

Histopathologic Cancer Detection

Identify metastatic tissue in histopathologic scans of lymph node sections

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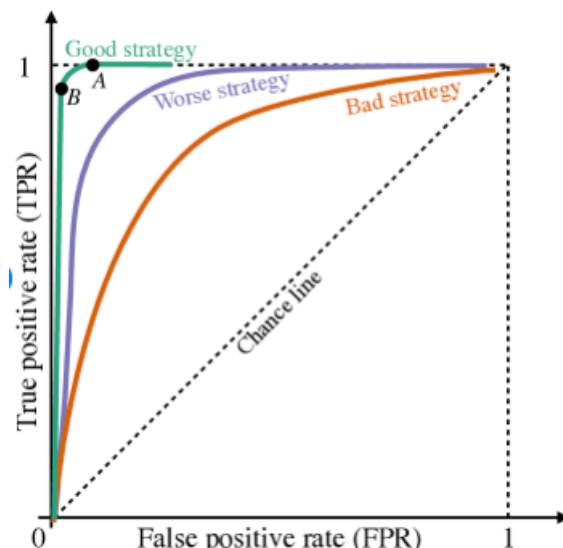
1. Exploratory Data Analysis (EDA)

Project Description

That which is measured, improves. – Karl Pearson

The goal of this project is building model to identify Binary image classification problem for Histopathologic Cancer Detection. The ROC curve will be used as measurement that shows how well a classifier performs by plotting the True Positive Rate (TPR) against the False Positive Rate (FPR) at different decision thresholds.

Model strategy is summarized by the below ROC curve:

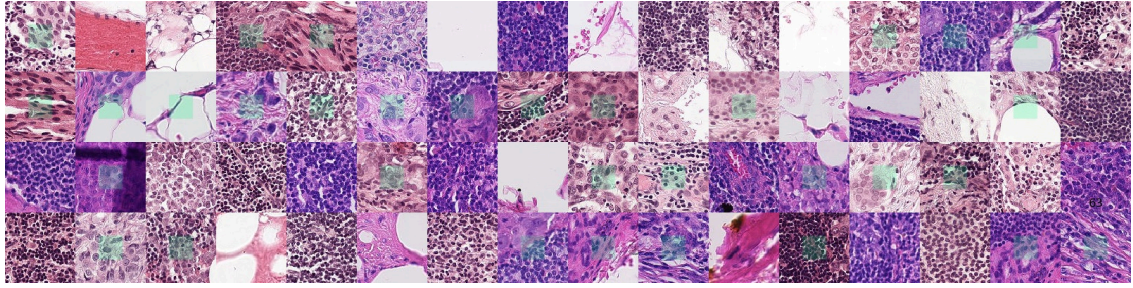


The area under the curve (AUC) represents the likelihood that the classifier will correctly rank a randomly chosen positive instance higher than a randomly chosen negative one. The ideal outcome is an AUC of 1 that can be translated that the classifier correctly identifies all positive samples without any false positives.

Data Understanding

1. PatchCamelyon benchmark

The PatchCamelyon benchmark is a new and challenging image classification dataset. It consists of 327,680 color images (96 x 96px) extracted from histopathologic scans of lymph node sections. Each image is annotated with a binary label indicating presence of metastatic tissue. PCam provides a new benchmark for machine learning models: bigger than CIFAR10, smaller than imagenet, trainable on a single GPU.



< Example images from PCam. Green boxes indicate tumor tissue in center region, which dictates a positive label >

The data for this competition is a slightly modified version of the PatchCamelyon (PCam) benchmark dataset (the original PCam dataset contains duplicate images due to its probabilistic sampling, however, the version presented on Kaggle does not contain duplicates).

The PatchCamelyon benchmark is a vital tool in the development and evaluation of machine learning models for digital pathology. By focusing on classifying small tissue patches, it enables researchers to develop automated systems that can assist in detecting cancer from histopathological images, which can ultimately improve early diagnosis and patient outcomes in oncology. The benchmark encourages progress in deep learning techniques for medical image analysis and contributes to the growing field of AI-assisted healthcare.

PatchCamelyon is derived from Camelyon16 and Camelyon17, which are existing datasets for breast cancer detection. The benchmark is used to evaluate machine learning models, particularly in histopathological image classification, where the goal is to determine whether a tissue patch contains cancerous cells or not.

1) Dataset Features:

- Number of Images: 327,680
- Image Size: 96 x 96 pixels
- Labels: Each image is annotated with a binary label indicating the presence of metastatic tissue.

2) Importance of the Benchmark:

- PCam is larger than CIFAR10 but smaller than ImageNet, designed to be trainable on a single GPU. This dataset provides a new standard for evaluating the performance of machine learning models.

3) Source of the Dataset:

- PCam is derived from the Camelyon16 challenge, based on 400 whole-slide images stained with H&E.
- The slides were digitized at 40x magnification and collected from two different centers.

4) Sampling Method:

- The dataset uses a probabilistic method to sample positive and negative patches.
- To avoid background patches, slides are converted to HSV, and patches with a maximum pixel saturation below 0.07 are filtered out.

5) Use Cases:

- PCam can be utilized for various machine learning tasks, including breast tumor classification, image compression, and image clustering.
- This dataset plays a crucial role in assessing advancements in machine learning within the medical imaging field.
- Benchmarking: PatchCamelyon is often used in research papers to evaluate and compare the performance of different machine learning models, especially deep learning architectures, on the same dataset.

5) Importance in Medical AI:

- **Pathology Automation:** The PatchCamelyon benchmark plays a critical role in automating pathology by enabling models to assist pathologists in detecting and diagnosing cancer from tissue slides. This can reduce the burden on medical professionals and improve diagnostic efficiency.
- **Transferability:** While PatchCamelyon is focused on breast cancer, the techniques and models trained on it can be applied to other types of cancer and pathology datasets, making it an important stepping stone in the broader field of medical image analysis.

2. TIFF (Tagged Image File Format)

TIFF files are a high-quality image format ideal for use cases that require detailed and lossless image preservation, such as in medical imaging, professional photography, and scanning. While the file sizes can be large, the format's ability to maintain image integrity makes it the preferred choice for industries where image quality is paramount.

TIFF files are commonly used in medical imaging (e.g., histopathology, radiology, X-rays, MRI scans), as they preserve the high detail and accuracy needed for diagnosis. For instance, whole slide images (WSI) from biopsy samples are often saved in TIFF format for analysis by pathologists.

1) Lossless Compression:

- TIFF files can be stored using lossless compression, meaning no image data is lost during compression. This ensures that the image retains its full quality, which is essential in fields like medical imaging or archival purposes.
- TIFF can also support lossy compression, allowing for smaller file sizes if some data loss is acceptable (e.g., JPEG compression).

2) High-Quality Imaging:

- TIFF is capable of storing images with high color depth (e.g., 16 or 32 bits per channel), which allows for more detailed and accurate color representation. This makes TIFF ideal for images that require fine detail, such as scanned photographs, artwork, or satellite imagery.

3) Multi-layer and Multi-page Support:

- TIFF files can store multiple layers (each containing different image data) and multi-page images, making them useful for storing things like scanned documents or multi-image datasets. Flexibility in Color Models:
- TIFF can support a wide range of color models, such as RGB, CMYK, grayscale, and indexed colors. This flexibility makes it suitable for various use cases, including printing and medical imaging.

4) Metadata Support:

- TIFF files can contain metadata (additional information about the image), such as camera settings, GPS coordinates (in the case of photos), and other technical details. This is particularly useful in professional fields where context and image data are critical.

5) File Size:

- Since TIFF files often store images in high quality or without any compression, the file sizes can be quite large compared to other image formats like JPEG or PNG. This is one reason TIFF is used less in general consumer applications but more in professional environments.

3. Performance Evaluation Metrics

1) AUC (Area Under the Curve):

- One of the most commonly used evaluation metrics for the PatchCamelyon benchmark is AUC, which indicates how well the model can distinguish between positive and negative classes.

2) Accuracy:

- The overall accuracy of the model in correctly classifying patches is also a standard performance

measure.

3) Precision and Recall:

- These metrics can be useful for evaluating how well the model identifies cancerous patches (precision) and how well it detects all cancerous patches (recall).

Background Knowledge

Histopathological images

Histopathological images are microscopic images of tissue samples that are used in pathology to study and diagnose diseases. These images are captured after the tissue samples are processed, stained, and examined under a microscope, typically by pathologists.

Histopathological images help in the detailed examination of the cellular structure and tissue organization, which is essential for diagnosing various diseases, including cancers.

Histopathological images are crucial for understanding and diagnosing diseases at the microscopic level. By examining these images, healthcare professionals can make accurate diagnoses and treatment decisions. With the integration of AI, the process of analyzing histopathological images has become faster and more reliable, improving patient outcomes and reducing diagnostic errors.

1) Tissue Samples:

- These images are taken from tissue biopsies or surgical specimens. The tissues are often from organs or lesions, such as tumors, and may show healthy or diseased conditions.

2) Staining:

- Histopathological images are usually enhanced using staining techniques (e.g., Hematoxylin and Eosin (H&E) stain), which make certain components of the cells and tissues more visible, such as nuclei, cytoplasm, and extracellular matrices. Stains help differentiate structures in the tissue, making it easier to analyze pathological changes.

3) Microscopic Analysis:

- These images are captured using high-powered microscopes, often requiring magnifications ranging from 100x to 1000x. This level of detail allows pathologists to closely examine the fine structures of cells, tissues, and any abnormalities that may be present.

4) Cellular and Tissue Changes:

- Histopathological images reveal changes at the cellular level, such as abnormal cell morphology, infiltration by immune cells, tissue necrosis (cell death), inflammation, or tumor growth. The analysis of these changes is crucial for diagnosing conditions like cancer, inflammatory diseases, infectious diseases, and other disorders. Applications of Histopathological Images:

5) Cancer Diagnosis:

- One of the primary uses of histopathological images is in the diagnosis of cancer. Pathologists analyze the images to determine the type of cancer, the degree of differentiation of cancer cells, and whether cancer cells have spread (metastasized) to other parts of the body.

6) Disease Monitoring:

- Histopathological images are used to monitor the progression of diseases, such as inflammatory conditions or autoimmune diseases, by examining tissue damage or changes over time.

7) Surgical Planning and Outcome Prediction:

- These images help surgeons and oncologists in planning treatments, such as determining the extent of surgical resection needed for tumor removal. They also provide insight into how well a patient might respond to a particular treatment, based on tissue characteristics.

8) Role in Machine Learning and AI:

- Recent advancements in artificial intelligence (AI) and machine learning (ML) have enabled automated analysis of histopathological images. AI models can help pathologists by automatically detecting anomalies, identifying regions of interest, and classifying types of tissue or disease, thus speeding up diagnosis and improving accuracy. For example, deep learning models have been developed to detect tumors, estimate cancer stages, and even predict patient outcomes from histopathological data.

Exploring Data and Visualization

```
In [1]: import numpy as np
import pandas as pd
import os
import cv2
import matplotlib.pyplot as plt
import matplotlib.patches as patches
import random
from sklearn.utils import shuffle
from tqdm import tqdm_notebook
from scipy.stats import ttest_ind
import matplotlib.image as mpimg
from PIL import Image
```

```
In [2]: # Set global seeds for reproducibility
SEED = 42
np.random.seed(SEED)
random.seed(SEED)
```

Prepare dataframe

```
In [3]: # Define the file path for the directory containing training images
train_tif = '/kaggle/input/histopathologic-cancer-detection/train/'

# Define the file path for the CSV file that contains the labels for the images
label_csv = '/kaggle/input/histopathologic-cancer-detection/train_labels.csv'

# Load the CSV file into a pandas DataFrame
class_labels = pd.read_csv(label_csv)

# Append the '.tif' extension to each image ID in the 'id' column
class_labels['id'] = class_labels['id'] + '.tif'

# Convert the 'label' column to a string type
class_labels['label'] = class_labels['label'].astype(str)

# Add a new column 'image_path' to the DataFrame
class_labels['image_path'] = class_labels['id'].apply(lambda x: os.path.join(train_tif, x))
```

```
In [4]: class_labels.head()
```

```
Out[4]:
```

	id	label	image_path
0	f38a6374c348f90b587e046aac6079959adf3835.tif	0	/kaggle/input/histopathologic-cancer-detection...
1	c18f2d887b7ae4f6742ee445113fa1aef383ed77.tif	1	/kaggle/input/histopathologic-cancer-detection...
2	755db6279dae599ebb4d39a9123cce439965282d.tif	0	/kaggle/input/histopathologic-cancer-detection...
3	bc3f0c64fb968ff4a8bd33af6971ecae77c75e08.tif	0	/kaggle/input/histopathologic-cancer-detection...
4	068aba587a4950175d04c680d38943fd488d6a9d.tif	0	/kaggle/input/histopathologic-cancer-detection...

Distribution of labels in image dataframe

```
In [5]: # Calculate frequency distribution
label_distribution = (class_labels.label.value_counts(normalize=True) * 100).to_frame()

# Plotting the frequency distribution as a bar chart
plt.figure(figsize=(5, 4))
colors = ['palegreen', 'hotpink'] # Colors for benign and malignant

# Plotting bar chart with specified colors
label_distribution.iloc[:, 0].plot(kind='bar', color=colors)

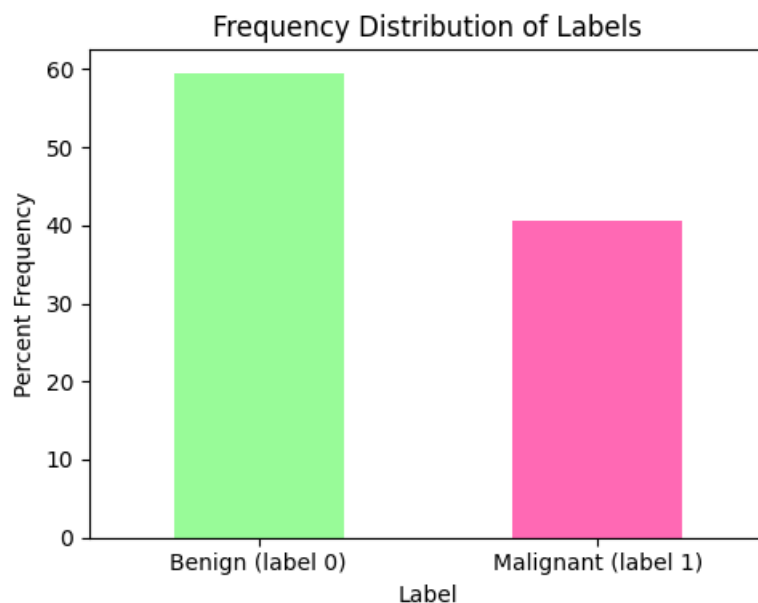
# Customizing chart
plt.title('Frequency Distribution of Labels')
plt.xlabel('Label')
plt.ylabel('Percent Frequency')
plt.xticks([0, 1], ['Benign (label 0)', 'Malignant (label 1)'], rotation=0)

# Displaying frequency distribution and counts
print("< Benign vs Malignant Distribution (%) >\n", label_distribution, "\n")
print("< Label Frequency (Count) >\n", class_labels.label.value_counts())

# Adjust layout and show the plot
plt.tight_layout()
plt.show()
```

```
< Benign vs Malignant Distribution (%) >
      proportion
label
0      59.496875
1      40.503125
```

```
< Label Frequency (Count) >
label
0      130908
1       89117
Name: count, dtype: int64
```



```
In [6]: # Sample images with label '0' and label '1'
sample_tif_lb_0 = class_labels[class_labels['label'] == '0'].sample(6)
sample_tif_lb_1 = class_labels[class_labels['label'] == '1'].sample(6)

# Combine the samples into a single DataFrame
sample_tiff = pd.concat([sample_tif_lb_0, sample_tif_lb_1])

# Set up the figure and axes
fig, axes = plt.subplots(4, 3, figsize=(12, 18))
fig.tight_layout(pad=1.0)

# Loop through sampled images and mark feature area.
for i, ax in enumerate(axes.flat):
    # Get the image and label
```



```

id = sample_tiff.iloc[i]['id']
label = sample_tiff.iloc[i]['label']

# Load the image from file
img = mpimg.imread(os.path.join(train_tif, id))

# Display the image
ax.imshow(img, cmap='gray')
ax.axis('off')

# Highlight the center 32x32 area
h, w = img.shape[:2]
center_x, center_y = w // 2, h // 2
rect_x, rect_y = center_x - 16, center_y - 16

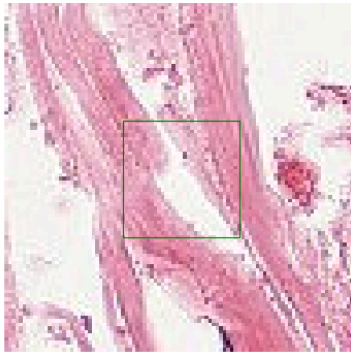
# Correctly determine the box color based on label
box_color = 'green' if label == '0' else 'red'

rect = patches.Rectangle(
    (rect_x, rect_y), 32, 32,
    linewidth=0.8,
    edgecolor=box_color,
    linestyle='-',
    facecolor='none'
)
ax.add_patch(rect)

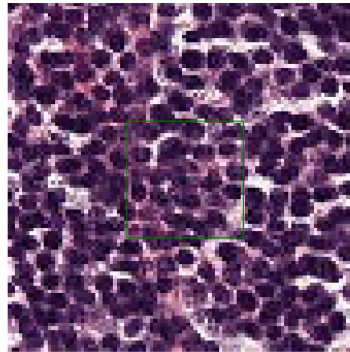
# Set title for the image
ax.set_title(f"Label: {label}")

```

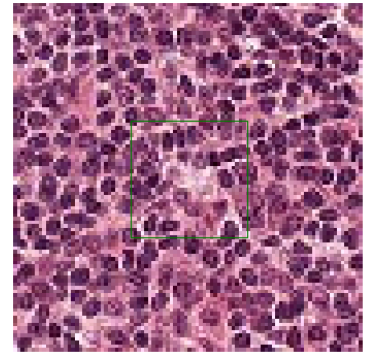
Label: 0



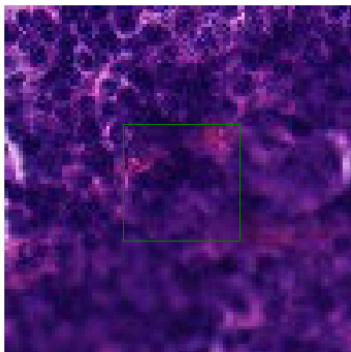
Label: 0



Label: 0



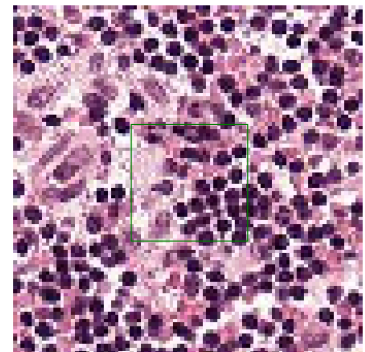
Label: 0



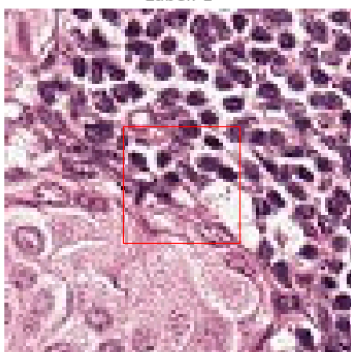
Label: 0



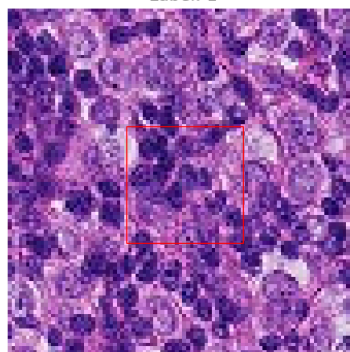
Label: 0



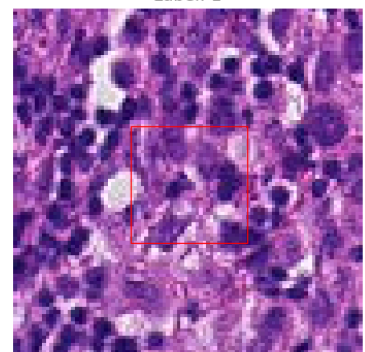
Label: 1

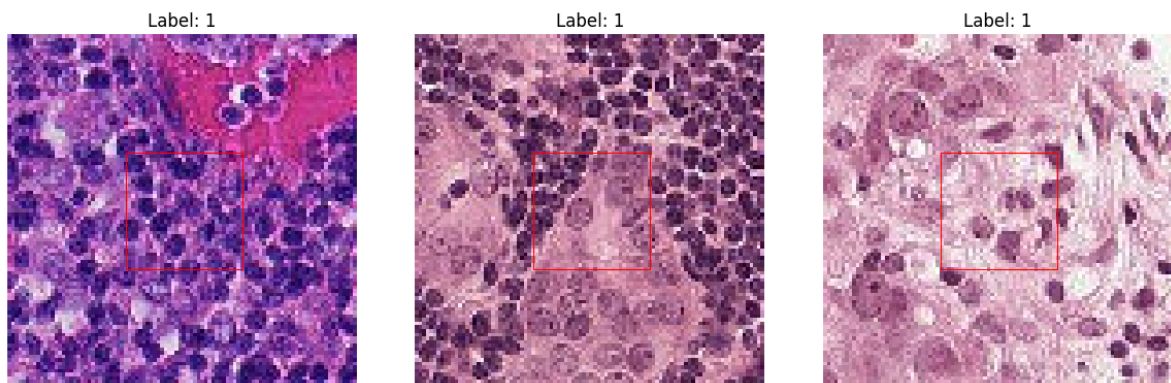


Label: 1



Label: 1





Histogram of RGB channel intensities for benign or malignant

```
In [7]: # Filter DataFrame for benign and malignant samples
benign_df = class_labels[class_labels['label'] == '0'] # Label 0 = benign
malignant_df = class_labels[class_labels['label'] == '1'] # Label 1 = malignant

def load_image(image_path, target_size=(96, 96)):
    """
    Load a single image, resize it, and convert to a NumPy array.
    """
    try:
        img = Image.open(image_path) # Load the image
        img = img.resize(target_size) # Resize
        img_array = np.array(img) # Convert to NumPy array
        return img_array
    except Exception as e:
        print(f"Error loading image: {image_path}")
        print(e)
        return None # Return None if loading fails

def load_images(df, max_images=None):
    """
    Load multiple images based on a DataFrame of paths.
    """
    images = []
    for path in df['image_path'][:max_images]:
        img = load_image(path)
        if img is not None:
            images.append(img)
    return np.array(images)

# Limit the number of images to load for testing
benign_tif = load_images(benign_df, max_images=100)
malignant_tif = load_images(malignant_df, max_images=100)

# Check the shapes of the loaded data
print(f"Benign data shape: {benign_tif.shape}")
print(f"Malignant data shape: {malignant_tif.shape}")
```

Benign data shape: (100, 96, 96, 3)
Malignant data shape: (100, 96, 96, 3)

```
In [8]: num_bins = 256 # Each possible pixel value (0-255) gets a bin
fig, axs = plt.subplots(4, 2, sharey=True, figsize=(8, 8), dpi=120) # Create a 4x2 plot grid
rgb_list = ["Red", "Green", "Blue", "RGB"]

# Loop through rows (RGB channels and combined) and columns (benign and malignant)
for row_idx in range(0, 4):
    for col_idx in range(0, 2):
        if row_idx < 3:
            axs[row_idx, 0].set_ylabel("Relative Frequency")
            axs[row_idx, 1].set_ylabel(rgb_list[row_idx], rotation="horizontal",
                                       labelpad=35, fontsize=10)
            # Plot histograms for RGB channels
            if col_idx == 0: # Benign (label 0)
                axs[row_idx, 0].hist(benign_tif[:, :, :, row_idx].flatten(),
                                     bins=num_bins, density=True, color='teal', alpha=0.7)
            elif col_idx == 1: # Malignant (label 1)
                axs[row_idx, 1].hist(malignant_tif[:, :, :, row_idx].flatten(),
                                     bins=num_bins, density=True, color='crimson', alpha=0.7)
```



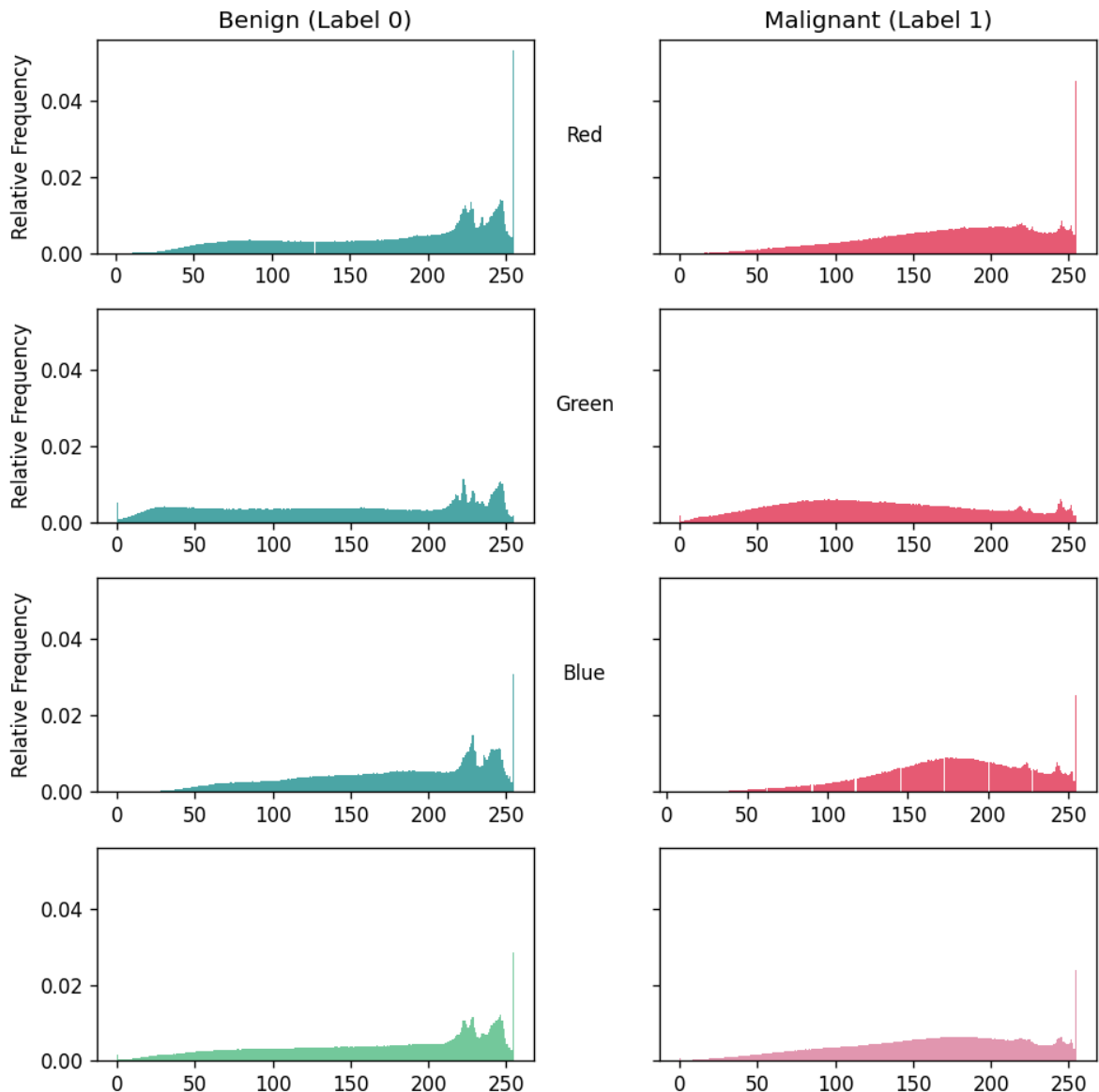
```

else:
    # Plot histograms for combined RGB intensities
    if col_idx == 0: # Benign (label 0)
        axs[row_idx, 0].hist(benign_tif.flatten(),
                             bins=num_bins, density=True, color='mediumseagreen', alpha=0.5)
    elif col_idx == 1: # Malignant (label 1)
        axs[row_idx, 1].hist(malignant_tif.flatten(),
                             bins=num_bins, density=True, color='palevioletred', alpha=0.5)

# Add titles for columns
axs[0, 0].set_title("Benign (Label 0)")
axs[0, 1].set_title("Malignant (Label 1)")

# Show the plots
plt.tight_layout()
plt.show()

```



Statistical Analysis comparing channel intensity between benign and malignant images

If the t-statistic is significantly high or low, and the p-value is below the chosen significance level (e.g., 0.05), it suggests that there is a statistically significant difference in the pixel intensity distributions between benign and malignant images. This analysis can help in understanding whether the characteristics of benign and malignant images differ in a meaningful way, which could be crucial for diagnostic purposes.

1) t-statistic (t_stat)

- The t-statistic is a measure that indicates how many standard deviations the sample mean difference is from the null hypothesis mean difference (usually zero)

represent the null hypothesis mean difference (usually zero).

- A higher absolute value of the t-statistic suggests a greater difference between the two groups' means relative to the variability in the data.
- It is calculated as:

$$[t = \frac{\bar{X}_1 - \bar{X}_2}{SE}]$$

where (\bar{X}_1) and (\bar{X}_2) are the sample means, and (SE) is the standard error of the difference between the means.

2) p-value (p_value)

- The p-value indicates the probability of obtaining a t-statistic as extreme as, or more extreme than, the observed value under the null hypothesis.
- A low p-value (typically less than 0.05) suggests that the observed difference between the groups is statistically significant, leading to the rejection of the null hypothesis.
- Conversely, a high p-value indicates insufficient evidence to conclude that a significant difference exists between the means of the two groups.

```
In [11]: def statistics_comparison(benign_images, malignant_images):

    stats = []
    channels = ["Red", "Green", "Blue"]

    for i, channel in enumerate(channels):
        # Flatten pixel intensities for the current channel
        benign_flattened = benign_images[:, :, :, i].flatten()
        malignant_flattened = malignant_images[:, :, :, i].flatten()

        # Calculate descriptive statistics for benign
        benign_mean = benign_flattened.mean()
        benign_median = np.median(benign_flattened)
        benign_std = benign_flattened.std()
        benign_min = benign_flattened.min()
        benign_max = benign_flattened.max()

        # Calculate descriptive statistics for malignant
        malignant_mean = malignant_flattened.mean()
        malignant_median = np.median(malignant_flattened)
        malignant_std = malignant_flattened.std()
        malignant_min = malignant_flattened.min()
        malignant_max = malignant_flattened.max()

        # Perform a two-sample t-test
        t_stat, p_value = ttest_ind(benign_flattened, malignant_flattened, equal_var=False)

        # Append results to the stats list
        stats.append({
            "Channel": channel,
            "Benign Mean": benign_mean,
            "Benign Median": benign_median,
            "Benign Std Dev": benign_std,
            "Malignant Mean": malignant_mean,
            "Malignant Median": malignant_median,
            "Malignant Std Dev": malignant_std,
            "t-statistic": t_stat,
            "p-value": p_value
        })

    # Convert stats list to a DataFrame
    return pd.DataFrame(stats)

# Compute statistics for all channels with significance
stats_comparison = statistics_comparison(benign_tif, malignant_tif)

# Display the statistics with t-tests
print("[Statistics and T-Test Results for Benign vs Malignant Images]\n")
print(stats_comparison)
```

[Statistics and T-Test Results for Benign vs Malignant Images]

	Channel	Benign Mean	Benign Median	Benign Std Dev	Malignant Mean	\
0	Red	177.239027	197.0	64.745381	177.150913	
1	Green	141.707395	145.0	75.322605	129.802393	

2	Blue	177.614376	188.0	58.059069	177.590972
	Malignant Median	Malignant Std Dev	t-statistic	p-value	
0	184.0	54.141419	1.002253	0.316222	
1	124.0	63.145928	116.276410	0.000000	
2	180.0	46.567179	0.301876	0.762746	

Summary of statistics & T-Test results

- The "green channel" is the only channel that shows a statistically significant difference between benign and malignant images, indicating that it may contain critical information for differentiating between these two types of tissues.
- The red and blue channels do not show significant differences, suggesting that they may not be as useful for classification purposes in this context.
- This analysis highlights the importance of the green channel in histopathological image analysis and suggests that further investigation into the features captured in this channel could be beneficial for improving diagnostic accuracy.
- The statistically significant difference in the green channel for histopathologic cancer detection data may be attributed to the distinct staining characteristics of benign and malignant tissues. The green channel often captures specific features related to cellular morphology and density, which can vary significantly between these tissue types, aiding in their differentiation.

1) Red Channel

Benign Mean: 177.24

Malignant Mean: 177.15

t-statistic: 1.002253

p-value: 0.316222

- The means of the benign and malignant groups are very close, indicating that there is little difference in the red channel intensity between the two groups.
- The t-statistic is low, and the p-value (0.316222) is greater than the common significance level of 0.05, suggesting that the difference is not statistically significant. This means that the red channel does not provide a reliable distinction between benign and malignant tissues.

2) Green Channel

Benign Mean: 141.71

Malignant Mean: 129.80

t-statistic: 116.276410

p-value: 0.000000

- The benign group has a significantly higher mean intensity in the green channel compared to the malignant group.
- The t-statistic is extremely high, and the p-value is 0.000000, which is far below 0.05. This indicates a statistically significant difference between the two groups. The green channel appears to be a strong indicator for distinguishing between benign and malignant tissues, suggesting that the green channel captures important features related to tissue characteristics.

3) Blue Channel

Benign Mean: 177.61

Malignant Mean: 177.59

t-statistic: 0.301876

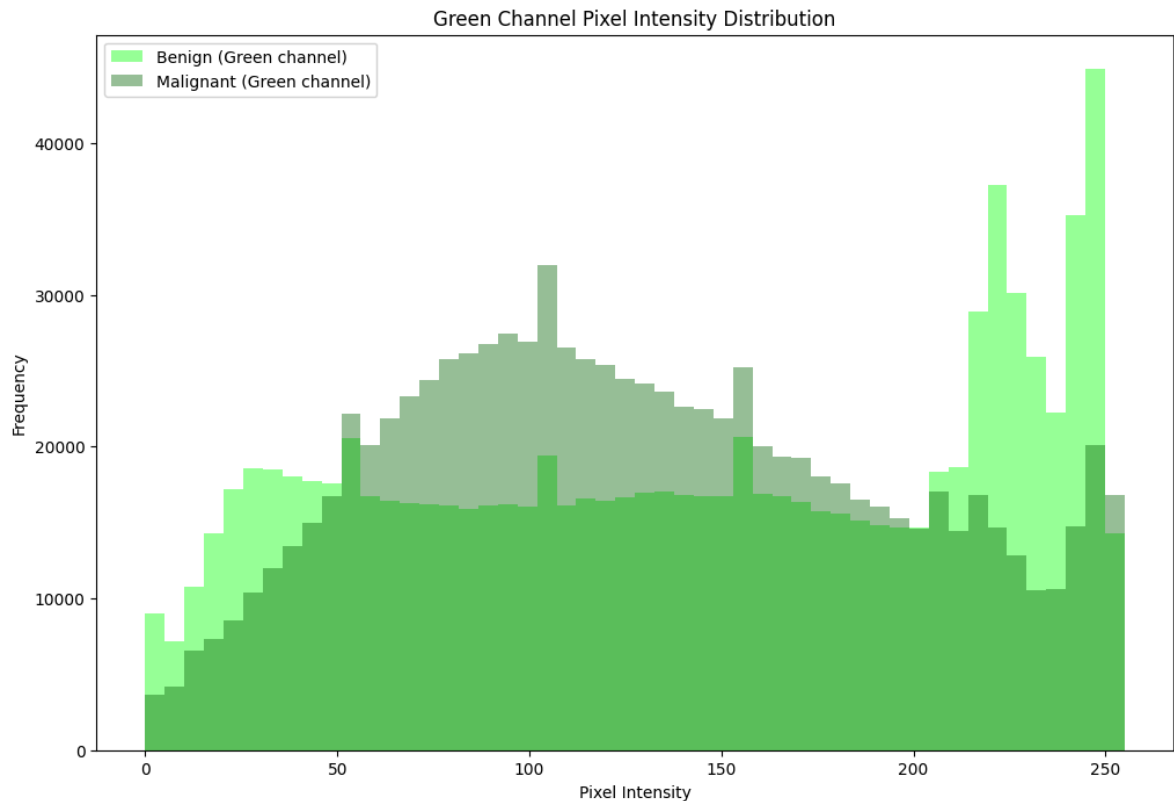
p-value: 0.762746

- Similar to the red channel, the means for the benign and malignant groups in the blue channel are very close, indicating little difference.
- The t-statistic is low, and the p-value (0.762746) is much greater than 0.05, suggesting that there is no statistically significant difference between the two groups in the blue channel. Thus, the blue channel does not provide useful information for distinguishing between benign and malignant tissues.

Visualization of Green channel pixel intensity

```
In [13]: # Compare Green channel pixel distributions

plt.figure(figsize=(12, 8))
plt.hist(benign_tif[:, :, :, 1].flatten(), bins=50, alpha=0.4, label="Benign (Green channel)")
plt.hist(malignant_tif[:, :, :, 1].flatten(), bins=50, alpha=0.4, label="Malignant (Green channel)")
plt.title("Green Channel Pixel Intensity Distribution")
plt.xlabel("Pixel Intensity")
plt.ylabel("Frequency")
plt.legend()
plt.show()
```



Result Summary of Visualization of Green channel pixel intensity

1. The green channel pixel intensity distributions in benign and malignant visualization differ significantly. This suggests that green channel intensity can be a useful feature for distinguishing between benign and malignant images.
2. The image displays the distribution of pixel intensities in the green channel for two classes of images: benign and malignant
 - Benign's Green Channel (lime color in histogram): The histogram shows a higher frequency of pixels with intensity values around 230-250.
 - Malignant's Green Channel (Dark green): The histogram shows a higher frequency of pixels with intensity values around 100-120.
3. Based on the visualization, it appears that there's a noticeable difference in the distribution of green channel pixel intensities between benign and malignant images. Benign images seem to have a higher concentration of bright green pixels (higher intensity values). Malignant images tend to have a higher concentration of darker green pixels (lower intensity values).

```
In [1]: import numpy as np
import pandas as pd
import tensorflow as tf
from tensorflow.keras.applications import MobileNetV2
from tensorflow.keras.applications.mobilenet_v2 import preprocess_input
from tensorflow.keras.layers import (Dense, GlobalAveragePooling2D, Input, Dropout,
                                     Flatten, Concatenate, GlobalMaxPooling2D)

from tensorflow.keras.models import Model
from tensorflow.keras.optimizers import Adam, RMSprop
from tensorflow.keras.callbacks import ModelCheckpoint, EarlyStopping, ReduceLROnPlateau
from tensorflow.keras.preprocessing.image import ImageDataGenerator

from keras.losses import binary_crossentropy

import os
from glob import glob
from random import shuffle
import cv2
import tifffile
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
```

```
In [2]: df_train = pd.read_csv("../input/histopathologic-cancer-detection/train_labels.csv")
id_label_map = df_train.set_index('id')['label'].to_dict()
```

```
In [3]: # 이미지 삭제코드 누락
import concurrent.futures
from pathlib import Path

def id_from_file_path(file_path):
    file_name = Path(file_path).name
    if file_name.endswith('.tif'):
        return file_name[:-4]
    return file_name

def get_file_paths_from_directory(directory):
    return [str(file) for file in Path(directory).rglob("*.tif")]

def process_files_in_parallel(file_paths):
    with concurrent.futures.ThreadPoolExecutor() as executor:
        # 병렬로 파일 경로 처리
        return list(executor.map(id_from_file_path, file_paths))

directory_path = "../input/histopathologic-cancer-detection/train"
tif_files = get_file_paths_from_directory(directory_path)

file_ids = process_files_in_parallel(tif_files)

print(file_ids[:5])

['d43c081bafa286f9c1f7e921883f26ceafebc912', '092d0eedebce504847715ee046b6ad74b57599b4', 'b0d
2582c6218a8764323fc940b41312282b99bf4', '187c99df762f13f99818e5593d4bab4c6577e7e3', '7c5270c8
3837de5a5cbb2dca511559dc39d19d53']
```

```
In [4]: labeled_tif = glob('../input/histopathologic-cancer-detection/train/*.tif')
test_tif = glob('../input/histopathologic-cancer-detection/test/*.tif')
```

```
In [5]: print("Number of labeled tif :", len(labeled_tif))
print("Number of test tif :", len(test_tif))
```

```
Number of labeled tif : 220025
Number of test tif : 57458
```

```
In [6]: train, val = train_test_split(labeled_tif, test_size=0.1, random_state=42)
```

```
In [7]: def chunker(seq, size):
    return (seq[position: position + size] for position in range(0, len(seq), size))
```

```
In [8]: def increase_green_channel(image):
    image[:, :, 1] = np.clip(image[:, :, 1] * 1.5, 0, 255)
    return image
```



```

    return image

def image_to_green_histogram(image_path):
    with tiffFile.TiffFile(image_path) as tif:
        image = tif.asarray()

        if image.ndim == 3:
            green_channel = image[:, :, 1]
        else:
            green_channel = image

        hist, _ = np.histogram(green_channel, bins=256, range=(0, 256))

    return hist

def convert_images_to_histograms(directory, num_images):
    histograms = []
    count = 0

    for filename in os.listdir(directory):
        if filename.endswith(".tif"):
            image_path = os.path.join(directory, filename)
            histogram = image_to_green_histogram(image_path)
            histograms.append(histogram)
            count += 1

            if count >= num_images:
                break

    return np.array(histograms)

```

In [9]:

```

def data_gen(list_files, id_label_map, batch_size, augment=False):
    tif_gen = ImageDataGenerator(
        rotation_range=8,
        width_shift_range=0.1,
        height_shift_range=0.1,
        horizontal_flip=True,
        vertical_flip=True,
        zoom_range=0.15,
        shear_range=4,
        preprocessing_function=increase_green_channel
    )

    while True:
        shuffle(list_files)
        for batch in chunker(list_files, batch_size):
            X = [cv2.imread(x) for x in batch]
            Y = [id_label_map[id_from_file_path(x)] for x in batch]
            histograms = [image_to_green_histogram(x) for x in batch]

            if augment:
                X = [tif_gen.random_transform(x) for x in X]

            X = [preprocess_input(x.astype(np.float32)) for x in X]

            X = np.array(X)
            histograms = np.array(histograms)
            Y = np.array(Y)

            yield (X, histograms), Y

```

In [10]:

```

# 히스토그램 추가해서 예측하는 코드
def mobilenetv2(histogram_input_shape=(256,), image_input_shape=(96, 96, 3)):
    # 이미지 입력
    image_inputs = Input(shape=image_input_shape)

    # MobileNetV2 모델
    base_model = MobileNetV2(include_top=False, input_shape=image_input_shape)
    x = base_model(image_inputs)

    # 다양한 풀링 레이어
    out1 = GlobalMaxPooling2D()(x)
    out2 = GlobalAveragePooling2D()(x)
    out3 = Flatten()(x)

    # 풀링 결과를 결합
    combined_features = Concatenate(axis=-1)([out1, out2, out3])
    combined_features = Dropout(0.5)(combined_features)

```

```

combined_features = Dropout(0.5)(combined_features)

# 히스토그램 입력
histogram_inputs = Input(shape=histogram_input_shape)

# 히스토그램 데이터를 처리하는 Dense 레이어
histogram_dense = Dense(128, activation='relu')(histogram_inputs)

# 이미지와 히스토그램 데이터를 결합
combined = Concatenate(axis=-1)([combined_features, histogram_dense])

# 최종 출력 레이어
out = Dense(1, activation="sigmoid", name="output")(combined)

# 모델 정의
model = Model(inputs=[image_inputs, histogram_inputs], outputs=out)
model.compile(optimizer=Adam(0.0001), loss=binary_crossentropy, metrics=['acc'])
model.summary()

return model

```

In [11]: `model = mobilenetv2()`

Downloading data from https://storage.googleapis.com/tensorflow/keras-applications/mobilenet_v2/mobilenet_v2_weights_tf_dim_ordering_tf_kernels_1.0_96_no_top.h5
9406464/9406464 ————— 1s 0us/step

Model: "functional"

Layer (type)	Output Shape	Param #	Connected to
input_layer (InputLayer)	(None, 96, 96, 3)	0	—
mobilenetv2_1.00_96 (Functional)	(None, 3, 3, 1280)	2,257,984	input_layer[0]
global_max_pooling2d (GlobalMaxPooling2D)	(None, 1280)	0	mobilenetv2_1.
global_average_pooling2d (GlobalAveragePooling2D)	(None, 1280)	0	mobilenetv2_1.
flatten (Flatten)	(None, 11520)	0	mobilenetv2_1.
concatenate (Concatenate)	(None, 14080)	0	global_max_poo global_average flatten[0][0]
input_layer_2 (InputLayer)	(None, 256)	0	—
dropout (Dropout)	(None, 14080)	0	concatenate[0]
dense (Dense)	(None, 128)	32,896	input_layer_2
concatenate_1 (Concatenate)	(None, 14208)	0	dropout[0][0], dense[0][0]
output (Dense)	(None, 1)	14,209	concatenate_1

Total params: 2,305,089 (8.79 MB)

Trainable params: 2,270,977 (8.66 MB)

Non-trainable params: 34,112 (133.25 KB)

In [12]: `from tensorflow.keras.callbacks import ReduceLRonPlateau, EarlyStopping, ModelCheckpoint`

```

h5_path = "model.keras"

# ModelCheckpoint 콜백
checkpoint = ModelCheckpoint(
    h5_path,          # 모델 가중치를 저장할 경로
    monitor='val_acc', # 모니터링할 지표
    verbose=1,        # 로그 출력 여부
    save_best_only=True, # 성능이 개선된 경우에만 저장
    mode='max'         # val_acc가 최대가 될 때 모델 저장
)

# 여기 스텝이 코백 (거즈 저장드 모니터링)

```

```

early_stopping_acc = EarlyStopping(monitor='val_acc', patience=3, verbose=1, mode='max', res

# 얼리 스톱핑 콜백 (검증 손실 모니터링)
early_stopping_loss = EarlyStopping(monitor='val_loss', patience=5, restore_best_weights=True

# 학습률 감소 콜백
lr_scheduler = ReduceLRonPlateau(monitor='val_loss', patience=3, factor=0.5, min_lr=0.00001,

```

In []:

```

# 첫 번째 학습
batch_size = 32
history = model.fit(
    data_gen(train, id_label_map, batch_size, augment=True),
    validation_data=data_gen(val, id_label_map, batch_size),
    epochs=2, verbose=1,
    callbacks=[checkpoint, early_stopping_acc, early_stopping_loss, reduce_lr],
    steps_per_epoch=len(train) // batch_size,
    validation_steps=len(val) // batch_size)

# 두 번째 학습
batch_size = 64
history = model.fit(
    data_gen(train, id_label_map, batch_size, augment=True),
    validation_data=data_gen(val, id_label_map, batch_size),
    epochs=6, verbose=1,
    callbacks=[checkpoint, early_stopping_acc, early_stopping_loss, reduce_lr],
    steps_per_epoch=len(train) // batch_size,
    validation_steps=len(val) // batch_size)

# 세 번째 학습
model.compile(optimizer=Adam(0.00001), loss=binary_crossentropy, metrics=['acc'])
history = model.fit(
    data_gen(train, id_label_map, batch_size, augment=True),
    validation_data=data_gen(val, id_label_map, batch_size),
    epochs=6, verbose=1,
    callbacks=[checkpoint, early_stopping_acc, early_stopping_loss, reduce_lr],
    steps_per_epoch=len(train) // batch_size,
    validation_steps=len(val) // batch_size)

# 모델 가중치 로드
model.load_weights(h5_path)

```

```

Epoch 1/2
6188/6188 _____ 0s 360ms/step - acc: 0.8468 - loss: 0.4539
Epoch 1: val_acc improved from -inf to 0.91626, saving model to model.keras
6188/6188 _____ 2484s 395ms/step - acc: 0.8468 - loss: 0.4538 - val_acc: 0.916
3 - val_loss: 0.2240 - learning_rate: 1.0000e-04
Epoch 2/2
6188/6188 _____ 0s 166ms/step - acc: 0.9184 - loss: 0.2156
Epoch 2: val_acc improved from 0.91626 to 0.93514, saving model to model.keras
6188/6188 _____ 1118s 178ms/step - acc: 0.9184 - loss: 0.2156 - val_acc: 0.935
1 - val_loss: 0.1804 - learning_rate: 1.0000e-04
Restoring model weights from the end of the best epoch: 2.
Restoring model weights from the end of the best epoch: 2.
Epoch 1/6
3094/3094 _____ 0s 310ms/step - acc: 0.9427 - loss: 0.1555
Epoch 1: val_acc did not improve from 0.93514
3094/3094 _____ 1051s 333ms/step - acc: 0.9427 - loss: 0.1555 - val_acc: 0.915
2 - val_loss: 0.2263 - learning_rate: 1.0000e-04
Epoch 2/6
3094/3094 _____ 0s 318ms/step - acc: 0.9481 - loss: 0.1425
Epoch 2: val_acc improved from 0.93514 to 0.93600, saving model to model.keras
3094/3094 _____ 1055s 341ms/step - acc: 0.9481 - loss: 0.1425 - val_acc: 0.936
0 - val_loss: 0.1626 - learning_rate: 1.0000e-04
Epoch 3/6
3094/3094 _____ 0s 328ms/step - acc: 0.9537 - loss: 0.1254
Epoch 3: val_acc did not improve from 0.93600
3094/3094 _____ 1095s 354ms/step - acc: 0.9537 - loss: 0.1254 - val_acc: 0.924
2 - val_loss: 0.2074 - learning_rate: 1.0000e-04
Epoch 4/6
3094/3094 _____ 0s 321ms/step - acc: 0.9579 - loss: 0.1185
Epoch 4: val_acc improved from 0.93600 to 0.93664, saving model to model.keras
3094/3094 _____ 1051s 340ms/step - acc: 0.9579 - loss: 0.1185 - val_acc: 0.936
6 - val_loss: 0.1690 - learning_rate: 1.0000e-04
Epoch 5/6
3094/3094 _____ 0s 292ms/step - acc: 0.9599 - loss: 0.1116
Epoch 5: val_acc did not improve from 0.93664

```

Epoch 5: ReduceLRonPlateau reducing learning rate to 4.999999873689376e-05.

```

3094/3094 ————— 958s 310ms/step - acc: 0.9599 - loss: 0.1116 - val_acc: 0.9178
- val_loss: 0.2410 - learning_rate: 1.0000e-04
Epoch 6/6
3094/3094 ————— 0s 294ms/step - acc: 0.9677 - loss: 0.0922
Epoch 6: val_acc improved from 0.93664 to 0.93965, saving model to model.keras
3094/3094 ————— 963s 311ms/step - acc: 0.9677 - loss: 0.0922 - val_acc: 0.9397
- val_loss: 0.1660 - learning_rate: 5.0000e-05
Restoring model weights from the end of the best epoch: 6.
Restoring model weights from the end of the best epoch: 2.
Epoch 1/6
3094/3094 ————— 0s 307ms/step - acc: 0.9577 - loss: 0.1165
Epoch 1: val_acc did not improve from 0.93965
3094/3094 ————— 1042s 325ms/step - acc: 0.9577 - loss: 0.1165 - val_acc: 0.9357
- val_loss: 0.1642 - learning_rate: 1.0000e-05
Epoch 2/6
3094/3094 ————— 0s 289ms/step - acc: 0.9609 - loss: 0.1070
Epoch 2: val_acc did not improve from 0.93965
3094/3094 ————— 961s 306ms/step - acc: 0.9609 - loss: 0.1070 - val_acc: 0.9371
- val_loss: 0.1664 - learning_rate: 1.0000e-05
Epoch 3/6
3094/3094 ————— 0s 279ms/step - acc: 0.9618 - loss: 0.1042
Epoch 3: val_acc did not improve from 0.93965
3094/3094 ————— 913s 295ms/step - acc: 0.9618 - loss: 0.1042 - val_acc: 0.9335
- val_loss: 0.1768 - learning_rate: 1.0000e-05
Epoch 3: early stopping
Restoring model weights from the end of the best epoch: 1.
Restoring model weights from the end of the best epoch: 1.

```

In [14]:

```

preds = []
ids = []
batch_size = 32

# 데이터 제너레이터를 사용하여 예측
for batch in chunker(test_tif, batch_size):
    # 이미지 읽기 및 전처리
    X = [cv2.imread(x) for x in batch]
    ids_batch = [id_from_file_path(x) for x in batch]

    # 전처리 및 히스토그램 계산
    histograms = [image_to_green_histogram(x) for x in batch] # 히스토그램 계산
    X = [preprocess_input(x.astype(np.float32)) for x in X]

    # NumPy 배열로 변환
    X = np.array(X)
    histograms = np.array(histograms) # 히스토그램 배열로 변환

    # 예측 수행
    preds_batch = (
        (model.predict([X, histograms]).ravel() *
         model.predict([X[:, :-1, :, :], histograms]).ravel() *
         model.predict([X[:, :-1, :-1, :], histograms]).ravel() *
         model.predict([X[:, :, :-1, :], histograms]).ravel()) ** 0.25
    ).tolist()

    preds += preds_batch
    ids += ids_batch

# 결과를 DataFrame으로 변환하고 CSV로 저장
df = pd.DataFrame({'id': ids, 'label': preds})
df.to_csv("submission.csv", index=False)
df.head()

```

```

1/1 ————— 2s 2s/step
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```

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1/1	3s	3s/step
1/1	0s	24ms/step
1/1	0s	22ms/step
1/1	0s	22ms/step


Out[14]:

		id	label
0	a7ea26360815d8492433b14cd8318607bcf99d9e		0.023997
1	59d21133c845dff1ebc7a0c7cf40c145ea9e9664		0.000669
2	5fde41ce8c6048a5c2f38eca12d6528fa312cdabb		0.101719
3	bd953a3b1db1f7041ee95ff482594c4f46c73ed0		0.104361
4	523fc2efd7aba53e597ab0f69cc2cbded7a6ce62		0.009658

```
In [15]: df.head()
```

Out [15]:

		id	label
0	a7ea26360815d8492433b14cd8318607bcf99d9e		0.023997
1	59d21133c845dff1ebc7a0c7cf40c145ea9e9664		0.000669
2	5fde41ce8c6048a5c2f38eca12d6528fa312cdbb		0.101719
3	bd953a3b1db1f7041ee95ff482594c4f46c73ed0		0.104361
4	523fc2efd7aba53e597ab0f69cc2cbded7a6ce62		0.009658

Submission and Description		Private Score ⓘ	Public Score ⓘ
	submission.csv Complete (after deadline) · now · MobileNetV2G	0.9341	0.9364

Conclusion

Due to the GPU quotation issue, I focused solely on the MobileNet v2 model, achieving a public score of 9.364 at this stage. To enhance the results and improve accuracy, I plan to explore alternative data processing techniques and experiment with various CNN models, potentially employing ensemble methods for even greater performance. Additionally, I could consider techniques such as data augmentation to increase the diversity of the training set, transfer learning to leverage pre-trained models, and hyperparameter tuning to optimize model performance.