# The EndoTect 2020 Challenge: Evaluation and Comparison of Classification, Segmentation and Inference Time for Endoscopy

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Abstract. The EndoTect challenge at the International Conference on Pattern Recognition 2020 aims to motivate the development of algorithms that aid medical experts in finding anomalies that commonly occur in the gastrointestinal tract. Using HyperKvasir, a large dataset containing images taken from several endoscopies, the participants competed in three tasks. Each task focuses on a specific requirement for making it useful in a real-world medical scenario. The tasks are (i) high classification performance in terms of prediction accuracy, (ii) efficient classification measured by the number of images classified per second, and (iii) pixel-level segmentation of specific anomalies. Hopefully, this can motivate different computer science researchers to help benchmark a crucial component of a future computer-aided diagnosis system, which in turn, could potentially save human lives.

**Keywords:** GI endoscopy · Anomaly detection · Segmentation · Accuracy · Efficient processing · Challenge.

# 1 Introduction

The human digestive system is prone to suffer from many different diseases and abnormalities throughout a human lifetime. Some of these may be lifethreatening and pose a severe risk to a patient's health and well-being. In most cases, if the detection of lethal disease is done early enough, it can be treated with a high chance of being fully healed. Therefore, it is important that all lesions are identified and reported during a routine investigation of the gastrointestinal (GI) tract. Currently, the gold-standard in performing these investigations is through video endoscopies, which is a procedure involving a small camera attached to a tube that is inserted either orally or rectally. However, there is one major downside to this procedure. The method is highly dependent on the skills and experience of the person operating the endoscope, which in turn results in a high operator variation and performance [18, 28, 47]. This is one of the reasons for high miss-rates when measuring polyp detection performance, with some miss-rates

being as high as 20% [25]. Polyps are small mushroom-like growths that appear on the inner-lining of the GI wall and are the leading cause to colorectal cancer.

Automated detection of GI anomalies has been a research topic for at least two decades, and in the last few years, there have been various AI-based solutions have been proposed using both hand-crafted features and representation learning methods (such as neural networks). However, even though there are many approaches for detecting [1, 4, 7, 13, 32, 33, 35, 37, 42, 45, 48, 44] and segmenting [23, 24, 14] GI findings, even some targeting real-time analysis [2, 39, 40], there is room for improvement. One popular way of benchmarking and improving the state-of-the-art in machine learning is through publicly hosted challenges that motivate researchers to contribute to a use-case they otherwise would not work on. For GI automatic image and video analysis, there have been several such challenges hosted the last few years [19, 38, 41, 3], with each bringing new insights into the current state of the field.

This year, we present three different tasks for participants to complete. The tasks are as follows: (i) The *detection* task which aims for high classification accuracy among 23 different classes, (ii) the *efficient detection* task which targets real-time performance for the same 23 classes of the *detection* task, and (iii) the *segmentation* task that aims to segment polyps in GI images. To participate, the teams had to solve at least one of the provided tasks. Overall, six teams participated, where all participants, in one way or another, utilize deep neural networks to solve the provided tasks. The results vary between teams, but most are able to achieve satisfactory scores in terms of what is suitable for use in clinics [36].

We see this as an opportunity to aid medical doctors by helping them detect lesions through automatic frame analysis done live during endoscopy examinations. The pattern recognition community has a lot of knowledge that could assist in this task, making this challenge a perfect fit for the International Conference on Pattern Recognition (ICPR). The work done in this competition, detecting and segmenting medical findings in the GI tract, has the potential of making a real societal impact, as it directly affects the quality of care that healthcare professionals can provide.

# 2 Dataset Details

For this challenge, we provided the participants with a development dataset that was to be used to train their algorithms. This year, we provided HyperKvasir [6], which is a large GI dataset consisting of labeled and unlabeled images taken from several different GI endoscopies. The dataset is split into four distinct parts; Labeled image data, unlabeled image data, segmented image data, and annotated video data. In total, the dataset contains 110,079 images (see Figure 1 for examples) and 374 videos where it captures anatomical landmarks, pathological findings, and normal findings. The result is more than one million images and video frames altogether.



Fig. 1: One example taken from each of the classes contained within the development dataset.

For the *detection* and *efficient detection* tasks, participants used the 23 classes provided in the labeled part of the dataset to develop their algorithms. The number of images per class is not balanced, which is a general challenge in the medical field due to the fact that some findings occur more often than others. This adds an additional challenge for researchers since methods applied to the data should also be able to learn from a small amount of training data. The participants could also use the unlabeled part of the dataset to further improve their algorithm by using, for example, a student-teacher approach or the pseudo labels provided in the HyperKvasir GitHub repository<sup>4</sup>.

For the *segmentation* task, we provide the original image, a segmentation mask, and a bounding box for 1,000 images containing polyps. An example is shown in Figure 2, where we see six samples taken from the segmentation dataset. For the image masks, the white pixels depict the area of the image containing a

<sup>&</sup>lt;sup>4</sup> https://github.com/simula/hyper-kvasir



Fig. 2: Some example images of polyps and their corresponding masks and bounding boxes.

polyp, while the black background pixels do not. The bounding box is defined as the outermost pixels of the found polyp.

## 3 Tasks

With the end-goal of helping medical experts detect more lesions, we present three different tasks that each target a different requirement for in-clinic use. In the following, we give a detailed description of each task and describe how each was evaluated using the appropriate metrics. The script used to evaluate each task is on GitHub<sup>5</sup>.

## 3.1 Detection Task

The detection task stems from the requirement of the high detection accuracy needed to be viable for use in a clinical setting. Participants are asked to develop algorithms that achieve high classification scores on the 23 different classes present in the labeled part of the development dataset (further described in Section 2). Submissions to this task was a comma-separated values (CSV) file, where each line contained the filename of the predicted image in the test dataset, the predicted label, and a confidence score ranging from 0 to 1 for the predicted label.

For this detection task, we use several standard metrics commonly used to evaluate classification tasks. We collect all true and false positives and negatives, and we then calculate metrics such as precision, recall/sensitivity, specificity,

<sup>&</sup>lt;sup>5</sup> https://github.com/simula/endotect-2020-submission-evaluation

F1, and Matthews correlation coefficient (MCC) for multi-classification (also called  $R_k$  statistic for multiclass classification). The officially reported metric for evaluating this task is the MCC, which will also be the metric used to rank the submissions.

### 3.2 Efficient Detection Task

The efficient detection task focuses on the real-time analysis needed to deliver instant feedback to doctors performing endoscopies. To satisfy this requirement, the algorithm must achieve good classification scores while also being able to classify images as fast as they are put on screen, which is approximately 30 frames per second. For the efficient detection task, we asked participants to submit a Docker [31] image so that we can evaluate the speed and efficiency of the proposed algorithm on the same hardware. The Docker image was set up to produce a submission file similar to the one described for the detection task, but in addition to the aforementioned value entries, the classification processing time was also appended to the end of each row. All submissions submitted to this task were run on what could be considered consumer-grade hardware, that is, a computer running Arch Linux with an Intel Core i9-10900K processor, an Nvidia GeForce 1080 Ti graphics processing unit (GPU), and 32 gigabytes of RAM.

As one could generally achieve higher processing speeds with an algorithm with lower prediction accuracy, the evaluation used a combination of the MCC classification score and the number of frames processed per second. The focus here is on the "speed" aspect of the algorithm, so the only requirement from a classification standpoint is that it exceeds a set MCC threshold so that it is still viable for in-clinic use. We set the threshold of 85% as it is considered standard for automatic detection systems for colonoscopies [36].

#### 3.3 Segmentation Task

In the segmentation task, we asked participants to use the segmented images provided in the dataset to generate segmentation masks of polyps automatically. Polyps are clumps of cells that form on the mucosal wall of the GI tract and come in a variety of shapes and sizes. Polyps are among the most critical findings in an endoscopy procedure as they are a precursor to different cancer types, including colorectal cancer, which is one of the most lethal cancer types worldwide [22]. The motivation behind this task is rooted in the requirement for not only detecting that a frame contains a polyp, but also showing where it is so that it can be properly removed. A typical example of a segmented polyp is shown in Figure 2.

For the evaluation of this task, we use the standard metrics commonly used to evaluate segmentation tasks. This includes precision, recall, the Dice coefficient, and the Intersection over Union (IoU, also known as the Jaccard index). The metric which will be used to rank submissions will be the IoU. To calculate the metrics, we use the implementation provided by the Python library scikitlearn [34].

## 4 Participants

This year, we received 26 registrations, of which six submitted results. Each participating team was allowed to submit as many runs to each task as they wished. In the following, we give a short summary of each participant's approach. A more detailed description of each approach can be found in the teams' corresponding challenge papers.

## 4.1 Team DeepBlueAI

Team *DeepBlueAI* participated in the detection and segmentation tasks. For the detection task, they trained a series of convolutional neural networks (CNNs), of which the best performing approach is an ensemble network consisting of a ResNet-50 [15] with batch normalization and an EfficientNet B7 [43]. For the segmentation task, they used two different approaches, namely instance and semantic segmentation. The instance segmentation approach used the Mask Scoring R-CNN [21] with ResNeXt-101 [49] as the backbone. As for the semantic segmentation, they used DeepLab V3 plus [9] with multi-scale training. More information on the specific implementation for both tasks can be found in [30].

## 4.2 Team Spearheads

Team *Spearheads* participated in all three tasks, where two runs were submitted to the detection and efficient detection tasks, and one run to the segmentation task. For the detection and efficient detection task, they used a Tiny Darknet model<sup>6</sup>, which was trained using an augmented version of the provided development dataset. For the segmentation task, they used a standard UNet architecture trained on the provided segmentation dataset, which was expanded using augmentation by Augmentor [5]. More information about team *Spearheads* approach can be found in [11].

### 4.3 Team NKT

Team NKT participated in the segmentation task, where they submitted one run. Their approach used a novel CNN-based architecture, which they named Dual Decoder Attention Network (DDANet). The architecture uses a single encoder network together with multiple decoders that use a combination of residual learning [16] and squeeze and excitation networks [20]. A more detailed explanation of the approach can be found in [46].

### 4.4 Team aggcmab

Team aggcmab participated in the detection and segmentation tasks, for which they submitted one run to each. For the detection task, aggcmab used a ResNet-50x1 with a BiT-M [27] backbone trained with a hierarchical loss function. For

<sup>&</sup>lt;sup>6</sup> https://pjreddie.com/darknet/tiny-darknet/

	Macro Average			Mi			
Team Name	Precision	Recall	F1-score	Precision	Recall	F1-score	MCC $(R_K)$
howard	0.683	0.646	0.659	0.913	0.913	0.913	0.903
DeepBlueAI	0.629	0.568	0.590	0.874	0.874	0.874	0.860
aggcmab	0.598	0.533	0.558	0.870	0.870	0.870	0.856
FAST-NU-DS	0.453	0.431	0.413	0.603	0.603	0.603	0.568
Spearheads	0.333	0.220	0.223	0.440	0.440	0.440	0.388

Table 1: Results for the best runs from the **detection** task. The table entries are ordered after the best MCC score.

	Macro Average			Micro Average				
Team Name	Precision	Recall	F1-score	Precision	Recall	F1-score	MCC $(R_K)$	$\mathbf{FPS}$
howard	0.528	0.496	0.503	0.785	0.785	0.785	0.765	129.748
Spearheads	0.333	0.220	0.223	0.440	0.440	0.440	0.388	49.132

Table 2: Results for the best runs from the **efficient detection** task. Please note that FPS signifies the average FPS calculated over the provided test dataset.

Team Name	Precision	Recall	F1-score / Dice	IoU
aggcmab DeepBlueAI howard NKT Spearheads	$\begin{array}{c} 0.928 \\ 0.907 \\ 0.915 \\ 0.858 \\ 0.801 \end{array}$	$\begin{array}{c} 0.937 \\ 0.947 \\ 0.882 \\ 0.799 \\ 0.801 \end{array}$	$\begin{array}{c} 0.920 \\ 0.915 \\ 0.879 \\ 0.787 \\ 0.754 \end{array}$	$\begin{array}{c} 0.871 \\ 0.861 \\ 0.822 \\ 0.701 \\ 0.656 \end{array}$

Table 3: Resultss for the best runs from the **segmentation** task. The table entries are ordered after according to the best IoU score.

the segmentation task, they use a double encoder-decoder network with a dual path network [10] for the encoders and a Feature-Pyramid [29] for the decoders. More information on the specifics of team *aggcmab's* approach can be found in [12].

#### 4.5 Team FAST-NU-DS

Team *FAST-NU-DS* participated in the detection task, where they submitted three runs. Their approach used bagging with 11 DenseNet169 models, where the final classification was made through hard majority voting. More information on the method can be found in [26].

#### 4.6 Team howard

Team *howard* participated in all three tasks, where they submitted one run to each. For the detection and efficient detection task, they used a CNN based on the ResNet152 [15] architecture trained with a hybrid loss. During training, they also applied some data augmentation, namely, contrast augmentation, color shift, brightness augmentation, flipping, perspective transformation, and blur. For the segmentation task, their solution is based on Cascade Mask R-CNN [8]. More information about their solution can be found in [17].

## 5 Results and Discussion

Tables 1, 2, and 3 show the results for all tasks in the challenge. Looking at the results for the *detection* task (Table 1), we see that team *howard* achieved the best result with their use of ResNet-152 together with a custom hybrid loss. They achieved an MCC score of 0.903, 0.043 ahead of DeepBlueAI, who came in second place. For the efficient detection task (Table 2)), only two teams participated, but also here, team *howard* achieved the best average frames per second (FPS) while also keeping the classification performance high. None of the teams reached the target MCC threshold of 85%, but team howard achieved an MCC of 0.765 at an FPS of 129, far above the real-time requirement. Thus, maybe some speed can be traded for a more complex model, achieving a slightly higher MCC while still reaching a real-time speed of 30 FPS. A common trend in this task was using neural networks with less parameters, like MobileNet or Tiny Darknet, to achieve a higher FPS. For the segmentation task (Table 3), team aggcmab achieved the highest IoU with their double encoder-decoder network approach. They reached an IoU score of 0.871, which is quite close to the runner up score of 0.861 submitted by team *DeepBlueAI*. Overall, the results prove that deep learning works well for analyzing GI image data and confirms the potential of computer-assisted detection and segmentation of GI anomalies, but they also suggest that there is still some room for improvement.

From an organizational perspective, the challenge went smoothly, without any significant hiccups or sudden difficulties. Docker submissions seem to work well, but may require some extra effort from the participants, which may explain why we only got two submissions to the *efficient detection* task. The difficulty level of the tasks appears to be quite balanced as the different teams achieved a variety of scores. Next year, we plan to hold the challenge again, but this time with an extended evaluation dataset and an additional task for efficient segmentation.

## 6 Conclusion

This paper described the EndoTect 2020 challenge, which asked participants to build algorithms that automatically detect different findings commonly found in the GI tract. The challenge consisted of three distinct tasks, where participants were given a large open dataset composed of videos from real endoscopies. We believe that computer scientists can make a real impact on the field of medicine, and the results presented in this paper show that we are at the point where machine learning algorithms have much potential in helping doctors detect more diseases.

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