PlutoNet: An Efficient Polyp Segmentation Network with Modified Partial Decoder and Consistency Training

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ABSTRACT
Deep learning models are used to minimize the number of polyps that goes unnoticed by the experts and to accurately segment the detected polyps during interventions. Although state-of-the-art models perform well, they require too many parameters, which can pose a problem with real-time applications. To address this problem, we propose a novel segmentation model called PlutoNet which requires only 2,626,537 parameters while outperforming state-of-the-art models on several datasets. With PlutoNet, we propose a novel consistency training approach that consists of a shared encoder, the modified partial decoder, and the auxiliary decoder that are trained with a combined loss to enforce consistency. We use a lightweight architecture and propose the modified partial decoder, which is a combination of the partial decoder and full-scale connections that further reduces the number of parameters required, as well as captures semantic details. We use asymmetric convolutions to handle varying polyp sizes and then we weigh each feature map by using a squeeze and excitation block. Then, we enforce consistency by combining the loss of the modified partial decoder and the auxiliary decoder, which helps improve the encoder’s representations without losing learned relevant semantic details. This way we are able to reduce false positive rates. We perform extensive experiments to show that our model outperforms the state-of-the-art models and is able to generalize well to several datasets. Our model outperforms the state-of-the-art models on the EndoScene dataset, Etis dataset, 2018 Data Science Bowl Challenge dataset, and Kvasir Instrument dataset. We also perform an ablation study to show the effectiveness of each component of our model.

1. Introduction

According to World Health Organisation (WHO), colon cancer is the third most common and the second most deadly cancer. Polyps in the colon can turn into cancerous cells if not removed with early intervention. Studies show that during colonoscopy, depending on their type and size, 14-30% of polyps go unnoticed by the experts [14]. Deep learning models are used to minimize the number of polyps that goes unnoticed by the experts and to accurately segment the detected polyps during these interventions. Although state-of-the-art models perform well, they require too many parameters, which can pose a problem with real-time applications. In this work, we propose a novel segmentation model called PlutoNet which requires only 2,626,537 parameters while outperforming state-of-the-art models on several datasets.

We propose a novel consistency training approach, which ensures a balance between the semantic details learned through our modified partial decoder and the more relevant higher-level features learned through the auxiliary decoder without losing semantic details. PlutoNet architecture adopts a lightweight encoder-decoder structure [22], and we also propose the novel modified partial decoder which is a combination of partial decoder [32] and full scale connections [11]. Higher-level encoder layers carry both low-level and high-level features [32]. Using modified partial decoder, we are able to reduce the number of parameters by ignoring skip connections to the low-level features which may be redundant. Polyps in colonoscopy images have varying sizes, appearances, and aspect ratios. In order to handle these variations, we use asymmetric convolutions. We increase the representation of the more relevant features by weighting each feature map using a squeeze and excitation block. Then we enforce consistency by combining the loss of the modified partial decoder and the auxiliary decoder, which helps improve the encoder’s representations without losing learned relevant semantic details in most cases. This way we are able to focus on the polyps and reduce false positive rates.

An overview of our model is demonstrated in Figure 1.

We tested our model extensively for the segmentation of polyps in colonoscopy images on five different public datasets. In addition to polyp segmentation in colonoscopy, we tested our model on the segmentation of nuclei and surgical instruments to demonstrate its generalizability to different medical image segmentation tasks. To segment polyps in colonoscopy images, we trained our model with Kvasir [14] and CVC-ClinicDB [2] datasets. We tested our model on ETIS [24], Endosence [29] and CVC-ColonDB [27] datasets. We tested our model for nuclei segmentation on the 2018 Data Science Bowl Challenge dataset [12], and for surgical instrument segmentation on the Kvasir-instrument dataset [15]. We outperformed the state-of-the-art models with a Dice score of 82.9% in Etis dataset and 91.9% on EndoScene dataset, a Dice score of 91.73% on the 2018 Data Science Bowl Challenge dataset, and a Dice score of 94.8% on Kvasir-instrument dataset. Our experiments and ablation studies show that our model outperforms state-of-the-art models, and it is able to generalize to several datasets and different medical image segmentation tasks. Moreover, PlutoNet requires only 2,626,537 parameters, which is far fewer than the state-of-the-art models.

Our paper is organized as follows: In section 2, we review the literature on state-of-the-art approaches in medical
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Figure 1: The overview of PlutoNet. In the top left corner (a), a simple representation of our proposed model is shown. In PlutoNet, a shared encoder, the modified partial decoder, and the auxiliary decoder are trained with a combined loss to enforce consistency. In the top right corner (b), the auxiliary decoder is shown. It carries out elementwise multiplication of higher-level encoders and then concatenates them. In the bottom left corner (c), the modified partial decoder, which is a combination of the partial decoder and full-scale connections is shown. In the bottom right corner (d), the details of the decoder layers which use a combination of asymmetric convolutions and a squeeze and excitation block are shown.

2. Related Work

Ronneberger et al. introduced U-Net [22] which uses an encoder-decoder structure with symmetrical contracting (down-sampling) and expansive (up-sampling) paths, and skip connections, to capture both low and high-level information for medical image segmentation. Due to its success, the U-Net architecture has been widely adopted in medical image segmentation with a focus on polyp segmentation. In section 3, we present our model in detail. In section 4, we provide information about the experiments and the datasets, along with the metrics used in these experiments. In section 5, we share our results and compare our model’s performance to the state-of-the-art models. In section 6, we provide a brief conclusion of our work and discuss our findings.
segmentation, and similar models [1, 20, 19] that build on this architecture have been proposed.

Jha et al. proposed a model titled ResUNet++ [6] for polyp segmentation in colonoscopy, which is a combination of ResNet [9] and UNet [22]. They used residual blocks to prevent the gradient vanishing problem. They also proposed to use Atrous Spatial Pyramid Pooling (ASPP) [3] to capture contextual information within the network and squeeze and excitation blocks [10] to reduce the redundant information.

In another work, Jha et al. [13] connected two U-Nets, namely, the double U-Net. The main motivation of double U-Net is to capture more semantic details [13]. They carried out experiments on different medical image segmentation tasks including colonoscopy, dermoscopy, and nuclei images. They demonstrated that they were able to capture more details by using two connected U-Nets back to back. Zhou et al. [34] proposed a nested U-Net architecture. The main idea behind this work is to redesign skip connections to reduce the gap between encoder and decoder layers. The authors tested their model on different medical image segmentation tasks that focus on the segmentation of nuclei, polyps in colonoscopy, lung nodules, and liver, outperforming U-Net on these datasets.

Huang et al. [11] proposed UNET 3+, a U-Net based architecture with full-scale connections. The motivation for this study is to capture details and semantics by combining low and high-level features at different scales. They used VGG-16 [25] and ResNet-101 [9] as backbone. While UNET 3+ showed that full-scale connections improve segmentation, the following work showed that lower layers are mostly redundant as the higher levels capture both low and high-level features. Wu et al. [32] proposed using cascaded partial decoder for the problem of salient object detection. Their experiments showed that the third encoder layer carried low-level features as well as high-level ones, therefore concatenations of lower layers are mostly redundant. Based on these findings, they developed the partial decoder which does not use the features of the first two encoder layers in the attention module. Using partial decoder and attention module, they outperformed state-of-the-art models. Wei et al. [30] proposed a novel polyp segmentation network titled Shallow Attention Network. Following the findings of Wu et al. [32], the authors ignored the connections from the first two encoder layers. To prevent bias in training, they also proposed a color exchange operation to decouple the image contents and colors. Moreover, they developed a probability correction strategy to increase segmentation accuracy at inference time. Meanwhile, Fan et al. [7] introduced a parallel reverse attention network for polyp segmentation. They reduced the number of parameters required by using a parallel partial decoder. They also proposed to use reverse attention [4] to better capture structural details.

Ding et al. [5] developed asymmetric convolutions which strengthen the square convolution kernels. Asymmetric and basic convolutions were tested separately as part of AlexNet [18] and ResNet [9] architectures, and the asymmetric convolutions were shown to be more successful in image classification tasks. Hu et al. [10] proposed squeeze and excitation networks. The main idea of this network is to weight each feature map in order to improve the representational power of relevant features. Similarly, Jha et al. [16] proposed a real-time polyp segmentation model which consists of residual and squeeze excitation blocks with fewer parameters. Their model demonstrated a significant frame per second (fps) improvement over the state-of-the-art models. Zhao et al. [33] proposed a polyp segmentation model titled MSNET. They developed a Multi-scale Subtraction Module to reduce inaccurate localization and the problem of blurred edges in polyp segmentation.

Consistency training has been used in semi-supervised learning to leverage unlabeled data by creating variations of the available data and combining the loss with the loss that comes from training the data available. Ouali et al. [21] proposed cross-consistency training which improves the encoder’s representations through different perturbations for semi-supervised semantic segmentation. Sohn et al. [26] presented consistency training for image classification. They used pseudo labels with weak and strong augmentations of images. More recently, Wu et al. [31] proposed mutual consistency learning for semi-supervised medical image segmentation. They used a shared encoder and slightly different decoders using up-sampling strategies.

In this work, we propose a novel segmentation model called PlutoNet which requires only 2,626,537 parameters. We propose a novel consistency training approach, which ensures a balance between the semantic details learned through our modified partial decoder and the higher-level features learned through the auxiliary decoder without losing semantic details. With PlutoNet, we also propose the novel modified partial decoder which is a combination of partial decoder [32] and full scale connections [11]. Inspired by the findings of [32], we are able to reduce the number of parameters by ignoring skip connections to the low-level features which may be redundant. As polys have varying sizes, appearances, and aspect ratios, we use asymmetric convolutions, and then we increase the representation of the more relevant features by weighting each feature map using a squeeze and excitation block. Our experiments on the EndoScene dataset, Etsi dataset, 2018 Data Science Bowl Challenge dataset, and Kvasir Instrument dataset show that PlutoNet outperforms the state-of-the-art models.

3. Proposed Model

In this section, we first introduce the architecture details and then explain the novel modified partial decoder which is a combination of partial decoder [32] and full-scale connections [11], the asymmetric convolutions and squeeze and excitation block which we use to capture semantic details of the polyps of varying sizes, appearances, and aspect ratios, and finally, the novel consistency training approach we propose, which enforces consistency by combining the loss of the modified partial decoder and the auxiliary decoder.

An overview of our model is demonstrated in Figure 1. As can be seen in the figure, we primarily adopt a lightweight
encoder-decoder structure using the last three encoder layers of EfficientNetB0 as the backbone of our network. We adopt full-scale skip connections as proposed in Huang et al.’s work [11]. Full-scale skip connections capture feature details at different scales. We then apply 64 convolution filters to the output of the encoder layers before they go into the full-scale connections, which further reduces the number of parameters. In order to handle variations in appearance, aspect ratio, and size of the polyps, we use asymmetric convolutions. Each decoder layer consists of an asymmetric convolution block followed by a squeeze and excitation block. Our motivation here is to first enrich the feature space using asymmetric convolutions and capture salient features, and then to weigh each feature map using a squeeze and excitation block to increase the representation of the more relevant features. Finally, we enforce consistency by combining the loss of the modified partial decoder and the auxiliary decoder, which helps improve the encoder’s representations without losing semantic details.

3.1. Modified Partial Decoder

Full-scale skip connections are proposed by Huang et al. [11]. These connections combine low-level features and high-level features. Integrating low and high-level information at different scales minimizes the loss of information. In this work, we also adopted full-scale connections, to capture more information at different scales. Wu et al. [32] proposed the partial decoder for fast and accurate salient object detection. An encoder-decoder structure that has five encoder layers: \( e^1, e^2, e^3, e^4, e^5 \) where the early layers \( e^1, e^2 \) extract the low-level features and \( e^3, e^4, e^5 \) extract the higher level features are common in segmentation models. Experiments of Wu et al. [32] showed that \( e^3 \) carries the low-level features that are learned through the earlier layers, therefore connections to these early layers carry redundant information. Moreover, they also showed that although \( e^1 \) and \( e^2 \) require more computation, they contribute less to the overall performance [32]. Based on these findings, in order to reduce the number of parameters of our model, we removed the full-scale skip connections of the earlier layers, \( e^1 \) and \( e^2 \). This way, we combined partial decoder and full-scale skip connections, coming up with the novel modified partial decoder which makes use of low and high-level information at different scales, while reducing the redundant and less informative features of the earlier layers, \( e^1 \) and \( e^2 \).

\[
\begin{align*}
d_1 &= \text{concatenate}(e^3, e^4, e^5) \\
d_2 &= \text{concatenate}(d_1, e^3, e^5) \\
d_3 &= \text{concatenate}(d_1, d_2, e^5)
\end{align*}
\]

In Equation 1, \( d_1, d_2, d_3, e^3, e^4 \) and \( e^5 \) represent decoder1, decoder2, decoder3, encoder3, encoder4 and encoder5, respectively. As mentioned earlier, we skip the connections to \( e^3 \) and \( e^4 \) as the higher layers carry the low-level features that are learned through the earlier layers which makes the connections to the two early layers redundant. \( e^3 \) and \( e^4 \) concatenate with the same and larger scale feature maps. \( e^5 \) is concatenated with all of the three decoder layers. We also concatenate inter-decoder layers at smaller and larger scales. These connections are demonstrated in Figure 1.

3.2. Asymmetric Convolution and Squeeze and Excitation Block

Ding et al. [5] proposed asymmetric convolutions to strengthen kernels, making them able to handle variations in appearance and size. They experimented with three different state-of-the-art models using asymmetric convolutions, and compared these models to the ones using basic convolutions. The models that have asymmetric convolutions outperformed the ones using the basic convolutions in image classification tasks. In our work, we use asymmetric convolutions to handle variations in appearance, aspect ratio and size of the polyps. After we enrich the feature space using asymmetric convolutions, we weight each feature map using a squeeze and excitation block to increase the representation of the more relevant features. A detailed view of the Asymmetric Convolution block and the Squeeze and Excitation Block can be seen in Figure 1.

\[
\text{relu}(bn(\text{conv}(3x1))) + bn(\text{conv}(1x3)) + bn(\text{conv}(3x3))
\]

Equation 2 shows the asymmetric convolution block structure. \( bn \) and \( conv \) represent batch normalization and convolution, respectively. In decoder layers, we used asymmetric convolutions. Three different convolutions are applied as part of the asymmetric convolution block. We then apply squeeze and excitation block to increase the representation of the more relevant features.

3.3. Consistency Training

We propose a novel consistency training approach that consists of a shared encoder, the modified partial decoder, and the auxiliary decoder that are trained with a combined loss to enforce consistency (Figure 1). While conventionally used in unsupervised segmentation problems Ouali et al. [21], we adopt consistency training to enforce consistency between the modified partial decoder which captures salient semantic details, and the more relevant features of the higher layers. Wei et al. [30] proposed a shallow attention network to focus on polyp details. We use this attention decoder as an auxiliary decoder and enforce consistency by combining the loss of the modified partial decoder and the auxiliary decoder. Equation 3 shows how this combined loss is calculated. This consistency training approach helps improve the encoder’s representations without losing learned relevant semantic details for most cases. With ablation studies, we show that consistency training helps our network better focus on the polyp regions.

\[
\frac{2 \sum P_{true} \cdot P_{main} + 0.2 \sum P_{main} \cdot P_{aux}}{\sum P_{true}^2 + \sum P_{main}^2 + \epsilon} + \frac{2 \sum P_{main} \cdot P_{aux} + 0.2 \sum P_{main}^2 + P_{aux}^2 + \epsilon}{\sum P_{aux}^2 + \sum P_{main}^2 + \epsilon}
\]

\( P_{true}, P_{main} \) and \( P_{aux} \) represents ground truth, output of modified partial decoder and output of auxiliary decoder, respectively. The auxiliary decoder adds only 200 parameters to
Table 1
A comparison of our model’s performance using Dice and IoU metrics to the state-of-the-art polyp segmentation models UNet [22], UNet++ [34], SFA [8], PraNet [7], MSNet [33] and Shallow Attention [30] are demonstrated. A comparison of the number of parameters for each benchmark model is also shown. According to the results, while our model requires fewer parameters, it achieved the best scores compared to state-of-the-art models with 92.3% Dice score in ClinicDB and 89.3% Dice score in Endoscape datasets (shown in bold).

| Methods          | Kvasir                | ClinicDB              | ColonDB              | Endoscape             | ETIS                  | Total Parameter |
|------------------|-----------------------|-----------------------|----------------------|-----------------------|-----------------------|-----------------|
|                  | Dice                  | IoU                   | Dice                 | IoU                   | Dice                  | IoU             | Million (Average) |
| UNet [2]         | 0.818                 | 0.746                 | 0.823                | 0.755                 | 0.512                 | 0.444           | 0.710 0.627 0.398 0.335 | 15.700.000 |
| UNet++ [12]      | 0.821                 | 0.743                 | 0.794                | 0.729                 | 0.483                 | 0.410           | 0.707 0.624 0.401 0.344 | 9.000.000  |
| SFA [18]         | 0.723                 | 0.611                 | 0.700                | 0.607                 | 0.469                 | 0.347           | 0.467 0.329 0.297 0.217 | -         |
| PraNet [8]       | 0.898                 | 0.840                 | 0.899                | 0.849                 | 0.709                 | 0.640           | 0.871 0.797 0.628 0.567 | 30.300.000 |
| MSNET [19]       | 0.907                 | 0.852                 | 0.921                | 0.879                 | 0.755                 | 0.678           | 0.869 0.807 0.719 0.664 | 27.700.000 |
| SANet [20]       | 0.904                 | 0.847                 | 0.916                | 0.859                 | 0.753                 | 0.670           | 0.888 0.815 0.750 0.654 | 23.900.000 |
| Ours             | 0.895                 | 0.811                 | 0.908                | 0.832                 | 0.694                 | 0.538           | 0.919 0.858 0.829 0.708 | 2.626.537  |

4. Experimental Details

We evaluated our model extensively for the segmentation of polyps in colonoscopy images on five different public datasets, and carried out ablation studies to show the effectiveness of each component of our model. In addition to polyp segmentation in colonoscopy, we also evaluated our model on the segmentation of nuclei and surgical instruments to demonstrate its generalizability to different medical image segmentation tasks.

The datasets we used to evaluate our model and the dataset properties are summarized in Table 2:

Table 2
Table shows the datasets we used to evaluate our model on several medical image segmentation tasks. "# images", "Image Size" and "Application" represent how many images there are in the corresponding dataset, the width, and height information of the images, and the application domain, respectively.

| Dataset            | #images | Image Size | Application   |
|--------------------|---------|------------|---------------|
| Kvasir SEG [14]    | 1000    | Variable   | Colonoscopy   |
| CVC-ClinicDB [2]   | 612     | 384x288    | Colonoscopy   |
| CVC-ColonDB [27]   | 380     | 574x500    | Colonoscopy   |
| Endoscape [29]     | 60      | 574x500    | Colonoscopy   |
| ETIS [24]          | 196     | 1225x966   | Colonoscopy   |
| 2018 Data Science Bowl [12] | 670 | 256x256 | Nuclei |
| Kvasir-Instrument [15] | 590 | Variable | Surgery |

4.1. Experimentation Details

We followed the experimentation set-up suggested by Fan et al. [7]; we split Kvasir and CVC-ClinicDB datasets as 80% training, 10% validation, and 10% testing, and carried out ablation studies on the Kvasir dataset. Then we tested our model further on ETIS, CVC-ColonDB, and Endoscape (CVC-300) datasets to show its generalizability across different datasets.

We tested our model on the segmentation of nuclei images using the 2018 Data Science Bowl Challenge dataset. We used 80% of this dataset for training, 10% for validation, and 10% for testing. We also tested our model on the segmentation of surgical instruments in the Kvasir-Instrument dataset and used 80% of this dataset for training, 10% for validation, and 10% for testing.

We resized all images to 224 × 224 × 3. We used common data augmentation techniques of random rotation and horizontal flip in all our experiments.

We trained our model on the Kvasir, CVC-ClinicDB, Kvasir-Instrument and 2018 data science bowl challenge datasets for 30 epochs. Using validation sets, we set up an early stopping scheme according to the validation loss. We set the initial learning rate to 1e−4 and used the Adam optimizer. We used Dice loss in all experiments.

4.2. Evaluation Metrics

We followed the evaluation metrics suggested by Jha et al. [14], and used Dice coefficient and Intersection over Union (IoU or also as known Jaccard) for our experiments on polyp segmentation. For the rest of our experiments, we used Dice, IoU, Area Under the Curve (AUC), precision, and recall metrics.

5. Results

We tested our model for segmentation of polyps in colonoscopy images, on the test split of Kvasir SEG [14] and CVC-ClinicDB [2], as well as the whole ETIS [24], Endoscape [29] and CVC-ColonDB [27] datasets. We also carried out two ablation studies to show the effectiveness of each component of our model.

Furthermore, we tested our model for nuclei segmentation on the 2018 Data Science Bowl Challenge dataset [12], and for surgical instrument segmentation on the Kvasir-instrument dataset [15] to evaluate our model’s generalizability to different medical domains.
5.1. Polyp Segmentation in Colonoscopy Images

For polyp segmentation, we compared our model’s performance to a benchmark consisting of the state-of-the-art models, namely, UNet [22], UNet++ [34], SFA [8], PraNet [7], MSNet [33] and Shallow Attention [30]. Table 1 shows our model’s results compared to the results of the benchmark studies. A comparison of the number of parameters each benchmark model requires is also shown.

Our model outperformed UNet, UNet++ and SFA on all datasets for Dice and IoU metrics. Even though we used about less than 10% of the parameters required by PraNet, MSNet, and Shallow Attention, our model outperformed state-of-the-art models on ETIS with an 82.9% Dice score and on EndoScene with a 91.9% Dice score.

5.2. Ablation Studies for Polyp Segmentation in Colonoscopy Images

We carried out our first ablation study on Kvasir dataset to evaluate the effectiveness of each added component of our architecture. First, we used EfficientNetB0 as the backbone with modified partial decoder. We achieved an 87.88% Dice and a 78.38% IoU score in polyp segmentation. Then, in addition to the first part, we added the asymmetric convolution block instead of using the basic convolution block. We reported an improvement of 0.51% Dice and 0.82% IoU score. Figure 2 demonstrates that by adding asymmetric convolutions we were able to capture more semantic details reducing false negatives and leading to more accurate segmentation.

Figure 2: As part of our ablation studies, sample outputs of each component on the Kvasir dataset [14] are shown. AS1, AS2, and AS3 represent Ablation Study 1, Ablation Study 2, and Ablation Study 3, respectively. AS1 contains Backbone and modified partial decoder. Please note how using an asymmetric convolution block (AS2) instead of a conventional convolution block (AS1) improved the segmentation output by reducing the number of false positives, in other words, the pixels that were segmented as polyps by mistake. An example of this can be clearly observed in the fourth row. Adding squeeze and excitation block (AS3) captured more semantic details reducing false negatives and leading to more accurate segmentation.

Figure 3: In our second ablation study, we compare our model’s performance with and without consistency on the Kvasir [14], ClinicDB [2], ColonDB [27], Etis [24], and EndoScene [29] datasets. Figures represent datasets, ground truth, our model with no consistency, and our model with consistency respectively. As shown in the sample results, consistency training reduced false positive rates as it better focuses on polyp regions.
Table 3
We carried out an ablation study on the Kvasir dataset [14] to evaluate the effectiveness of each component of our model. Backbone represents EfficientNetB0 in our experiments. PD, FSC, ACB, and SE represent Partial Decoder, Full-Scale Connection, Asymmetric Convolution Block, Squeeze and Excitation, respectively. AS1, AS2, and AS3 stand for Ablation Study 1, Ablation Study 2, and Ablation Study 3, respectively. Using an asymmetric convolution block (AS2) instead of the conventional convolution block (AS1) improved Dice, IoU, AUC, and recall scores. Using Squeeze and excitation block with asymmetric convolution block (AS3) achieved the best Dice, IoU, AUC, and recall scores which underlines the effectiveness of these components.

| Ablation Study                  | Dice    | IoU    | AUC    | Precision | Recall   | Parameter Sizes |
|--------------------------------|---------|--------|--------|-----------|----------|-----------------|
| Backbone + PD + FSC (AS1)      | 0.8788  | 0.7838 | 0.8951 | 0.9534    | 0.7979   | 2.192.545       |
| Backbone + PD + FSC + ACB (AS2)| 0.8839  | 0.7920 | 0.9046 | 0.9440    | 0.8188   | 2.620.961       |
| Backbone + PD + FSC + ACB + SE (AS3)| 0.9097 | 0.8345 | 0.9306 | 0.9380    | 0.8727   | 2.626.337       |

Table 4
We carried out a second ablation study to show the effectiveness of consistency training on Kvasir [14], ClinicDB [2], ColonDB [27], Etis [24], and EndoScene [29] datasets. The results of our model’s performance with and without consistency training are shown in Dice, IoU, Precision, and Recall metrics.

| Ablation Study                  | Dice    | IoU    | Precision | Recall |
|--------------------------------|---------|--------|-----------|--------|
| Kvasir No Consistency           | 0.8839  | 0.7920 | 0.9251    | 0.8315 |
| Kvasir With Consistency         | 0.8954  | 0.8107 | 0.9599    | 0.8267 |
| ClinicDB No Consistency         | 0.8964  | 0.8122 | 0.9492    | 0.8452 |
| ClinicDB With Consistency       | 0.9083  | 0.8320 | 0.9514    | 0.8660 |
| ColonDB No Consistency          | 0.7177  | 0.5597 | 0.7921    | 0.6556 |
| ColonDB With Consistency        | 0.6936  | 0.5308 | 0.8845    | 0.5703 |
| ETIS No Consistency             | 0.8041  | 0.6724 | 0.7927    | 0.8166 |
| ETIS With Consistency           | 0.8296  | 0.7088 | 0.8343    | 0.8255 |
| EndoScene No Consistency        | 0.8979  | 0.8147 | 0.8905    | 0.9024 |
| EndoScene With Consistency      | 0.9192  | 0.8505 | 0.9220    | 0.9186 |

5.3. Nuclei Segmentation
For nuclei segmentation, we compared our model’s performance to a benchmark consisting of the state-of-the-art models DoubleU-Net [13], UNet [22] and UNet++ [34]. We used VGG19 [25] as the backbone for DoubleU-Net, and ResNet101 as the backbone for UNet and UNet++. Table 5 shows our model’s performance results for Dice and IoU metrics compared to the results of the benchmark studies. Figure 4 demonstrates sample segmentation outputs of our model for the 2018 Data Science Bowl Challenge dataset, compared to the ground truth.

Our model outperformed all benchmark nuclei segmentation models with a Dice score of 91.73% even though it requires only 2.626.537 parameters while the benchmark model with the closest performance requires 11.15 times more parameters.

Table 5
A comparison of our model’s performance in 2018 Data Science Bowl Challenge [12] for Dice and IoU metrics to the state-of-the-art models UNet [22], UNet++ [34] and DoubleU-Net [13] are demonstrated. A comparison of the number of parameters each benchmark model requires is also shown. According to the results, while our model requires far fewer parameters, it achieved the best scores compared to state-of-the-art models using the Dice metric (shown in bold).

| Method     | Backbone    | Dice    | IoU    | Parameters |
|------------|-------------|---------|--------|------------|
| U-Net      | Resnet101   | 0.7573  | 0.9103 | 7.076.000  |
| U-Net++    | Resnet101   | 0.8974  | 0.9255 | 9.004.000  |
| DoubleU-Net| VGG-19      | 0.9133  | 0.8407 | 29.297.570 |
| Ours       | EfficientNetB0 | 0.9173 | 0.8473 | 2.626.537  |

5.4. Surgical Instrument Segmentation
For surgical instrument segmentation, we compared our model’s performance to a benchmark consisting of the state-of-the-art models U-Net [22], DoubleU-Net [13], ResUNet++ [6], NanoNet A [17], NanoNet B [17] and NanoNet C [17]. Table 6 shows our model’s performance results for Dice, IoU, AUC, precision, and recall metrics compared to the results of the benchmark models. Figure 5 demonstrates sample segmentation results of our model for the Kvasir-Instrument dataset [15], compared to the ground truth. Our model outperformed state-of-the-art models with a Dice metric of 94.8%.
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Table 6
A comparison of our model’s performance using Dice, IoU, precision and recall metrics to the state-of-the-art models used in Kvasir-Instrument dataset [15]; U-Net, DoubleU-Net, ResUNet++ [6], NanoNet-A [17], NanoNet-B [17] and NanoNet-C [17] are demonstrated. A comparison of the number of parameters each benchmark model requires is also shown. Our model outperformed all state-of-the-art models for Dice, IoU and recall metrics (shown in bold), while being among the models that require fewer parameters in the benchmark.

| Method   | Backbone      | Dice  | IoU  | Precision | Recall | Number of Parameters (~) |
|----------|---------------|-------|------|-----------|--------|--------------------------|
| UNet[22] | -             | 0.916 | 0.858 | 0.900     | 0.949  | 7,076,000                |
| DoubleU-Net[13] | VGG-19 [25] | 0.904 | 0.843 | 0.897     | 0.928  | 29,297,570               |
| ResUNet++[6] | ResNet[9]    | 0.914 | 0.864 | 0.935     | 0.910  | 4,070,385                |
| NanoNet-A[17] | MobileNetV2 [23] | 0.925 | 0.877 | 0.954     | 0.914  | 235,425                  |
| NanoNet-B[17] | MobileNetV2 [23] | 0.928 | 0.879 | 0.948     | 0.920  | 132,049                  |
| NanoNet-C[17] | MobileNetV2 [23] | 0.914 | 0.860 | 0.945     | 0.903  | 36,561                   |
| Ours     | EfficientNetB0 [28] | **0.948** | **0.901** | **0.971** | **0.924** | **2,626,537**          |

Figure 4: Sample segmentation results (predicted masks) of our model for the 2018 Data Science Bowl Challenge dataset, compared to the ground truth.

Figure 5: Sample segmentation results (predicted masks) of our model for the Kvasir-Instrument dataset, compared to the ground truth.

IoU metric of 90.1%, and Recall metric of 94.2% while remaining among the models that require fewer parameters.

5.5. Limitations and Future Work

Although our model achieves state-of-the-art results, there are some limitations to it. By ignoring lower-level features, we are able to largely decrease redundant information; however, we might be missing tiny polyps. This is a trade-off in order to reduce the number of parameters and false positives. Enforcing consistency by combining the loss of the modified partial decoder and the auxiliary decoder, we are able to improve the encoder’s representations without losing learned relevant semantic details in most cases. In Table 4, we see that the Precision is higher as the false positive rate is much smaller for all experiments that span five different datasets, however, the Recall is noticeably lower for the ColonDB dataset which suggests an increase of false negatives. In all other experiments with the remaining four datasets, we see that the Recall is higher or comparable to the state-of-the-art with consistency training.

6. Discussion and Conclusion

Colon cancer is preventable with early intervention. Recent advances in deep learning models are used to minimize the number of polyps that go unnoticed during colonoscopy, and to accurately segment the detected polyps. However, these models often require too many parameters, which may pose a problem with real-time applications. We propose a novel model named PlutoNet, to address these problems. PlutoNet requires only 2,626,537 parameters in test time while outperforming state-of-the-art models on multiple medical image segmentation tasks.

We use EfficientNetB0 architecture as a backbone which
achieves a high accuracy using fewer parameters. We propose the novel modified partial decoder, which is a combination of the partial decoder and full-scale connections. The modified partial decoder further reduces the number of parameters required, as well as captures semantic details at higher and lower levels, without being redundant. We use asymmetric convolutions to handle varying polyp appearances, aspect ratios, and sizes. We weight each feature map to improve segmentation results. Finally, we use consistency training to enable our network to focus on the polyp regions, which reduces false positive rates. In our ablation studies, we show that consistency training ensures higher Precision as the false positive rate is much smaller for all experiments, moreover, the Recall is also higher or comparable for most experiments 4. Our ablation studies also emphasize how using asymmetric convolutions and squeeze and excitation block improves semantic accuracy (Table 3 and Figure 2).

Our model requires only 2.626.537 parameters while U-Net++: the model that requires the least number of parameters in the benchmark for polyp segmentation, requires 9.042.177 parameters (Table1). This suggests a substantial improvement over the state-of-the-art, as our model requires only 29% of U-Net++.

Our experiments span five different datasets for polyp segmentation in colonoscopy images, as well as two more datasets on different medical image segmentation tasks; the 2018 Data Science Bowl Challenge for nuclei segmentation and the Kvasir-Instrument dataset for surgical instrument segmentation. Our model outperformed UNet, UNet+++, and SFA on all datasets for Dice and IoU metrics. Even though we used about less than 10% of the parameters required by PraNet, MSNet, and Shallow Attention, our model outperformed state-of-the-art models on ETIS dataset with an 82.9% Dice score and on Endoscope dataset with a 91.9% Dice score. Moreover, our model outperformed state-of-the-art models for the segmentation of nuclei and surgical instruments, with a Dice score of 91.73% on the 2018 Data Science Bowl Challenge dataset, and a Dice score of 94.8% on the Kvasir-Instrument dataset.

Our experiments and ablation studies support our model’s robustness and superiority in terms of accuracy and show that it is able to generalize well to several medical image segmentation tasks.

CRediT authorship contribution statement

Tugberk Erol: Conceptualization, Methodology, Software, Validation, Writing - original draft Duygu Sarikaya: Conceptualization, Methodology, Supervision, Validation, Writing - original draft

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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