

Gastro-intestinal Disease Prediction

Course- CS5704

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About



- Gastrointestinal (GI) diseases are widespread and strain healthcare systems. These conditions create patient discomfort and can lead to serious health problems.
- This project develops an image-based, machine learning tool to classify GI diseases. Leveraging advanced models like LLM Meta Llama 3.0 B parameters for enhanced processing and interpretation of medical imagery. It aims to be a non-invasive solution to aid medical professionals.
- A successful system could enhance diagnosis, increase accessibility of expert knowledge, reduce the need for endoscopies, and improve healthcare efficiency.
- We need a reliable, efficient way to classify GI diseases using endoscopic images to support faster, more accurate diagnoses.

This anatomical illustration shows the stomach and the first part of the small intestine, the duodenum. The stomach is a large, sac-like organ with a pinkish, textured surface. The duodenum is a C-shaped tube that receives chyme from the stomach. The pylorus, the opening of the stomach into the duodenum, is shown as a small, circular structure at the junction. The duodenal bulb, the first part of the duodenum, is shown as a larger, rounded structure. The illustration highlights the anatomical relationship between the stomach, pylorus, and duodenum.



Dyed-Resection-Margins



Normal-Cecum

- 3

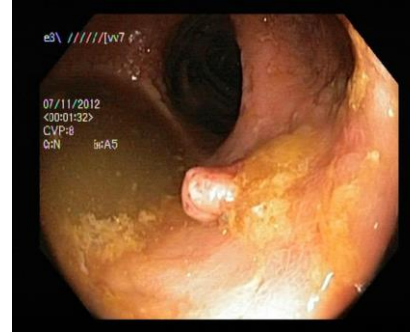
Diseases



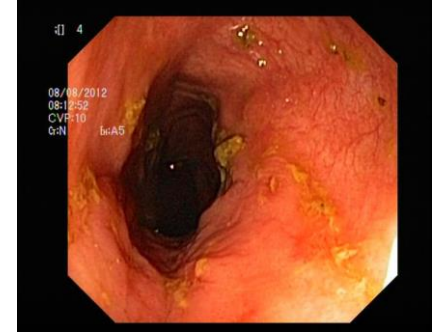
Normal-Pylorus



Normal-Z-Line



Polyps



Ulcerative-Colitis

- **Normal-pylorus:** Images of a healthy pylorus, the muscular valve connecting the stomach to the small intestine.
- **Normal-z-line:** Images of a healthy z-line, the squiggly line marking the transition between the esophagus and the stomach.
- **Polyps:** Images of polyps, which are growths on the lining of the colon or rectum.
- **Ulcerative-colitis:** Images showing inflammation and ulcers in the colon and rectum, characteristic of this chronic inflammatory bowel disease.



Dataset

KVASIR Dataset:

A Multi-Class Image Dataset for Computer Aided Gastrointestinal Disease Detection

Link :

<https://www.kaggle.com/datasets/meetnagadia/kvasir-dataset/data>

The dataset consists of 4000 images, where 500 images belonging to each class of diseases discussed.

Data

Sample Images from Dataset:





Data Preprocessing



- Data exploration revealed that all the images have different sizes , hence making it difficult during defining the model parameters. Hence we reduce to the image size to ensure reproducibility.
- Since our model requires images in RGB format, we convert them from BGR to RGB using the `cv2.COLOR_BGR2RGB` function in Python, ensuring compatibility with the model's input requirements.

Disease Labels

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Label Number	Disease Name
0	Dyed-Lifted-Polyps
1	Dyed-Resection-Margins
2	Esophagitis
3	Normal-Cecum
4	Normal-Pylorus
5	Normal-Z-Line
6	Polyps
7	Ulcerative-Colitis

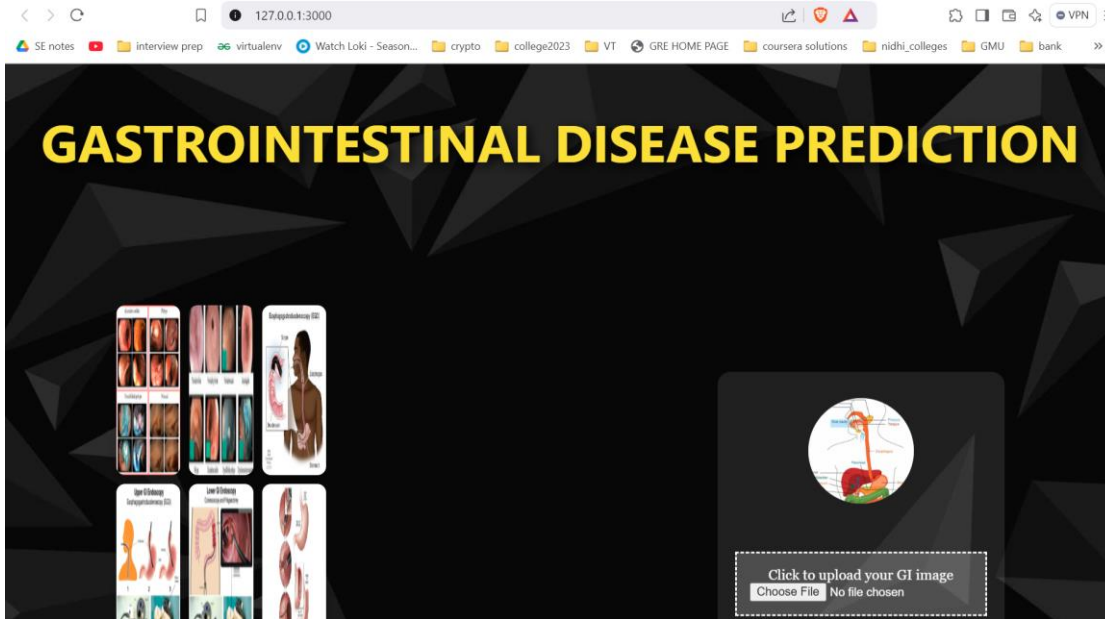
$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Methodologies

- FrontEnd: HTML, CSS, JS
- Backend: Flask, Postgres DB, Python
- LLM : Meta-Llama-3-8B-Instruct-GGUF
- Final ML model: DenseNet 121
- Scrum tools Used: Jira, Team gantt
- Communication: Zoom, Slack, Whatsapp

FrontEnd:

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$



Backend: Postgres

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

The screenshot displays the PostgreSQL pgAdmin web interface. On the left, the 'Browser' pane shows a tree view of the database structure, with the 'users' table selected under the 'public' schema. The main pane shows the 'Query' editor with the following SQL query:

```
1 SELECT * FROM public.users
2 ORDER BY id ASC
```

Below the query editor, the 'Data Output' tab displays the results of the query in a table format:

	id	name	email	password_hash
	[PK] integer	character varying (150)	character varying (150)	character varying (200)
1	1	Gautham Gali	ggali14@vt.edu	scrypt:32768:8:1\$Hd7C6EmPuwKyK4ru\$8170e319fba493ba702bd31f5

At the bottom of the interface, a status bar indicates: 'Total rows: 1 of 1', 'Query complete 00:00:00.220', and a green message: 'Successfully run. Total query runtime: 220 msec. 1 rows affected.'

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Backend: Flask

- User Authentication APIs:
- Login (/login): Validates user credentials and grants access to the application.
- Register (/register): Allows new users to create an account.
- Logout (/logout): Logs out the current user securely.
- Chatbot API:
- Chat (/chat): Processes user queries and generates AI-based responses using the Meta-Llama-3.0 model.
- Prediction API:
- Predict (/predict): Handles image uploads, classifies gastrointestinal conditions using a pre-trained model, and returns detailed disease information.
- Home API:
- Home (/): Renders the home page for logged-in users, providing access to core functionalities.

ML Model prediction

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

```
PROBLEMS 64 OUTPUT DEBUG CONSOLE TERMINAL PORTS GITLENS JUPYTER AZURE python - app + v [ ] [ ] ... ^ x

* Debugger PIN: 584-907-237
C:\Users\gauth\Desktop\jobs\EHR\gi-website\app\app.py:52: LegacyAPIWarning: The Query.get() method is considered legacy as of the 1.x series of SQLAlchemy and becomes a legacy construct in 2.0. The method is now available as Session.get() (deprecated since: 2.0) (Background on SQLAlchemy 2.0 at: https://sqlalche.me/e/b8d9)
    return User.query.get(int(user_id))
127.0.0.1 - - [03/Dec/2024 10:27:20] "GET / HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI2.jpg HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI3.jpg HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI5 HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI6.jpg HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI1.jpeg HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI7.jpeg HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI2.jpeg HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI4.jpg HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI8 HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /static/images/GI.jpeg HTTP/1.1" 200 -
127.0.0.1 - - [03/Dec/2024 10:27:21] "GET /favicon.ico HTTP/1.1" 404 -
./static/uploads/0a3d11f8-f994-4b2b-9fb1-57e4e346861f.jpg
1/1 9s 9s/step
Predicted gastrointestinal condition: normal-z-line
```

LLM Output

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

The screenshot displays the LM Studio application interface. At the top, it shows system resources: RAM Usage 5.65 GB and CPU 0.00 %. The main header indicates the current model is 'lmstudio-community • Meta Llama 3 Instruct 7B Q4_K_M gguf'. Below this, the interface is divided into several panels:

- Configuration:** Includes fields for 'Server Port' (set to 1234), 'Cross-Origin-Resource-Sharing (CORS)' (ON), 'Request Queuing' (ON), and 'Verbose Server Logs' (ON).
- My Models:** A section for managing local models, currently showing 'Formatting' as ON.
- Embedding Model Settings:** A panel for loading text embedding models. It features a search bar, a list of models (e.g., 'nomic-ai/nomic-embed-text-v1.5'), and a 'Download' button.
- Server Model Settings:** A panel for configuring the server model. It includes a 'Preset' dropdown (set to 'Llama 3'), a 'Danger Zone' with 'Discard Changes' and 'Override Preset' buttons, and a 'System Prompt' field.
- Model Inspector:** A panel showing detailed information about the selected model, including its name, architecture, quantization, context length, embedding length, number of layers, rope frequency base, and dimension count.

The 'Server logs' panel is highlighted, showing the following output:

```
complications, such as:\n\n1. **Gastric cancer**: Increased risk of developing gastric adenocarcinoma.\n2. **Gastrointestinal bleeding**: Bleeding from the stomach lining due to mucosal damage.\n3. **Stomach perforation**: Perforation of the stomach wall, which can lead to peritonitis or abscess formation.\n\nIn conclusion, Normal-Z-line disease is a condition characterized by the loss of normal gastric mucosa and the formation of a distinct Z-line in the stomach. While often asymptomatic, it can lead to complications if left untreated. Early diagnosis and treatment are essential to prevent long-term consequences."
```

The logs also show a JSON object indicating the completion of the task:

```
{\n  "finish_reason": "stop",\n  "usage": {\n    "prompt_tokens": 760,\n    "completion_tokens": 759,\n    "total_tokens": 1519\n  }\n}
```

Output

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Detailed Information

As a healthcare assistant, I'd be happy to provide you with detailed information about Normal-Z-line Gastrointestinal Disease.

What is Normal-Z-line (N-Z) disease?

Normal-Z-line disease, also known as N-Z line disease or gastric mucosal atrophy, is a type of gastrointestinal disorder characterized by the loss of normal gastric mucosa and the formation of a distinct "Z-line" or "Normal-Z-line" in the stomach. This condition is often asymptomatic but can lead to complications if left untreated.

Causes and Risk Factors

The exact causes of Normal-Z-line disease are not fully understood, but several factors are believed to contribute to its development:

- **Helicobacter pylori (H. pylori) infection**

: H. pylori bacteria have been linked to the development of N-Z line disease.

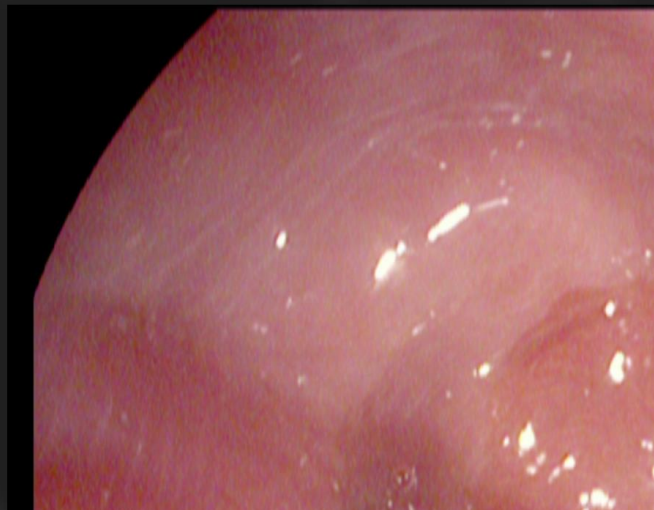
- **Gastritis**

: Chronic gastritis can lead to mucosal atrophy and the formation of a Z-line.

- **Gastroesophageal reflux disease (GERD)**

Prediction Result

Predicted gastrointestinal condition: normal-z-line



Model One - VGG16



Model: "sequential"

Layer (type)	Output Shape	Param #
vgg16 (Functional)	(32, 7, 7, 512)	14,714,688
flatten (Flatten)	(32, 25088)	0
dense (Dense)	(32, 256)	6,422,784
dropout (Dropout)	(32, 256)	0
dense_1 (Dense)	(32, 8)	2,056

Total params: 33,989,210 (129.66 MB)

Trainable params: 6,424,840 (24.51 MB)

Non-trainable params: 14,714,688 (56.13 MB)

Optimizer params: 12,849,682 (49.02 MB)

Base Model: Utilizes VGG16, a powerful pre-trained convolutional neural network.

Architecture:

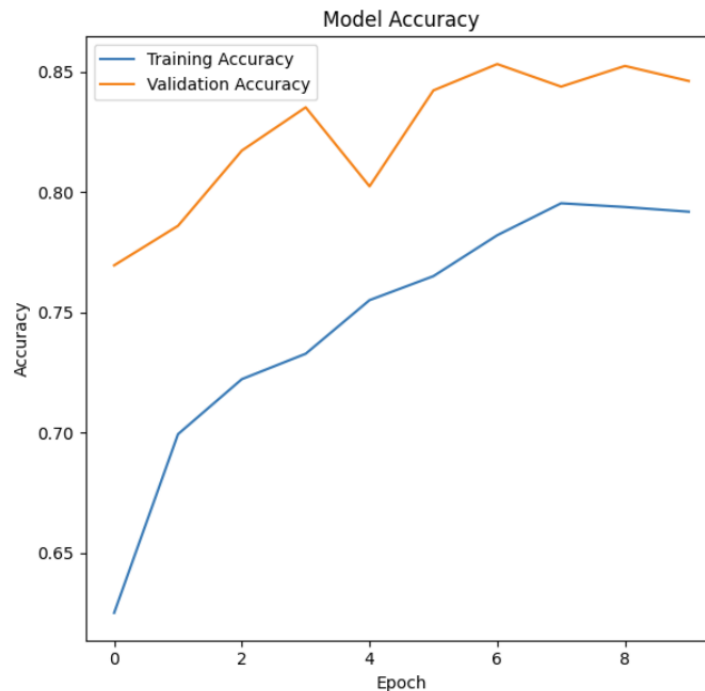
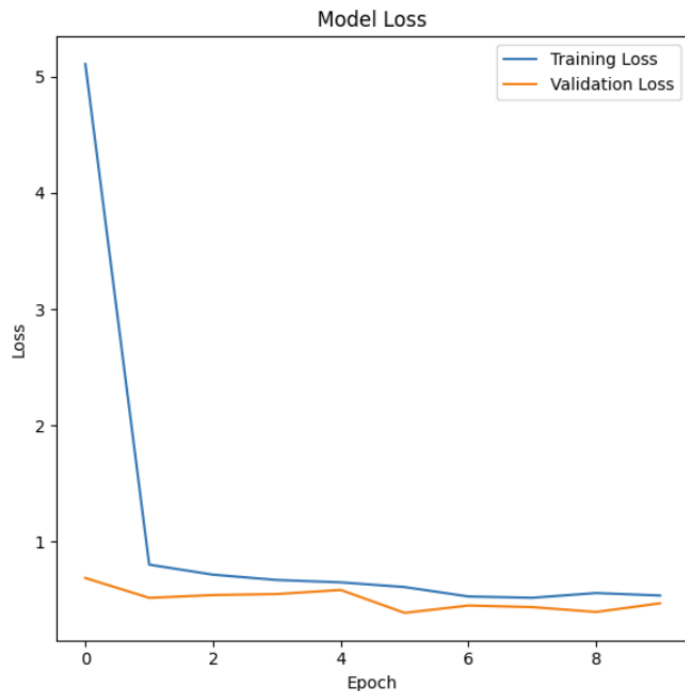
- Input: 224x224 RGB image
- Convolutional Blocks:
 - Multiple convolutional layers (with 3x3 filters)
 - Max-pooling layers for downsampling
- Fully Connected Layers:
 - Layers to map the extracted features to the final output classes
- Output: 1000-dimensional vector (corresponding to 1000 ImageNet classes)

Total Parameters: 33,989,210

Trainable Parameters: 6,424,840

Non-trainable Parameters: 14,714,688

Model One - VGG16

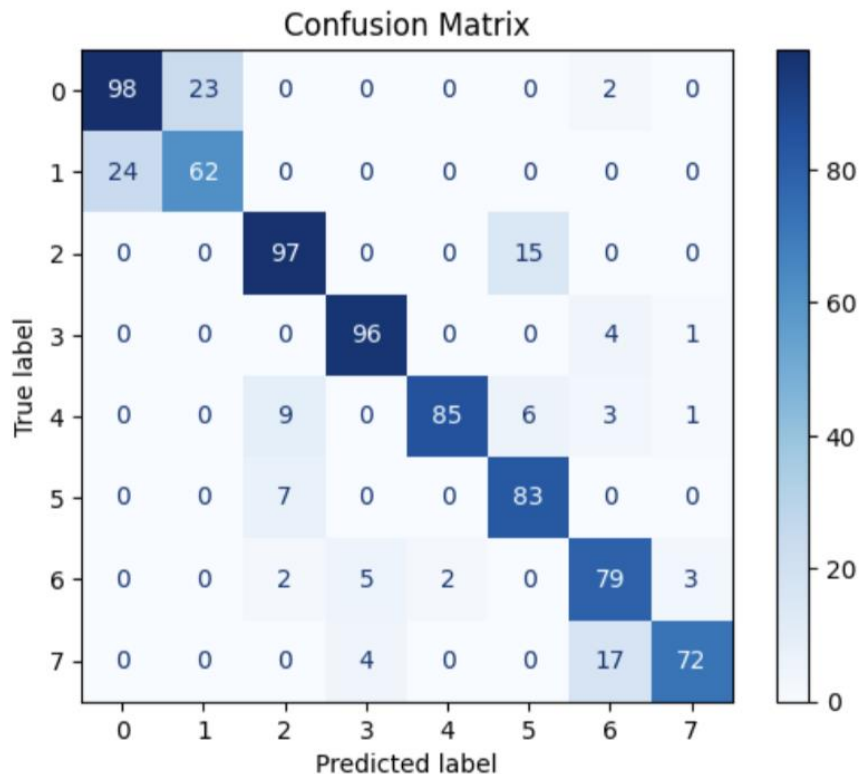


Test Accuracy: 0.8387500047683716

Precision: 0.8441235916451795

Recall: 0.8395125011453841

Model One - VGG16



→ High Correct Predictions:

The model accurately predicted 'dyed-lifted-polyps' (98), 'esophagitis' (97), and 'normal-cecum' (96) with high counts, indicating strong performance in recognizing these classes.

→ Confusion between Similar Classes:

Confusion occurred between 'dyed-lifted-polyps' and 'dyed-resection-margins' (24 instances), and between 'polyps' and 'ulcerative-colitis' (17 instances). This suggests similarities or overlapping features between these classes, leading to misclassifications.

→ Rare Misclassifications:

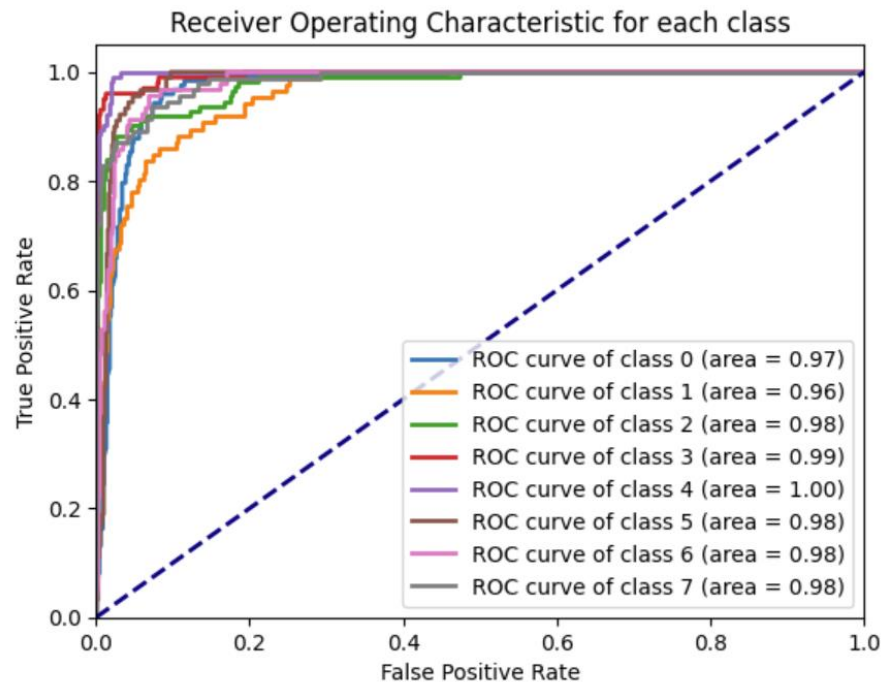
Some classes experienced rare misclassifications, such as 'normal-z-line' being predicted as 'esophagitis' (15 instances) and 'normal-pylorus' being predicted as 'esophagitis' (9 instances), indicating potential areas for model improvement.

Model One - VGG16



ROC Plot

ROC AUC Score: 0.9811764244794556



Model Two - VGG19



Model: "sequential"

Layer (type)	Output Shape	Param #
vgg19 (Functional)	(None, 7, 7, 512)	20024384
flatten (Flatten)	(None, 25088)	0
dense (Dense)	(None, 256)	6422784
dropout (Dropout)	(None, 256)	0
dense_1 (Dense)	(None, 8)	2056

Total params: 26449224 (100.90 MB)

Trainable params: 6424840 (24.51 MB)

Non-trainable params: 20024384 (76.39 MB)

Base Model: Utilizes VGG19, a powerful pre-trained convolutional neural network.

Additional Layers:

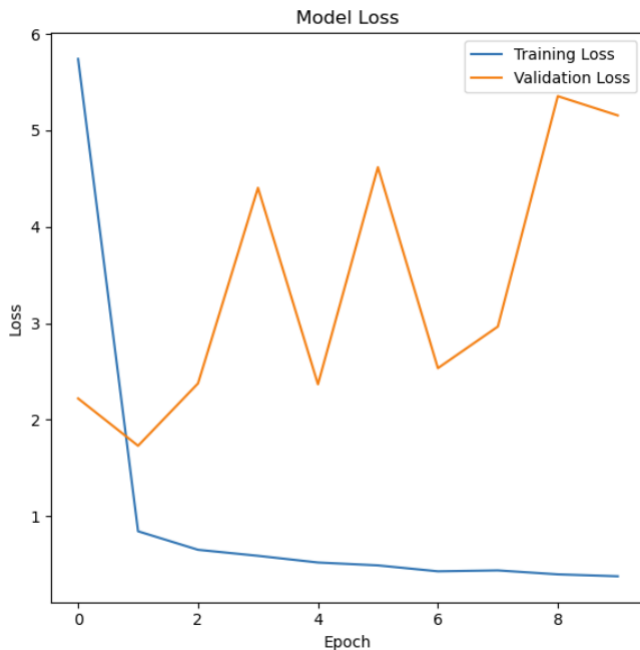
- Flatten Layer: converts the multi-dimensional output of a convolutional or pooling layer into a one-dimensional array or vector.
- Dense Layer: computes a weighted sum of its inputs from the previous layer, adds a bias term, and then applies an activation function.
- Dropout: Prevents overfitting by randomly deactivating some units during training.

Total Parameters: 26,449,224

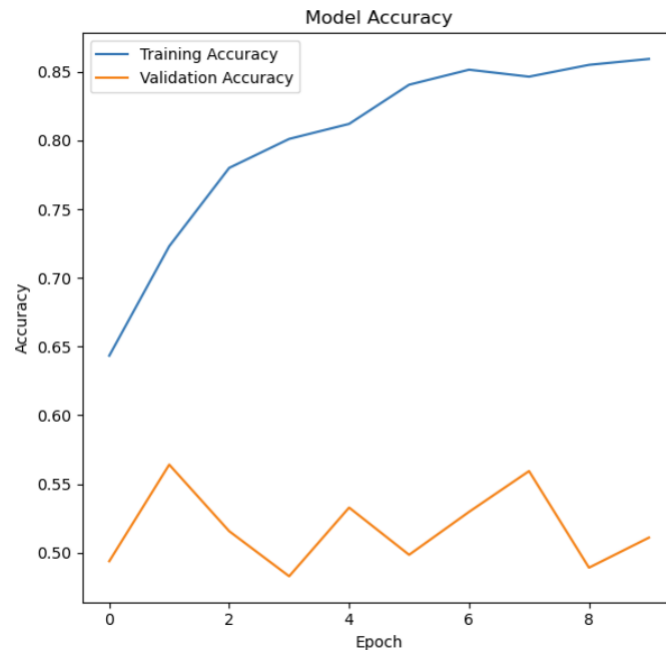
Trainable Parameters: 6,424,840

Non-trainable Parameters: 20,024,384

Model Two - VGG19



Test Accuracy: 0.8512499928474426



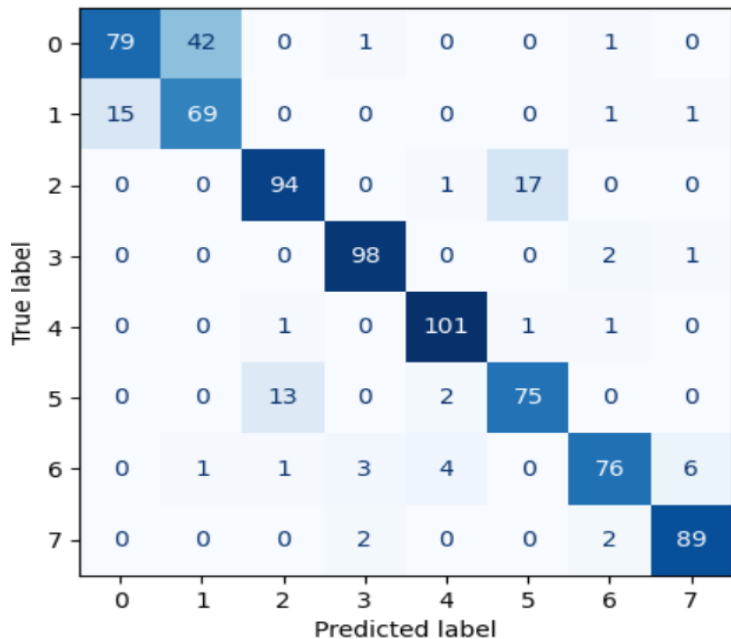
Precision: 0.8545018994727036

Recall: 0.856353251264013

Model Two - VGG19



Confusion Matrix



→ High Correct Predictions:

The model accurately predicted 'normal-pylorus' (101), 'normal-cecum' (98), and esophagitis' (94) with high counts, indicating strong performance in recognizing these classes.

→ Confusion between Similar Classes:

Confusion occurred between 'dyed-lifted-polyps' and 'dyed-resection-margins' (42 instances), and between 'normal-cecum' and 'polyps' (2 instances). This suggests similarities or overlapping features between these classes, leading to misclassifications.

→ Rare Misclassifications:

Some classes experienced rare misclassifications, such as 'normal-z-line' being predicted as 'esophagitis' (17 instances) indicating potential areas for model improvement.

→ Misclassification of Rare Classes:

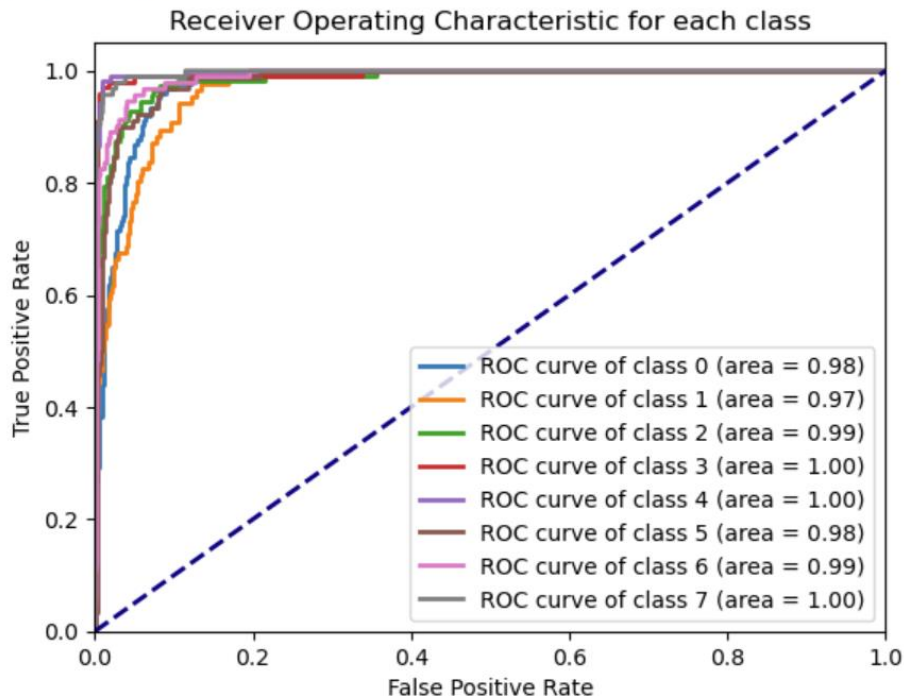
The class 'esophagitis' was occasionally misclassified as 'normal-z-line' (13 instances), possibly due to their similar visual characteristics, requiring further investigation to improve the model's performance on distinguishing between them.

Model Two - VGG19



ROC Plot

ROC AUC Score: 0.9865346411069655



Model Three - RESNET50



Model: "sequential"

Layer (type)	Output Shape	Param #
resnet50 (Functional)	(32, 7, 7, 2048)	23,587,712
flatten (Flatten)	(32, 100352)	0
dense (Dense)	(32, 256)	25,690,368
dropout (Dropout)	(32, 256)	0
dense_1 (Dense)	(32, 8)	2,056

Total params: 100,664,986 (384.01 MB)

Trainable params: 25,692,424 (98.01 MB)

Non-trainable params: 23,587,712 (89.98 MB)

Optimizer params: 51,384,850 (196.02 MB)

Base Model: Utilizes ResNet50, a powerful pre-trained convolutional neural network.

Additional Layers:

- Flatten Layer: converts the multi-dimensional output of a convolutional or pooling layer into a one-dimensional array or vector.
- Dense Layer: computes a weighted sum of its inputs from the previous layer, adds a bias term, and then applies an activation function.
- Dropout: Prevents overfitting by randomly deactivating some units during training.

Total Parameters: 100,664,986

Trainable Parameters: 25,692,424

Non-trainable Parameters: 23,587,712

Model Three - RESNET50

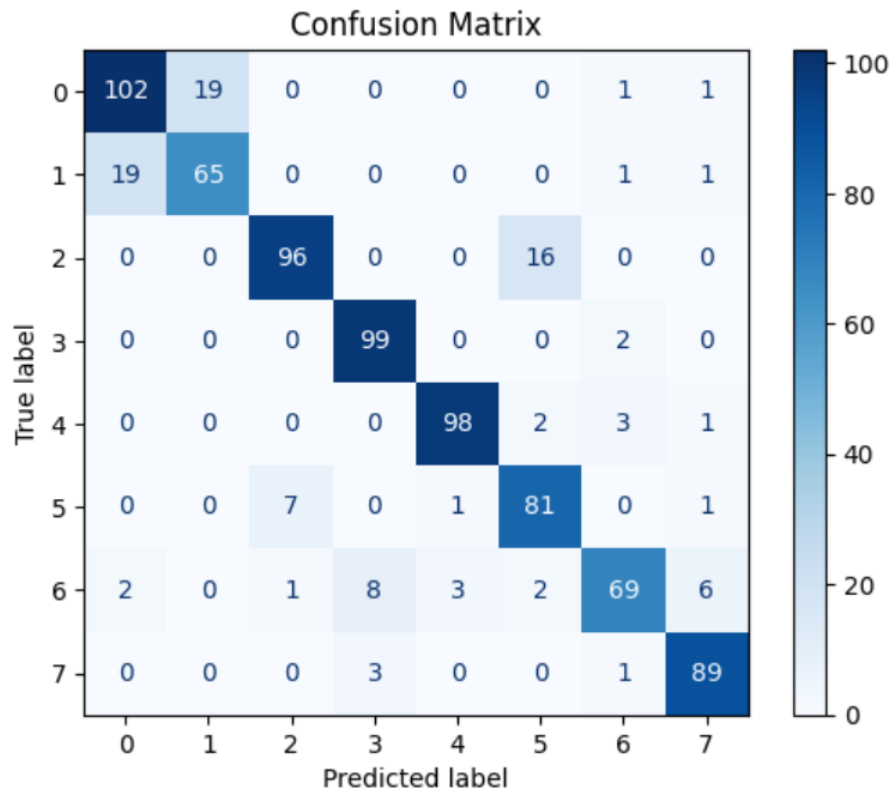


Test Accuracy: 0.8737499713897705

Precision: 0.8730016308010576

Recall: 0.8724952276221769

Model Three - RESNET50



→ High Correct Predictions:

The model accurately predicted 'dyed lifted polyps' (102), 'normal-cecum' (99), and 'normal pylorus' (98) with high counts, indicating strong performance in recognizing these classes.

→ Confusion between Similar Classes:

Confusion occurred between 'dyed-lifted-polyps' and 'dyed-resection-margins' (19 instances), and between 'normal-cecum' and 'ulcerative-colitis' (2 instances). This suggests similarities or overlapping features between these classes, leading to misclassifications.

→ Rare Misclassifications:

Some classes experienced rare misclassifications, such as 'normal-z-line' being predicted as 'esophagitis' (7 instances) and 'polyps' being predicted as 'normal-cecum' (8 instances), indicating potential areas for model improvement.

→ Misclassification of Rare Classes:

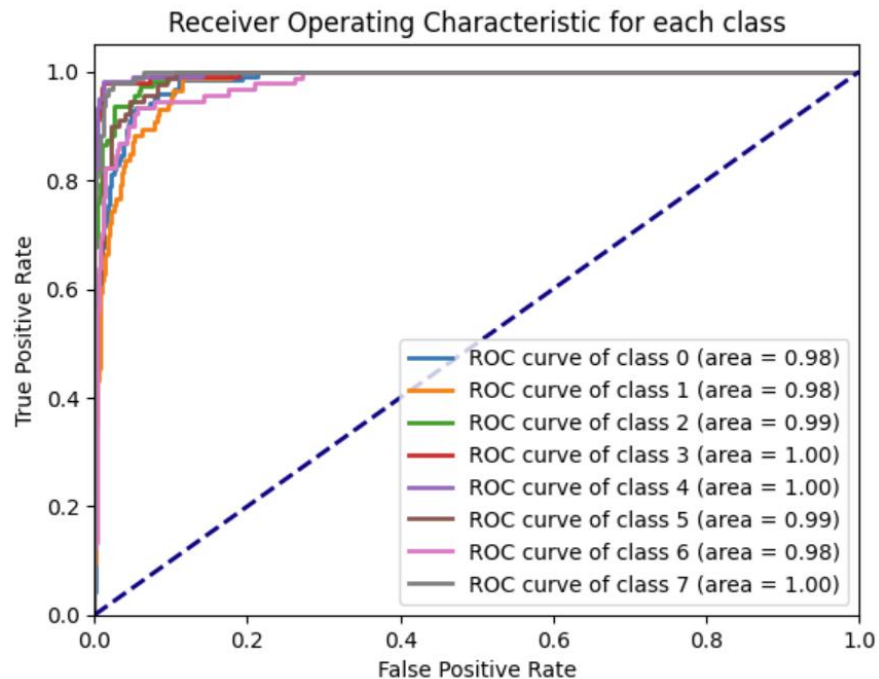
The class 'esophagitis' was occasionally misclassified as 'normal-z-line' (16 instances), possibly due to their similar visual characteristics, requiring further investigation to improve the model's performance on distinguishing between them.

Model Three - RESNET50



ROC Plot

ROC AUC Score: 0.9891276576654061



Model Four - DENSENET121



Model: "sequential"

Layer (type)	Output Shape	Param #
densenet121 (Functional)	(32, 7, 7, 1024)	7,037,504
global_average_pooling2d (GlobalAveragePooling2D)	(32, 1024)	0
dense (Dense)	(32, 256)	262,400
dropout (Dropout)	(32, 256)	0
dense_1 (Dense)	(32, 8)	2,056

Total params: 7,830,874 (29.87 MB)

Trainable params: 264,456 (1.01 MB)

Non-trainable params: 7,037,504 (26.85 MB)

Optimizer params: 528,914 (2.02 MB)

Base Model: Utilizes DenseNet121, a powerful pre-trained convolutional neural network.

Additional Layers:

- GlobalAveragePooling2D: Reduces spatial dimensions while retaining important information.
- Dense Layer: Adds non-linearity to the model with 256 units and ReLU activation function.
- Dropout: Prevents overfitting by randomly deactivating some units during training.

Total Parameters: 7,830,874

Trainable Parameters: 264,456

Non-trainable Parameters: 7,037,504

Model Four - DENSENET121

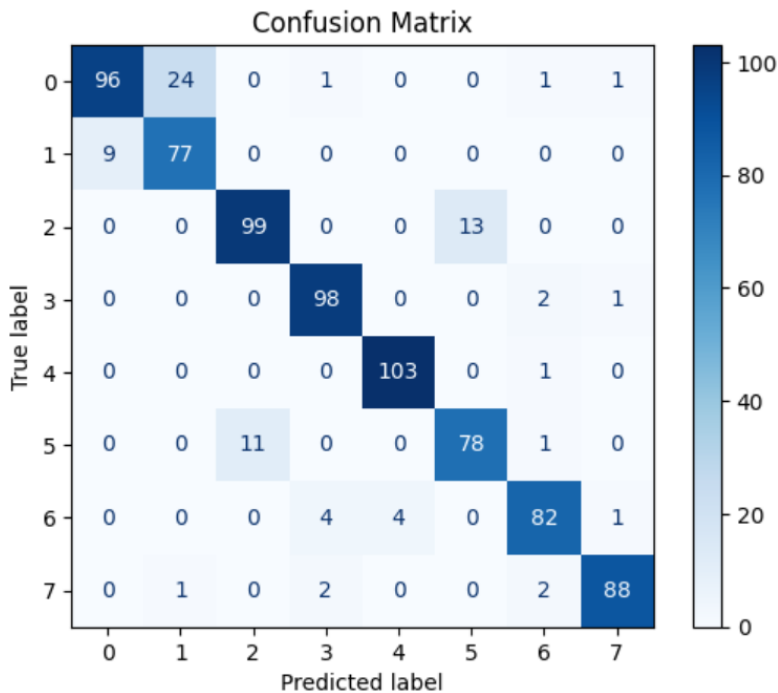


Accuracy: 0.9012500047683716

Precision: 0.9030350354188442

Recall: 0.9058453335771437

Model Four - DENSENET121



→ High Correct Predictions:

The model accurately predicted 'normal-pylorus' (103), and ulcerative-colitis' (88) with high counts, indicating strong performance in recognizing these classes.

→ Confusion between Similar Classes:

Confusion occurred between 'dyed-lifted-polyps' and 'dyed-resection-margins' (24 instances), and between 'normal-cecum' and 'ulcerative-colitis' (2 instances). This suggests similarities or overlapping features between these classes, leading to misclassifications.

→ Rare Misclassifications:

Some classes experienced rare misclassifications, such as 'normal-z-line' being predicted as 'esophagitis' (11 instances) and 'polyps' being predicted as 'normal-cecum' (4 instances), indicating potential areas for model improvement.

→ Misclassification of Rare Classes:

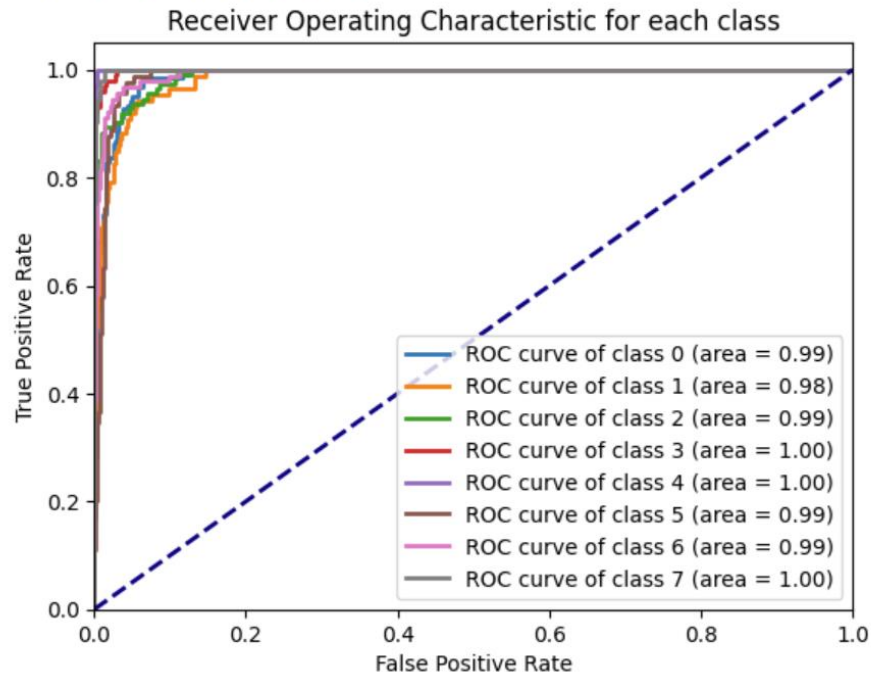
The class 'esophagitis' was occasionally misclassified as 'normal-z-line' (13 instances), possibly due to their similar visual characteristics, requiring further investigation to improve the model's performance on distinguishing between them.

Model Four - DENSENET121



ROC Plot

ROC AUC Score: 0.9930187375286718



Model Five - MOBILENET



Model: "sequential_2"

Layer (type)	Output Shape	Param #
mobilenet_1.00_224 (Functional)	(None, 7, 7, 1024)	3228864
global_average_pooling2d_2 (GlobalAveragePooling2D)	(None, 1024)	0
dense_4 (Dense)	(None, 256)	262400
dropout_2 (Dropout)	(None, 256)	0
dense_5 (Dense)	(None, 8)	2056
Total params: 3493320 (13.33 MB)		
Trainable params: 264456 (1.01 MB)		
Non-trainable params: 3228864 (12.32 MB)		

Base Model: Utilizes Mobilenet, a powerful pre-trained convolutional neural network optimised for mobile applications

Additional Layers:

- **Global_Average_Pooling Layer:** This layer reduces each of the incoming feature map's dimensions to a single value, condensing the spatial information, thus lowering the model's complexity and total parameter count.
- **Dense Layer:** computes a weighted sum of its inputs from the previous layer, adds a bias term, and then applies an activation function.
- **Dropout:** Prevents overfitting by randomly deactivating some units during training.

Total Parameters: 3,493,320

Trainable Parameters: 264,456

Non-trainable Parameters: 3,228,864

Model Five - MOBILENET

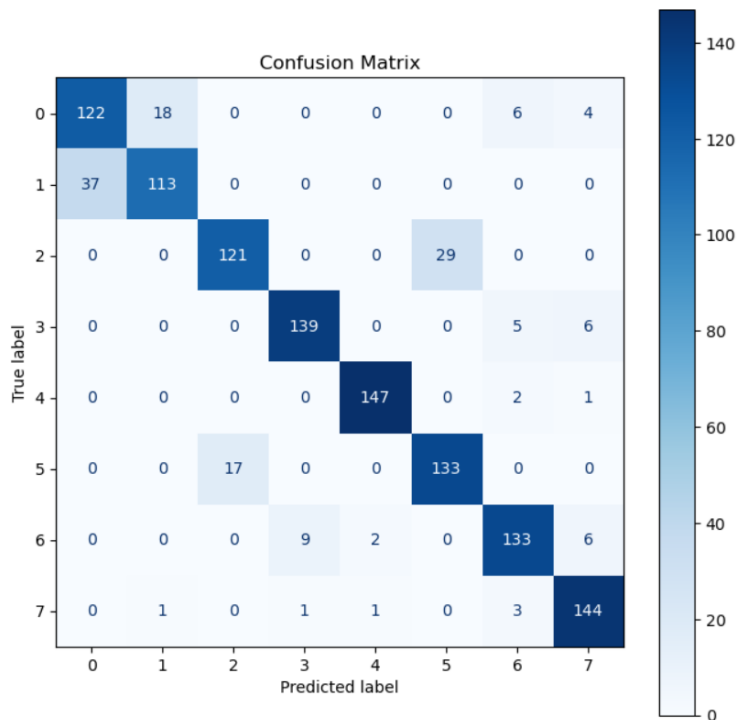


Test Accuracy: 0.8766666650772095

Precision (MobileNet): 0.8776335932077083

Recall (MobileNet): 0.8766666666666667

Model Five - MOBILENET



→ High Correct Predictions:

The model accurately predicted 'normal-pylorus' (147), 'normal-z-line' (133), and ulcerative colitis' (144) with high counts, indicating strong performance in recognizing these classes.

→ Confusion between Similar Classes:

A noticeable confusion was observed between 'esophagitis' and 'normal-z-line' with 29 instances misclassified. Confusion occurred between 'dyed-lifted-polyps' and 'dyed-resection-margins' (37 instances). This pattern has been predominant over the other cases as well.

→ Rare Misclassifications:

There were rare instances of misclassification across various classes, such as 'dyed-lifted-polyps' being mistaken for 'ulcerative-colitis' and 'normal-cecum' confused with 'normal-pylorus', each with a few cases.

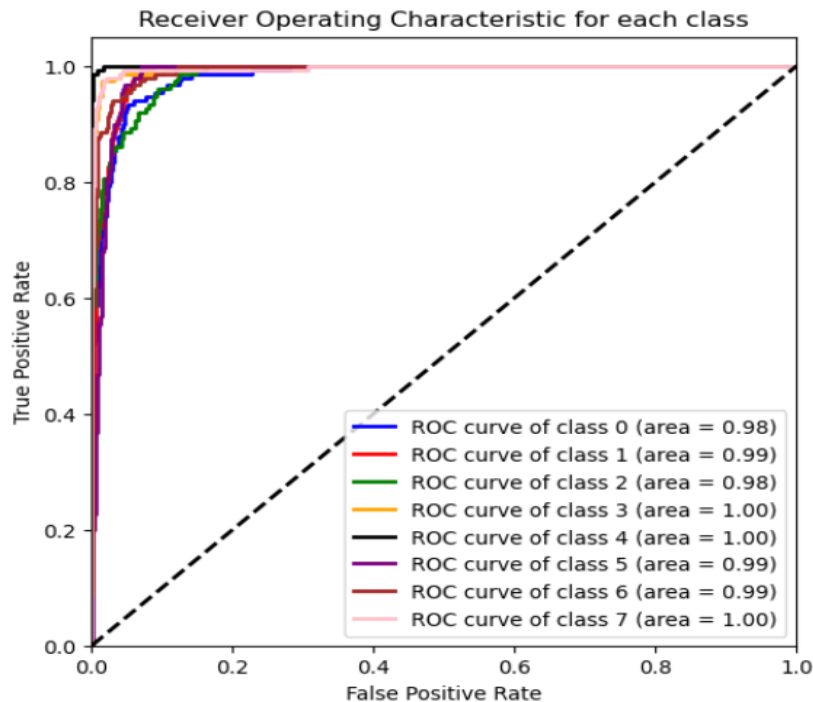
→ Misclassification of Rare Classes:

The class 'esophagitis' was occasionally misclassified as 'normal-z-line' (29 instances), possibly due to their similar visual characteristics, requiring further investigation to improve the model's performance on distinguishing between them.

Model Five - MOBILENET



ROC Plot



Model Six - EFFICIENTNET



Model: "sequential"

Layer (type)	Output Shape	Param #
efficientnetb2 (Functional)	(None, 9, 9, 1408)	7768569
global_average_pooling2d_1 (GlobalAveragePooling2D)	(None, 1408)	0
dense_1 (Dense)	(None, 256)	360704
dropout (Dropout)	(None, 256)	0
dense_2 (Dense)	(None, 8)	2056
Total params: 8131329 (31.02 MB)		
Trainable params: 362760 (1.38 MB)		
Non-trainable params: 7768569 (29.63 MB)		

Base Model: Utilizes efficientNet_B2, a powerful pre-trained convolutional neural network optimised for classification of larger datasets

Additional Layers:

- **Global_Average_Pooling Layer:** This layer reduces each of the incoming feature map's dimensions to a single value, condensing the spatial information, thus lowering the model's complexity and total parameter count.
- **Dense Layer:** computes a weighted sum of its inputs from the previous layer, adds a bias term, and then applies an activation function.
- **Dropout:** Prevents overfitting by randomly deactivating some units during training.

Total Parameters: 8,131,329

Trainable Parameters: 362,760

Non-trainable Parameters: 7,768,569

Model Six - EFFICIENTNET



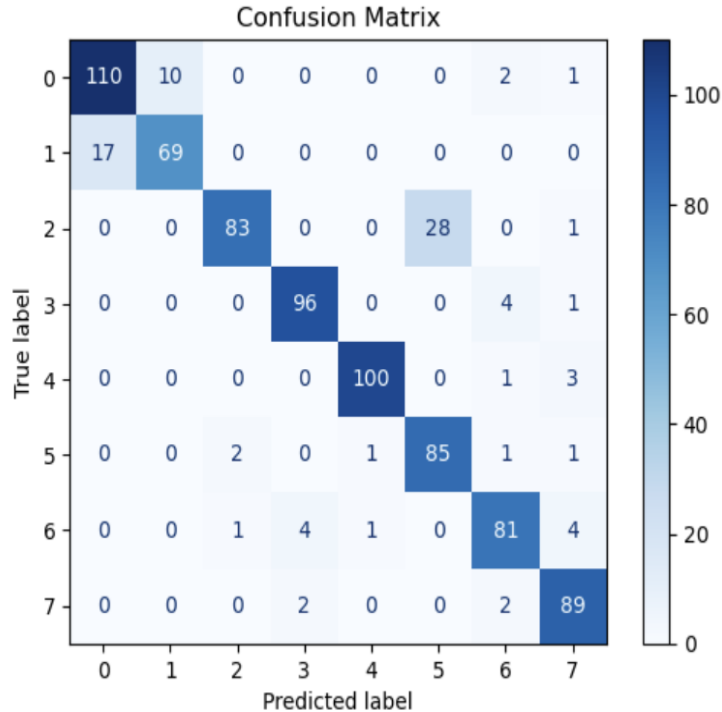
Test Accuracy: 0.8912500143051147

Precision: 0.8948208299767026

Recall: 0.8926603807457228



Model Six - EFFICIENTNET



High Correct Predictions:

- The model accurately predicted 'dyed-lifted-polyps' with 110 correct instances, 'normal-cecum' with 96 instances, and 'normal-pylorus' with 100 instances, showing a strong ability to recognize these classes.

Confusion between Similar Classes:

- There is notable confusion between 'dyed-lifted-polyps' and 'dyed-resection-margins', with 17 instances misclassified as 'dyed-resection-margins'. Additionally, 'normal-cecum' was occasionally mistaken for 'esophagitis' in 28 cases.

Rare Misclassifications:

- Rare misclassifications can be observed in instances where 'dyed-lifted-polyps' were incorrectly predicted as 'ulcerative-colitis', and 'normal-z-line' mistaken for 'normal-cecum', both with only a few cases. These highlight specific instances where the model's performance could be improved.

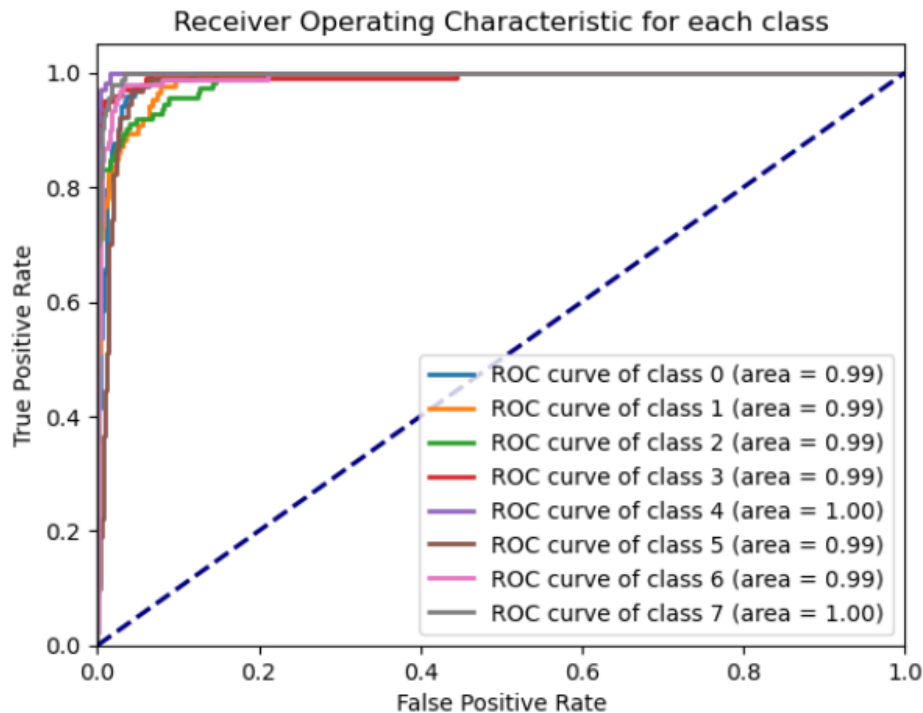
Misclassification of Rare Classes:

- 'Polyps' were sometimes confused with 'normal-pylorus' and 'ulcerative-colitis', with a few misclassifications noted. This misidentification suggests that 'polyps' may share similar characteristics with these classes or that there may be a need for better representation in the training data for 'polyps'.

Model Six - EFFICIENTNET



ROC Plot



Summary



Model Number	Model Name	Test Accuracy	Precision	Recall	Mean Cross Validation Accuracy
1	VGG16	0.839999973	0.8441235916	0.8395125011	0.816015625
2	VGG19	0.851249992	0.8545018994	0.8563532512	0.808984375
3	RESNET50	0.873749971	0.8730016306	0.8724952276	0.847265625
4	DENSENET121	0.901250004	0.9030350354	0.9058453335	0.855078125
5	MOBILENET	0.876666665	0.8776335932	0.8766666667	0.8732265999
6	EFFICIENTNET	0.891250014	0.8948208299	0.8926603807	0.888671875



Conclusion

Our comparative analysis of six models on the KVASIR dataset for gastrointestinal disease prediction has yielded important insights:

- Misclassifications occurred mostly between classes with similar visual characteristics, suggesting a need for improved feature extraction methods.
- Some models have exhibited strength in some classes
- Overall, no single model outperformed the others across all disease classes. The choice of the model should be informed by the specific clinical needs and the prevalence of diseases in the patient population.
- The findings advocate for the potential of using machine learning as a support tool in gastroenterology, promising enhancements in diagnosis accuracy and patient care.

THANK YOU!



Demo





Observations

Misclassifications Analysis:

- Misclassifications primarily occur between classes with similar visual features. For instance, Dyed-Lifted-Polyps (Class 0) and Dyed-Resection-Margins (Class 1) often share similar color and texture once stained, leading to confusion.
- The varying shades and inflammation levels in Esophagitis (Class 2) can resemble the normal tissue appearance, causing confusion with the Normal-Z-Line (Class 5).
- Ulcerative-Colitis (Class 7) can sometimes present with less pronounced visual symptoms, leading to misidentification as Normal-Cecum or Polyps (Class 6), depending on the severity and imaging clarity.



Observations

Model-Specific Performance:

- VGG16 has shown commendable performance in identifying Normal-Cecum (Class 3), with high correct predictions and fewer misclassifications.
- VGG19 has excelled in accurately classifying Normal-Cecum (Class 3) and Normal-Pylorus (Class 4), evidenced by its almost perfect prediction rate.
- ResNet50 has demonstrated strong performance across most classes, with particularly high accuracy for Normal-Cecum (Class 3) and Normal-Pylorus (Class 4).
- DenseNet121 stands out in its ability to distinguish between Normal-Cecum (Class 3), Normal-Pylorus (Class 4) and Ulcerative-Colitis (Class 7) with high accuracy.
- MobileNet offers the best performance for Normal-Pylorus (Class 4) and Ulcerative-Colitis (Class 7), indicating its strength in differentiating subtle textural differences.
- EfficientNet shows an impressive ability to correctly classify Dyed-Lifted-Polyps (Class 0), suggesting it might be best for datasets where this class is predominant.



Observations

Overall Best Model Considerations:

- No single model uniformly outperforms others across all classes; thus, the choice of model may depend on the specific clinical requirements and the prevalence of certain conditions in the target population.
- Ensemble methods that combine predictions from multiple models might be explored to leverage the strengths of individual models, potentially leading to better overall accuracy and robustness.



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