A Comparative Analysis of EfficientNet Architectures for Identifying Anomalies in Endoscopic Images

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Abstract: The gastrointestinal tract is part of the digestive system, fundamental to digestion. Digestive problems can be symptoms of chronic illnesses like cancer and should be treated seriously. Endoscopic exams in the tract make detecting these diseases in their initial stages possible, enabling an effective treatment. Modern endoscopy has evolved into the Wireless Capsule Endoscopy procedure, where patients ingest a capsule with a camera. This type of exam usually exports videos up to 8 hours in length. Support systems for specialists to detect and diagnose pathologies in this type of exam are desired. This work uses a rarely used dataset, the ERS dataset, containing 121.399 labelled images, to evaluate three models from the EfficientNet family of architectures for the binary classification of Endoscopic images. The models were evaluated in a 5-fold cross-validation process. In the experiments, the best results were achieved by EfficientNetB0, achieving average accuracy and F1-Score of, respectively, 77.29% and 84.67%.

1 INTRODUCTION

The gastrointestinal (GI) tract is part of the digestive system, being fundamental in digestion, breaking down food, and absorbing nutrients. Digestive issues such as bloating, constipation, or even diarrhoea can be symptoms of chronic diseases such as cancer and should be treated seriously. Cancers related to the GI tract (esophageal, gastric, and colorectal, for example) are some of the most common worldwide, corresponding to 9.6% of cancer cases in the world, with the second highest mortality rate (IARC/WHO, 2022b).

Worldwide, this type of cancer has the third highest incidence rate but has the second highest mortality rate among cancer types, being more than 8%, with lung cancer being the only one with a higher mortality rate. In Brazil specifically, 27% of the population is afflicted with some disease in the gastrointestinal

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tract. Colorectal cancer is among the three most common types of cancer among the entire Brazilian population, surpassing the number of cases of lung cancer (IARC/WHO, 2022a). The absence of specific symptoms in the initial stages results in delays in the diagnosis and treatment, with the prognosis of this disease being strongly associated with the stage at which it was diagnosed (Yeung et al., 2021).

By examining the interior of the GI tract, cancer can be detected at an early stage, allowing for an effective treatment. The patient survival rate reaches 90% if it is diagnosed at an early stage. However, this proportion drops to 14% in the case of an advancedstage cancer diagnosis (Siegel et al., 2020). Thus, endoscopy is one of the most used techniques for detecting and analyzing anomalies in the GI tract.

However, traditional endoscopies are characterized by being invasive and somewhat painful, and some complications, although rare, can include excessive sedation, perforations, hemorrhages, and infections in general (Kavic and Basson, 2001). Consequently, modern endoscopy has evolved into the Wireless Capsule Endoscopy (WCE) procedure over the past two decades. This exam consists of a patient ingesting a capsule a few millimetres in diameter, coupled with a camera, a light source, a wireless

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transmitter, and a battery. The patient uses a receiver on their waist to receive the images captured by the camera (Bao et al., 2015).

Despite being less uncomfortable for the patient, the sheer amount of details contained in this type of exam makes its analysis excessively time-consuming, with a usual video of about 8 hours requiring around 2 hours to be analyzed by an expert while requiring continuous focus (Hewett et al., 2010). As a result, several details present in the videos may go unnoticed by the expert, with up to 26% of polyps being undetected, depending on the endoscopist's experience, duration of the examination, patient's level of preparation and size of the polyps (Ramsoekh et al., 2010).

Therefore, a support system for the expert to analyze this exam is desirable. Computer-aided detection (CADe) and Diagnosis (CADx) Systems using Artificial Intelligence (AI) techniques have been proposed and used in several medical areas in the last decades (Litjens et al., 2017). Considering WCE images, several works have been published for detecting and diagnosing pathologies such as polyps, hemorrhages, colorectal tumours, and ulcers, among others (Zhuang et al., 2021), using Deep Learning techniques (DL). Thus, this work aims to evaluate convolutional neural network models from the EfficientNet family of architectures for the binary classification of Endoscopic images, focusing on the Endoscopy Recommendation System (ERS) dataset (Cychnerski et al., 2022).

The main contribution of this work is the evaluation of different versions of the EfficientNet architecture for binary classification in endoscopy and colonoscopy images using the ERS dataset, which contains over 100 different kinds of pathologies alongside images of healthy tissue from 6 distinct regions of the GI tract. Unlike the work of Brzeski et al. (Brzeski et al., 2023), which focused on classifying areas with endoscopic bleeding in the ERS dataset, this work considered all labels.

2 RELATED WORK

Recently, the focus of work related to endoscopic image processing has been directed toward WCE images. Muruganantham and Balakrishnan (Muruganantham and Balakrishnan, 2022) presented a two-step method that uses a convolutional network with a self-attention mechanism to estimate the region where a possible lesion would be located. This estimation, used as an attention map, is fused with the processed WCE image to refine the lesion classification process. This work considered ulcers, bleeding, polyps, and healthy classes, obtaining F_1 score values of 95.35%,

94.15%, 97.95%, and 93.55% for each class.

Goel et al. (Goel et al., 2022) proposed an automatic diagnostic method focused on angiodysplasia, polyps, and ulcers on WCE images. The authors presented a dilated convolutional neural network architecture to classify between normal and anomaly images. The authors did not process complete videos of the exams, but rather frames randomly selected and at least 4 frames apart, eliminating redundancies. Some regions of the edges of the images were removed to remove black edges resulting from the capsule camera capture process, which do not influence the presence or absence of pathology. Finally, by using a dilated convolutional neural network (i.e., with a particular spacing between the pixels of the convolution windows), it was possible to increase the receptive field of the network without the need to increase the number of parameters. The authors obtained an accuracy of 96%, sensitivity of 93%, and specificity of 97% using a private dataset.

The work of Yu et al. (Yu et al., 2022) presents a multitask model for classification (treated as an information retrieval task) and segmentation of pathologies in traditional gastroscopy images. The model shares characteristics between tasks, including individual characteristics for each one, aiming to improve the performance of each task. The information retrieval task determines whether an image has the presence of cancer, esophagitis, or no abnormalities, using a *deep retrieval* module (Lin et al., 2015). This module encodes image characteristics into a binary sequence and then performs similarity queries to determine the class of the analyzed image. The segmentation task uses a segmentation architecture inspired by SegFormer (Xie et al., 2021), which is a segmentation model based on Transformer (Dosovitskiy et al., 2020). Considering the classification task, the proposed method achieved 96.76% accuracy while achieving 82.47% F1 score for segmentation on a private dataset.

Ma et al. (Ma et al., 2023) also proposed a method to classify and segment pathologies in endoscopic images. The authors use their private dataset, which contains standard gastroscopic images and the presence of early-stage gastric cancer. The authors modified the ResNet-50 (He et al., 2016) architecture based on a guided attention inference network (Li et al., 2018) for the classification task between these two classes. On a private dataset, the authors achieved 98.84% accuracy and 98.18% *F1 Score* for classification and a Jaccard index value of 0.64 for segmentation.

Fonseca et al. (Fonseca et al., 2022) presented binary classification experiments (healthy and abnormal) on WCE images using three different convolutional neural network architectures. In the tests carried out, ResNet-50 obtained the best performance among the used models, reaching 98% and 81% of F_1 values for healthy and abnormal images, respectively, obtaining satisfactory results when working with a relatively small dataset.

The work of Brzeski et al. (Brzeski et al., 2023), the only other work in the literature that used the ERS dataset for the classification task, proposed a method for the binary classification of endoscopic bleeding. The authors defined high-level visual features to incorporate domain knowledge into deep learning models. The extracted features generated by the proposed feature descriptors were concatenated with the respective images and provided as input to the convolutional neural network architectures during the training and inference processes. The authors carried out experiments with the VGG19 (Simonyan and Zisserman, 2014), ResNet-50, ResNet-152, and Inception-V3 (Szegedy et al., 2016) architectures, with a performance improvement when including the high-level features in the first three architectures, reaching RO-CAUC values of up to 0.963.

Work involving the classification of endoscopic images in the literature tends to use datasets with a limited number of pathologies, usually focusing on images with the presence and absence of ulcers, polyps and bleeding alongside healthy images. Furthermore, the work by Brzeski et al., despite using the ERS dataset, focused only on images with endoscopic bleeding. Therefore, the difference in this work was the use of all pathologies present in the ERS dataset, in addition to considering images from both endoscopy and colonoscopy for the binary classification between healthy images and those with anomalies.

3 MATERIALS AND METHOD

3.1 Dataset

The ERS (Endoscopy Recommendation System) dataset (Cychnerski et al., 2022) contains 5,970 images labelled by experts from 1,136 different patients. This dataset was proposed to meet a need of the MAY-DAY 2012 (Blokus et al., 2012) project, where an attempt was made to create an ensemble of specialized classifiers for endoscopic video images. As part of a more extensive application, those classifiers were trained for multi-class classification and ROI detection to detect locations where potential diseases could occur.

Since this is a high-demand task for endoscopists

analyzing WCE videos, the authors tried to span numerous sets of endoscopic diagnosis, using terminology according to the Minimal Standard Terminology (MST 3.0) (Aabakken et al., 2009). This resulted in 27 types of colonoscopic findings and 54 findings regarding upper endoscopy pathologies. The dataset also included three miscellaneous terms applicable in machine learning applications: healthy GI tract tissues, image quality attributes, and images with endoscopic bleeding.

All terms collected were then separated into five distinct categories, namely:

- Gastro: Anomalies categorized according to MST 3.0 related to pathologies localizable by upper endoscopies, totalling 70 terms;
- **Colono:** Anomalies also categorized according to MST 3.0, but concerning pathologies that colono-scopies can detect, totalling 34 terms;
- Healthy: Labels of regions with no anomalies detected, totalling seven terms (which identity which region the image was captured from);
- **Blood:** Information indicating the presence of blood in the image, totalling two terms (presence and absence of bleeding);
- **Quality:** Categories referring to the quality of the endoscopic image (blurring, lack of focus, excessive light, etc.), as well as excess material in the image (such as undigested food, bile, feces, etc.), totalling ten terms.

Figure 1 presents an example of each category. The example of Gastro (1a) presents a frame of a case of duodenal ulcer. The example of Colono (1b) illustrates a case of Chrohns disease. The Healthy example (1c) is an esophagus image. An example of Blood is presented in 1d. Notably, all images in this category are labelled with a Gastro or Colono class. Finally, the Quality example (1e) is an image with low lighting.

Figure 2 presents other image examples from this dataset. The numbers in the upper left corner indicate the frame number from the respective exam video. The marked region shows the location of the anomaly contained in the image. The colour of numbers and markings indicate whether annotations are "Precise" or "Imprecise". Precise marks (in yellow, at frames 116, 12, and 180) were annotated by experts. The Imprecise ones (in blue, composed of the remaining frames) were defined using the neighbouring frames to those marked by experts, in which the authors performed a visual analysis and adjusted the binary mask to match the region of interest visually.

The dataset contains 115,429 images with labels categorized as Imprecise, significantly more than the



Figure 2: Example of images contained in the ERS dataset (Cychnerski et al., 2022).

number of images labelled by experts. Due to their high abundance, however, imprecise images can be instrumental in the training process of a deep learning model, even with lower label accuracy. Furthermore, the dataset has 866,612 images without any annotations and 366,656 images from 7 WCE exams with no labels.

In this dataset, images are split by patient, and each patient can contain images from up to six different exam videos. Each image may be associated with 0 or more labels (characterizing a multi-label dataset), in addition to the possibility of having a binary mask with the location of the finding for segmentation or object detection applications. Finally, each image is stored as a PNG file in the RGB colour space with an original resolution of 720x576.

3.2 EfficientNet

EfficientNet is a family of CNN architectures proposed by Tan and Le (Tan and Le, 2019), recognized for its high performance in image classification challenges such as ImageNet and ImageNet-V2 (Recht et al., 2019). The authors developed these architectures by combining coefficients to scale the network structure (the number of convolutional layers and their respective number of filters). This scaling process, defined as Compound Scaling, was done through a heuristic method based on *Grid Search*, which uniformly adjusts the width and depth of the network structure and regulates the feature maps from a fixed set of scale coefficients. Such coefficients are presented in the Equation 1:

$$\begin{cases} d = \alpha^{\phi} \\ w = \beta^{\phi} \\ r = \gamma^{\phi} \end{cases}$$
(1)

Where:

- d: Depth;
- *w*: Width;
- r: Image resolution;
- \$\overline\$: Coefficient that represents the amount of available computational resources, defined by the user;

The α , β , and γ coefficients define how the resources will be assigned in relation to depth, width, and resolution, respectively. These coefficients must assume values greater than or equal to 1, subject to the restriction presented in Equation 2:

$$\alpha \cdot \beta^2 \cdot \gamma^2 \approx 2 \tag{2}$$

These parameters can be estimated in 2 ways:

- 1. Assuming $\phi = 1$ and estimating α, β and γ ;
- 2. Assuming α, β and γ as constants and estimating different values of ϕ .

The EfficientNet family of networks was defined by this scaling method, being named from B0 to B7. The structure of these networks is composed of blocks called *MBConv*, being characterized by a combination between the Inverted BottleNecks (IB) (Sandler et al., 2018) and the Squeeze-and-Excitation (SAE) blocks (Hu et al., 2018). The IBs use depth-wise convolutions (DWConv) as alternatives to standard convolutions to reduce the computational cost of these operations since DWConv operations have a smaller amount of parameters to be adjusted (Howard et al., 2017).



Figure 3: Structure of the MBConv and SAE blocks.

Figure 3 illustrates the structure of the *MBConv* block and the SAE block. The input dimensions of the *MBConv* blocks are $H \times W \times F$, where H is the

height, W is the width, and F is the number of feature maps. More feature maps are generated after the first 1x1 convolution (followed by Batch Normalization and a Relu activation). This increases by a scaling factor S that multiplies F. Afterwards, the DWConv operations are applied, generating another increase in the number of feature maps, which will be used as input to the SAE block.

The SAE blocks, illustrated in Figure 3, assign weights to feature maps that are more relevant to the model's objective and will have greater weights. Finally, a last 1x1 convolution decreases the number of feature maps, assuming its initial value.

In this work, these models were chosen because they have comparatively lower computational costs (requiring fewer FLOPS in the inference process and with fewer adjustable parameters) and have better performances considering the top-1 and top-5 accuracy metrics in ImageNet (Recht et al., 2019), compared to other well-known CNN architectures. The experiments conducted in this work involving EfficientNet considered configurations from B0 to B3.

4 RESULTS AND DISCUSSION

4.1 Experiment Description

To conduct the experiments to evaluate the Efficient-Net architectures in the binary classification of endoscopic images, the same approach as (Cychnerski et al., 2022) was used to separate the images into healthy and anomaly classes. In this approach, images were selected from the **Healthy** categories and images without bleeding from the **Blood** category to compose the set of healthy images, and images from both the **Gastro** and **Colono** categories as well as images with bleeding from the **Blood** category composed the subset of images with pathologies.

A cross-validation method using five folds was used. The folds were separated per patient to ensure that exams from the same patient were not in separate folds to avoid data leakage (Kaufman et al., 2012). During each cross-validation stage, 20% of patients from the training set were randomly selected for validation. As each patient has a different number of exams, the absolute number of images for each fold will differ for each step. For the experiments, precise and imprecise images were used to train and validate the proposed models. For the evaluation, however, only precise images were utilized.

Each model was trained for 25 epochs using Binary Cross-Entropy (Yi-de et al., 2004) as the loss function, with the input resolutions ranging from 224x224 to 300x300, depending on which model was being trained. The network weights were initialized with the pre-trained weights on ImageNet (Recht et al., 2019), available through Keras (Chollet et al., 2015).

To evaluate the performance of each trained model, the Binary Accuracy value was used, as well as the *F1-Score* metric. This metric represents the harmonic mean of precision, the ratio of all true positives to all positive values returned, and sensitivity, which represents the ratio of true positives returned to all positive values present. This metric can be calculated as in Equation 3:

$$F_1 = 2\frac{precision * recall}{precision + recall} = \frac{2tp}{2tp + fp + fn}$$
(3)

With tp being the true positives, that is, the images with correctly classified anomalies; fp being the false positives, with the healthy images being incorrectly classified; and fn being the false negatives, these being the images with anomalies classified as healthy. F_1 values vary between 0 and 1, with higher values indicating better results for the model.

The only work in the literature that can be compared to the obtained results is (Cychnerski et al., 2022), in which the ERS dataset was published. In that work, the authors conducted some experiments to serve as a baseline for comparison. In the case of binary classification, the authors tested several deep neural network architectures, with MobileNet v1 (Sandler et al., 2018) obtaining the best result. The same cross-validation process was used for MobileNet v1, using the same five folds for a fair comparison.

4.2 **Results**

Table 1 compares the average results obtained with MobileNetV1 and different EfficientNet configurations (B0-B3) using the same cross-validation method and folds for each architecture. Each EfficientNet configuration uses a different input image resolution (as shown in the table), while the MobileNetV1 model was trained with 240x240 resolution images. Notably, all the different trained EfficientNet configurations obtained better results than the trained MobileNetV1 model, with differences of 8 to 15 percentage points in the average Accuracy and 8 to 11 percentage points in the average F1-Score. The standard deviation for the Precision metric with MobileNet was also significantly higher, resulting in a higher standard deviation for the F1-Score.

When analyzing the results between the Efficient-Net configurations, it is noticeable that the simplest configuration (B0 with the lowest resolution) obtained better results than the others regarding almost all metrics, with differences varying between 2 and 3 percentage points considering the F1-Score (with practically the same standard deviation).

In Table 2, we have the results for each individual fold of the cross-validation using EfficientNetB0, which was the best-performing variation of the tested architectures during the experiments. The Accuracy, Precision, Recall, and F1-Score values for each test fold and the mean and standard deviation for each in this experiment are presented. The results are promising, reaching average values above 76% in all metrics. However, the model's difficulty in correctly classifying healthy images is notable, as evidenced by the low precision in fold 5, resulting in a relatively high standard deviation for this metric. This also resulted in an accuracy value lower than the F1-Score achieved due to more false positives and, consequently, a lower number of true negatives (correctly classified healthy images). However, the model performed better in correctly classifying images with anomalies, with F1-Scores reaching 88.14% in fold 1 and obtaining an average of 84.67%.

4.3 Case Study

Aiming to understand better the performance of EfficientNet in classifying images from the ERS dataset, we selected the model that performed best during the experiments (EfficientNetB0 trained with folds 2-5) and verified which images the model had the most success and difficulties. To achieve this, we analyzed the model outputs for the test set. We selected the images for which the model generated the highest and lowest probabilities for correct and incorrect predictions for both the positive and negative classes.

In Figure 4, we have examples of positive classifications by the model. In Figure 4a and Figure 4c, we have the predictions with the highest probability for anomalies, for true positives and false positives, respectively. Similarly, the lowest probability model outputs for the positive class are presented in 4b and 4d. The positive case with the highest probability was a polyp in the colon region. This was probably an easy example of classification for the model because it was a frame with a very visually evident polyp. The case of the correct positive prediction with the lowest probability is an image of a duodenal ulcer. It is noticeable that there are bubbles in the image in this particular frame, which can complicate the model's inference process. However, it was still able to classify this example correctly.

Both examples of false positives are images of the

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Model	Resolution	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
EfficientNetB3	300x300	70.45 ± 4.64	69.84 ± 5.31	$\textbf{96.85} \pm \textbf{0.94}$	81.04 ± 3.63
EfficientNetB2	260x260	74.32 ± 5.44	75.04 ± 5.88	91.71 ± 3.44	82.40 ± 3.95
EfficientNetB1	240x240	73.81 ± 5.62	74.38 ± 5.67	92.26 ± 2.63	82.23 ± 3.87
EfficientNetB0	224x224	$\textbf{77.29} \pm \textbf{5.44}$	$\textbf{76.52} \pm \textbf{6.08}$	95.21 ± 1.42	$\textbf{84.67} \pm \textbf{3.51}$
MobileNetV1	240x240	61.93 ± 6.41	66.88 ± 6.85	83.88 ± 15.78	73.55 ± 7.79

Table 1: Comparison between different EfficientNet architectures and MobileNetV1.

Table 2: Results for cross-validation with EfficientNetB0.

Fold	Acc (%)	Precision (%)	Recall (%)	F1-Score (%)
Fold 1	84.46	81.95	95.35	88.14
Fold 2	78.19	78.90	95.78	86.53
Fold 3	74.05	74.07	94.98	83.23
Fold 4	80.86	81.89	92.78	87.00
Fold 5	68.89	65.78	97.17	78.45
Mean	77.29 ± 5.40	76.52 ± 6.08	9521 ± 142	84.67 ± 3.51

colon region, even though most healthy images in this dataset are from colonoscopies. The case in 4c probably resulted in a high probability for the class of pathologies due to the yellow spots along the tract tissue, which the model may have identified as features of some anomaly. The image presented in 4d generated a false positive, possibly because it is a lowquality image with some visual artifacts that could have been confused with pathology features.





(c) Maximum false positive. (d) Minimum false positive. Figure 4: Examples of predictions (correct and incorrect) as pathologies.

To visualize the network's decision process, the Grad-CAM algorithm (Selvaraju et al., 2016) was used to plot heatmaps that highlight the regions most crucial for target class prediction. This algorithm was applied to both the correct and incorrect cases presented previously to understand better the model's strengths and difficulties in detecting anomalies. Figure 5 shows the activation mappings of the last convolutional layer of EfficientNetB0 plotted over the corresponding images of the positive class. In 5a and 5b, it can be seen that the emphasis is around the lesion region, and in the case of 5b, little focus was given to the area with bubbles. For the case in 5c, it can be seen that the entire region with the yellow marks was highlighted, so, in fact, this was mistaken for a lesion. Finally, in 5d, it is noted that a small region in the middle of the image has been highlighted, but nothing particularly notable occurs in this location.



(a) Maximum true positive. (b) Minimum true positive.



(c) Maximum false positive. (d) Minimum false positive. Figure 5: Heatmaps mapping the activation for the positive class.

Similarly to the previous figure, in Figure 6, we have examples of the model's negative classifications, that is, predictions of healthy images. In 6a and 6b, we have the frames that had the highest and lowest probabilities for the negative class, respectively. This probability was given as 1 - p, with p being the probability for the positive class. Both cases are from images of healthy tissue from the colon region. In contrast, the low probability of healthy tissue in Figure

6b may be a consequence of the areas with high luminosity in the lower part of the image. Figures 6c and 6d, also parallel to the previous examples, are the frames that had the highest and lowest probabilities for the negative class, respectively, but were mistakenly classified as pathologies by the model. In Figure 6c, the model failed to recognize the region with a polyp in the frame, probably attributing more significant importance to the areas of healthy tissue in the image. In 6d, we have a severe case of false negative, where the pathology is significantly visually evident. Still, the probability of the positive class did not exceed the classification threshold and, therefore, was erroneously classified as healthy.





(c) Maximum false negative. (d) Minimum false negative. Figure 6: Examples of predictions (correct and incorrect) as healthy images.

As was done for positive examples, the Grad-CAM algorithm was also used to visualize the decision process in the classification examples for the healthy class. To this end, the gradient of the output of the network's last convolutional layer was also considered regarding the probability of the negative class, that is, 1 - p, as previously described. Figure 7 presents the output of Grad-CAM for the presented instances of classifications for the healthy class. In 7a, it can be seen that the activation for the healthy class in this frame is in the center of the image, coinciding with the incidence of light from the colonoscopic device and assigning less focus to the darker parts of the image. Something similar happens in 7b, and contrary to what was supposed, the regions with the highest incidence of light were the most important

for the model's decision in this classification.



(a) Maximum true negative. (b) Minimum true negative.



(c) Maximum false negative. (d) Minimum false negative. Figure 7: Heatmaps mapping the activation for the negative class.

For cases of incorrect classifications, 7c indicates that the model assigned similar importance to a significant portion of the image, including the region containing the polyp, pointing out that anomalies with these features may be a weakness of this model. Furthermore, the frame in 7d, despite pointing out that little importance was given to the region where the anomaly occurs for classification as a healthy image, the rest of the image had enough healthy tissue features to warrant a negative classification from the model.

4.4 Impact of Mislabeling

Finally, when carefully checking the labels assigned to the images used in the experiments, a problem was noticed in the separation chosen for healthy images and those with pathologies. In the same way as the binary classification experiments carried out in (Cychnerski et al., 2022), images were selected from the **Healthy** categories and images without bleeding from the **Blood** category to compose the set of healthy images. However, it was noted that 3 images (frame 4 of patient 12, and frames 1 and 2 from patient 944, all from the Precise subset) in the dataset were labelled both as "No blood" and as an anomaly in the **Gastro** or **Colono** category, which resulted in the same image being labelled as both healthy and unhealthy. Figure 8 shows the 3 frames where this occurred. The first frame is a colonoscopy exam, while the last two frames occur one after the other in another upper endoscopy exam. Interestingly, the three frames present cases of polyps.



(a) Frame 4 of patient 12.



(b) Frame 1 of patient 944.(c) Frame 2 of patient 944.Figure 8: Frames labelled both positive and negative.

The EfficientNetB0 model trained with folds 2-5 of the cross-validation process presented previously was also tested to evaluate the possible impact of this mislabeling during the experiments. The probability assigned to the positive class was verified. For the first image, a probability of 0.4656 was assigned, which would result in a wrong classification considering the threshold of 0.5 used in this work. For the other two images, the model assigned values of 0.6025 and 0.7797, respectively, correctly classifying the frames as pathologies. It is assumed that these cases harmed the learning of the model for pathology cases, in particular for polyp cases, even more so since the Keras API dealt with the situation of the same instance with multiple labels in a binary classification, keeping the last assigned label, which in turn was "healthy" for the 3 frames.

5 CONCLUSIONS

Various diseases in the gastrointestinal tract can be detected and prevented through CADe and CADx systems applied to endoscopic exam images. The automatic early identification of pathologies present in WCE exams can assist physicians in efficiently treating their patients. This work evaluated the performance of networks from the EfficientNet family of architectures for binary classification in WCE images. The experiments were conducted using an extensive dataset not used in the literature, and their results were compared with the benchmark presented by the dataset's authors.

The results indicate that the simplest Efficient-Net configurations obtained better results for binary classification, but all the results were superior to the best results obtained by the dataset authors. The values of the analyzed metrics indicate promising results for classifying anomalies in WCE images. Still, it is essential to highlight that no studies involving other possible tasks with this dataset, such as detecting pathologies in images or multiclass classification.

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