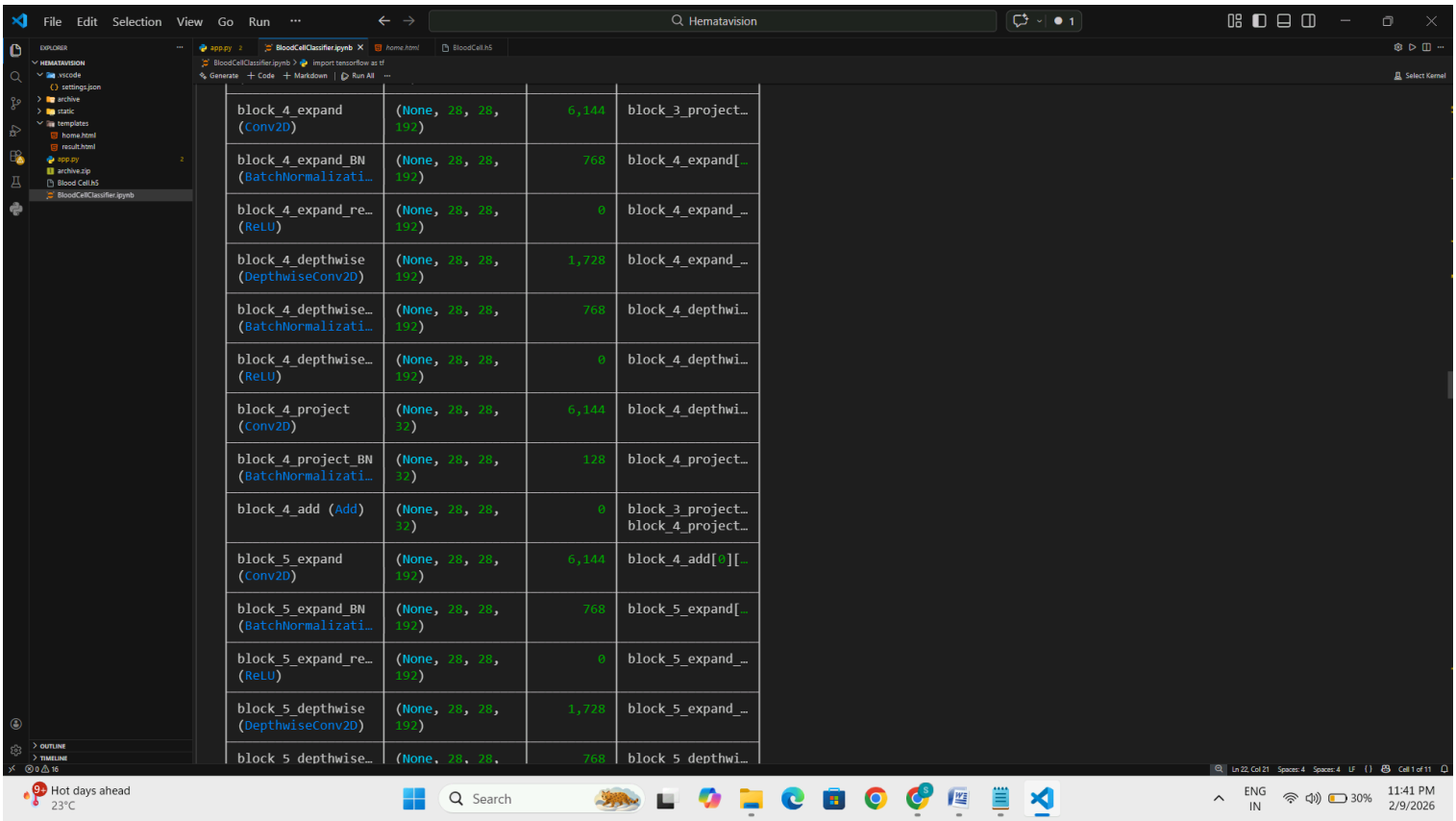
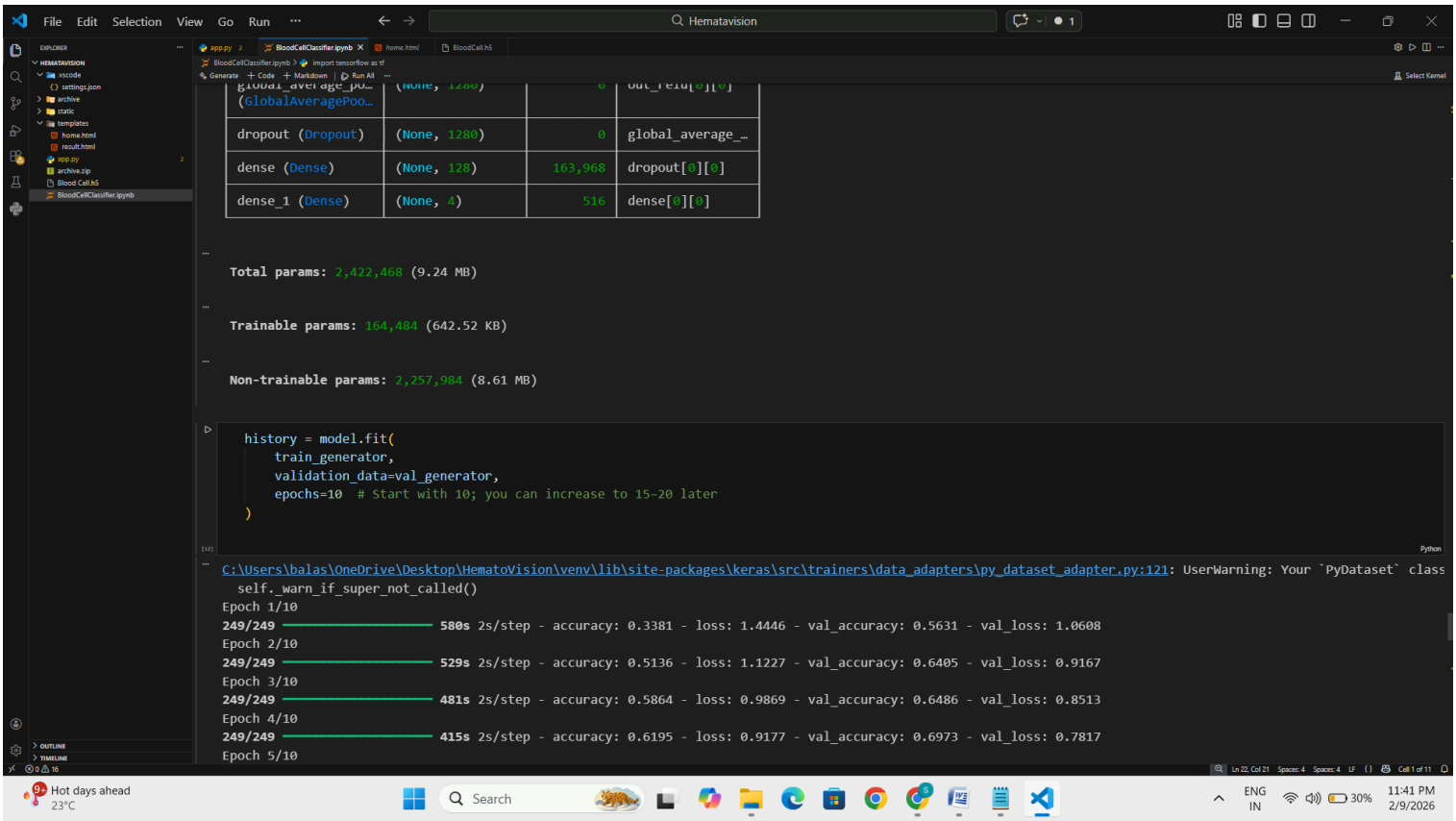


Layer (type)	Output Shape	Param #	Connected to
input_layer (InputLayer)	(None, 224, 224, 3)	0	-
Conv1 (Conv2D)	(None, 112, 112, 32)	864	input_layer[0][…
bn_Conv1 (BatchNormalizati…	(None, 112, 112, 32)	128	Conv1[0][0]
Conv1_relu (ReLU)	(None, 112, 112, 32)	0	bn_Conv1[0][0]
expanded_conv_dep… (DepthwiseConv2D)	(None, 112, 112, 32)	288	Conv1_relu[0][0]
expanded_conv_dep… (BatchNormalizati…	(None, 112, 112, 32)	128	expanded_conv_d…
expanded_conv_dep… (ReLU)	(None, 112, 112, 32)	0	expanded_conv_d…
expanded_conv_pro… (Conv2D)	(None, 112, 112, 16)	512	expanded_conv_d…
expanded_conv_pro… (BatchNormalizati…	(None, 112, 112, 16)	64	expanded_conv_p…
block_1_expand (Conv2D)	(None, 112, 112, 96)	1,536	expanded_conv_p…



block_4_expand (Conv2D)	(None, 28, 28, 192)	6,144	block_3_project…
block_4_expand_BN (BatchNormalizati…	(None, 28, 28, 192)	768	block_4_expand[…
block_4_expand_re… (ReLU)	(None, 28, 28, 192)	0	block_4_expand_…
block_4_depthwise (DepthwiseConv2D)	(None, 28, 28, 192)	1,728	block_4_expand_…
block_4_depthwise… (BatchNormalizati…	(None, 28, 28, 192)	768	block_4_depthwi…
block_4_depthwise… (ReLU)	(None, 28, 28, 192)	0	block_4_depthwi…
block_4_project (Conv2D)	(None, 28, 28, 32)	6,144	block_4_depthwi…
block_4_project_BN (BatchNormalizati…	(None, 28, 28, 32)	128	block_4_project…
block_4_add (Add)	(None, 28, 28, 32)	0	block_3_project… block_4_project…
block_5_expand (Conv2D)	(None, 28, 28, 192)	6,144	block_4_add[0][…
block_5_expand_BN (BatchNormalizati…	(None, 28, 28, 192)	768	block_5_expand[…
block_5_expand_re… (ReLU)	(None, 28, 28, 192)	0	block_5_expand_…
block_5_depthwise (DepthwiseConv2D)	(None, 28, 28, 192)	1,728	block_5_expand_…
block_5_depthwise…	(None, 28, 28,	768	block_5_depthwi…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app.py
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BloodCell.h5
BloodCellClassifier.ipynb > import tensorflow as tf
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(GlobalAveragePoo…
dropout (Dropout) (None, 1280) 0 global_average_…
dense (Dense) (None, 128) 163,968 dropout[0][0]
dense_1 (Dense) (None, 4) 516 dense[0][0]
Total params: 2,422,468 (9.24 MB)
Trainable params: 164,484 (642.52 KB)
Non-trainable params: 2,257,984 (8.61 MB)
history = model.fit(
train_generator,
validation_data=val_generator,
epochs=10 # Start with 10; you can increase to 15–20 later
)
Python
C:\Users\balas\OneDrive\Desktop\HematoVision\venv\lib\site-packages\keras\src\trainers\data_adapters\py_dataset_adapter.py:121: UserWarning: Your `PyDataset` class
self._warn_if_super_not_called()
Epoch 1/10
249/249 580s 2s/step - accuracy: 0.3381 - loss: 1.4446 - val_accuracy: 0.5631 - val_loss: 1.0608
Epoch 2/10
249/249 529s 2s/step - accuracy: 0.5136 - loss: 1.1227 - val_accuracy: 0.6405 - val_loss: 0.9167
Epoch 3/10
249/249 481s 2s/step - accuracy: 0.5864 - loss: 0.9869 - val_accuracy: 0.6486 - val_loss: 0.8513
Epoch 4/10
249/249 415s 2s/step - accuracy: 0.6195 - loss: 0.9177 - val_accuracy: 0.6973 - val_loss: 0.7817
Epoch 5/10
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app.py 2 | BloodCellClassifier.ipynb | home.html | BloodCell.h5

BloodCellClassifier.ipynb > import tensorflow as tf

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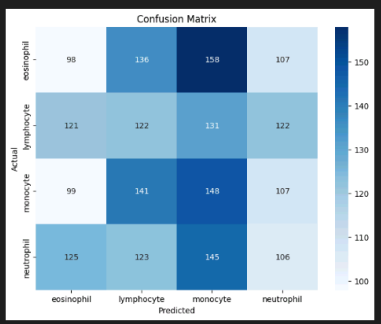
Select Kernel

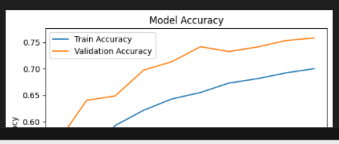
```
Classification Report:

              precision    recall  f1-score   support

  eosinophil       0.22      0.20      0.21       499
  lymphocyte       0.23      0.25      0.24       496
    monocyte       0.25      0.30      0.27       495
  neutrophil       0.24      0.21      0.23       499

    accuracy                           0.24      1989
   macro avg       0.24      0.24      0.24      1989
weighted avg       0.24      0.24      0.24      1989
```





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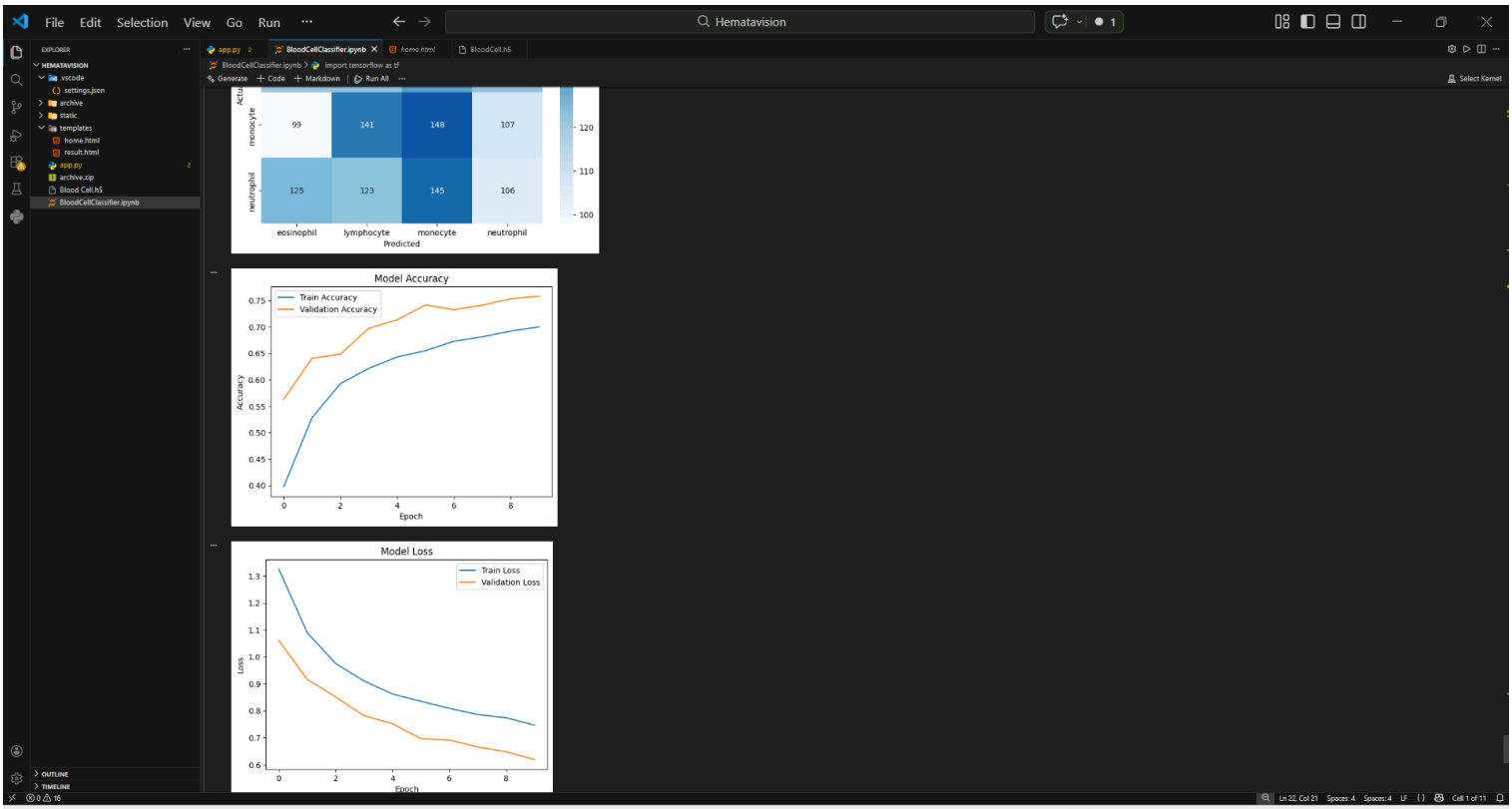
File Edit Selection View Go Run
Hematavision
99 141 148 107
125 123 145 106
monocyte
neutrophil
eosinophil lymphocyte monocyte neutrophil
Predicted
Model Accuracy
Train Accuracy
Validation Accuracy
Accuracy
Epoch
Model Loss
Train Loss
Validation Loss
Loss
Epoch