

## **Project Demonstration Phase**

## Stable Diffusion Model Initialization and Device

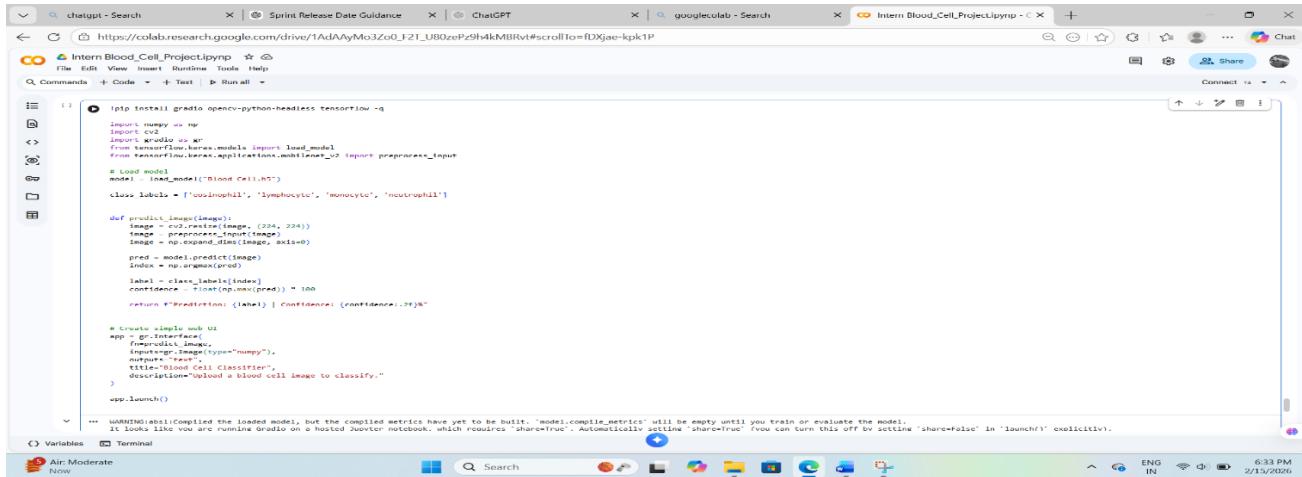
This section of the code initializes the Stable Diffusion v1.5 model using the Hugging Face Diffusers library. It first checks whether CUDA (GPU) is available and selects either GPU or CPU for execution to optimize performance. The appropriate data type (float16 for GPU or float32 for CPU) is selected to reduce memory usage. The pipeline is then loaded and moved to the selected device, enabling efficient image generation.

## Blood Smear Image Generation Using Text-to-Image Prompt

This part of the code defines the function `generate_blood_smear_image()` to create synthetic microscopic blood smear images. A detailed medical prompt describing eosinophils, lymphocytes, monocytes, and neutrophils is provided to the model. The Stable Diffusion pipeline generates a high-resolution image based on this prompt and saves it as `generated_blood_image.png`. The console output below confirms successful loading of model weights and components.

## Gradio-Based Deployment of Blood Cell Classification Model

This section of the code deploys the trained Blood Cell classification model using the Gradio library. The saved model Blood Cell.h5 is loaded, and class labels such as eosinophil, lymphocyte, monocyte, and neutrophil are defined. The predict\_image() function preprocesses the uploaded image by resizing it to 224×224 pixels, applying MobileNetV2 preprocessing, and expanding dimensions before making predictions. The predicted class is determined using argmax, and the confidence score is calculated and displayed as output.



```
!pip install gradio opencv-python-headless tensorflow -q
import numpy as np
import gradio as gr
from tensorflow.keras.models import load_model
from tensorflow.keras.applications.mobilenet_v2 import preprocess_input
# Load model
model = load_model('Blood Cell.h5')
class_labels = ['eosinophil', 'lymphocyte', 'monocyte', 'neutrophil']

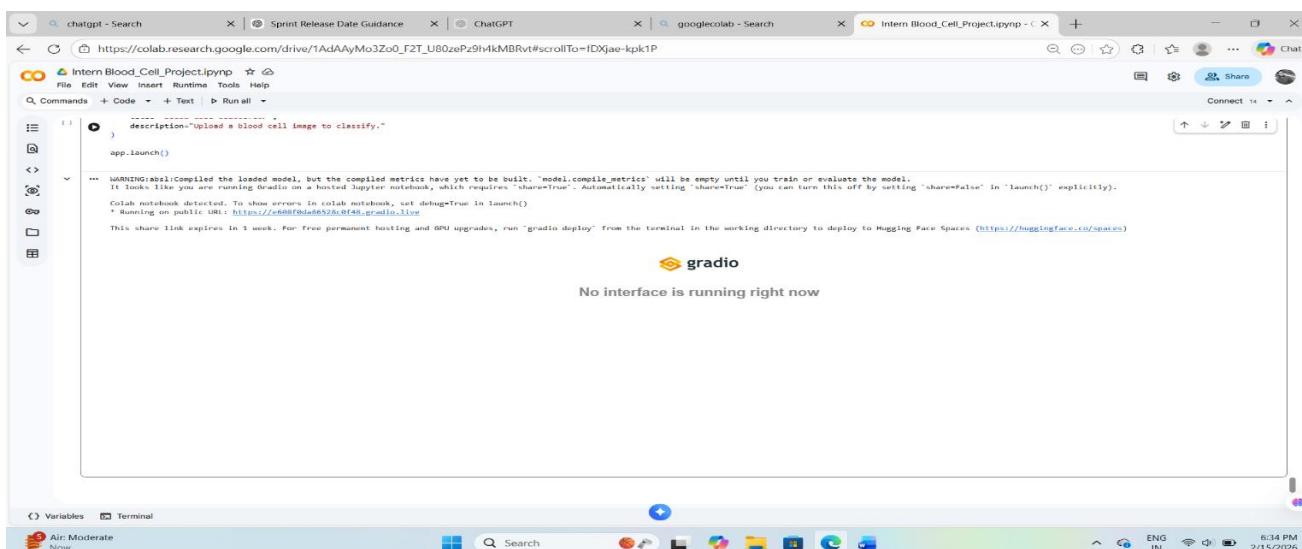
def predict_image(image):
    image = cv2.resize(image, (224, 224))
    image = preprocess_input(image)
    image = np.expand_dims(image, axis=0)
    pred = model.predict(image)
    index = np.argmax(pred)
    label = class_labels[index]
    confidence = float(np.max(pred)) * 100
    return f'Prediction: {label} | Confidence: {confidence:.2f}%'

# Create simple UI
app = gr.Interface(
    predict_image,
    inputs="image",
    outputs="text",
    title="Blood Cell Classification",
    description="Upload a blood cell image to classify."
)
app.launch()

*** WARNING! This compiled the loaded model, but the compiled metrics have yet to be built. 'model.compile_metrics' will be empty until you train or evaluate the model.
It looks like you are running Gradio on a hosted Jupyter notebook, which requires 'share=True'. Automatically setting 'share=True' (you can turn this off by setting 'share=False' in 'launch()' explicitly).
Colab notebook detected. To share servers in colab notebooks, set debug=True in launch()
* Running on public URL: https://e668fbda86528c0f48.gradio.live
This share link expires in 1 week. For free permanent hosting and GPU upgrades, run "gradio deploy" from the terminal in the working directory to deploy to Hugging Face Spaces (https://huggingface.co/spaces)
```

## Launching the Web Interface for Model Deployment

This part shows the execution of app.launch(), which starts the Gradio web interface for user interaction. Once launched, the application generates a public shareable link, allowing users to upload blood cell images and receive classification results in real time. The console output confirms successful deployment and provides the temporary URL for accessing the application online.



```
app.launch()

*** WARNING! This compiled the loaded model, but the compiled metrics have yet to be built. 'model.compile_metrics' will be empty until you train or evaluate the model.
It looks like you are running Gradio on a hosted Jupyter notebook, which requires 'share=True'. Automatically setting 'share=True' (you can turn this off by setting 'share=False' in 'launch()' explicitly).
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gradio
No interface is running right now
```

← → ⌛ 127.0.0.1:5000 ☆ 🗑️ 3 ⋮

## Welcome to the HematoVision

### About Blood Cells

Blood cells are vital components of our body, playing essential roles in immunity, oxygen transport, and clotting. Understanding different types of blood cells is crucial for diagnosing various medical conditions.

### Predict Blood Cell Type

Upload an image of a blood cell to determine its type using our state-of-the-art classification model.

No file chosen

By clicking on choose file it will ask us to upload the image , then by clicking on the predict button it will take us to the result.html.

Activity 1: Test For Class-1 – Neutrophil

## Predict Blood Cell Type

Upload an image of a blood cell to determine its type using our state-of-the-art classification model.

\_8\_9488.jpeg

## Prediction Result

**Predicted Class:** neutrophil



## Activity 2: Test For Class-2 – Monocyte

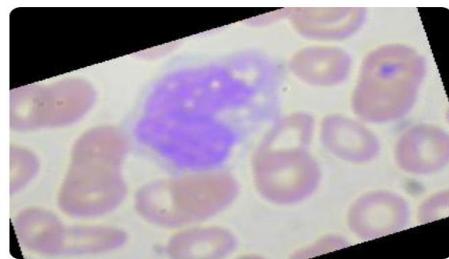
### Predict Blood Cell Type

Upload an image of a blood cell to determine its type using our state-of-the-art classification model.

\_3\_9423.jpeg

### Prediction Result

**Predicted Class:** monocyte



## Activity 3: Test For Class-3 – Lymphocyte

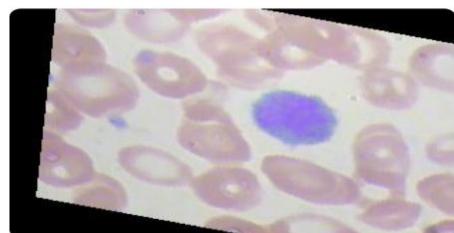
### Predict Blood Cell Type

Upload an image of a blood cell to determine its type using our state-of-the-art classification model.

\_5\_9201.jpeg

### Prediction Result

**Predicted Class:** lymphocyte



Activity 4: Test For Class-4 – Eosinophil

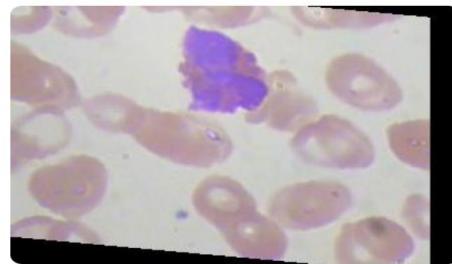
## Predict Blood Cell Type

Upload an image of a blood cell to determine its type using our state-of-the-art classification model.

\_3\_9885.jpeg

### Prediction Result

**Predicted Class:** eosinophil



Demo Link:

[https://drive.google.com/file/d/1oXSLu4IW-SQOzftMFpjtagMg\\_7hxfgKW/view?usp=drivesdk](https://drive.google.com/file/d/1oXSLu4IW-SQOzftMFpjtagMg_7hxfgKW/view?usp=drivesdk)

Google Colab Link :

<https://colab.research.google.com/drive/1nnHWn4UKBKx6oxfna4zrmP5ovKtj4S5b>