Image segmentation of gastrointestinal polyps in the human gastrointestinal tract using machine learning

Leo Lee

Abstract

Currently, colorectal cancer is one of the most common cancers in the world, with it contributing to over 10% of all cancers. With colorectal cancer being a significant contributor to the worldwide mortality rate, it is imperative to find effective methods for treatment and detection. Early disease detection has a huge impact on survival from colorectal cancer, and polyp detection is therefore important. Although colonoscopies have seemingly been perceived to search and find a large amount of potentially cancerous polyps, there are still many issues with thorough detection. Several studies have shown that many polyps are often overlooked during colonoscopies, with 38.69% of patients having at least one polyp missed during colonoscopy, along with a general polyp miss rate of 17.24%. Increasing the detection of polyps has been shown to decrease the risk of colorectal cancer. Thus, automatic detection of more polyps at an early stage can play a crucial role in improving both prevention of and survival from colorectal cancer. This convolutional neural network model, trained on an annotated medical dataset(KVAIR-SEG), is able to accurately detect gastrointestinal polyps with a state-of-the-art accuracy of 96.8%. This novel machine learning model built using the fast.ai library will immensely improve the polyp detection accuracy of colonoscopies in the future.

Introduction

Currently, colorectal cancer is one of the most common cancers in the world, with it contributing to over 10% of all cancers[1]. Colorectal cancer is caused by an abnormal growth of cells either in the human rectum or colon. Although not certain, doctors generally agree that this abnormal growth in cells is due to a change in DNA in colon cells, instructing them to multiply quickly, eventually leading to dangerous tumors[5]. Colorectal cancer typically occurs in older patients but can be found at any age. The cancer usually begins with small clumps of cells called polyps that form inside the colon[5]. Several studies have shown that many polyps are often overlooked during colonoscopies and have reported that 38.69% of patients have at least one polyp missed during colonoscopy, along with a general polyp miss rate of 17.24% [2]. Overall, polyps are typically not dangerous, but some can turn cancerous over time, making it essential for proper removal to negate this possibility. Colorectal cancer patients may experience symptoms such as rectal bleeding, weakness or tiredness, ongoing discomfort in the belly area, losing weight without trying, and a change in bowel habits[5]. Cancerous polyps also may not display these symptoms in the patient at first, making screenings for middle to older adults imperative. Increasing the detection of polyps has been shown to decrease the risk of colorectal cancer[3] This project uses machine learning to optimize the detection of gastrointestinal polyps as a checking tool in the case of human error. This convolutional neural network model, trained on an annotated medical dataset(KVAIR-SEG)[4]. The KVAIR-SEG dataset used for the image segmentation contained 2000 images(1000 base images and 1000 masks).

Machine learning is a computer science discipline that aims to code computers to operate like humans. Machine learning, especially when using convolutional neural networks, is extremely useful in different medical and computer vision tasks such as image segmentation and classification. Convolution neural networks(CNN) are a type of neural network that operates using convolutional layers within the neural network. Each layer in the neural network possesses different filters that identify the characteristics of what you are identifying, which would, in this case, be the gastrointestinal polyp. The deeper through the neural network the image travels, the more complex filters it encounters within the convolutional layers. This project uses the U-net convolutional neural network architecture. By changing the CNN's architecture, the modified architecture allows for better resolution on less-trained images, as pooling operations are replaced by upsampling operations[6]. A pre-trained model was also implemented using Resnet-34, which is a CNN model trained on Imagenet, a database with over 14 million images.

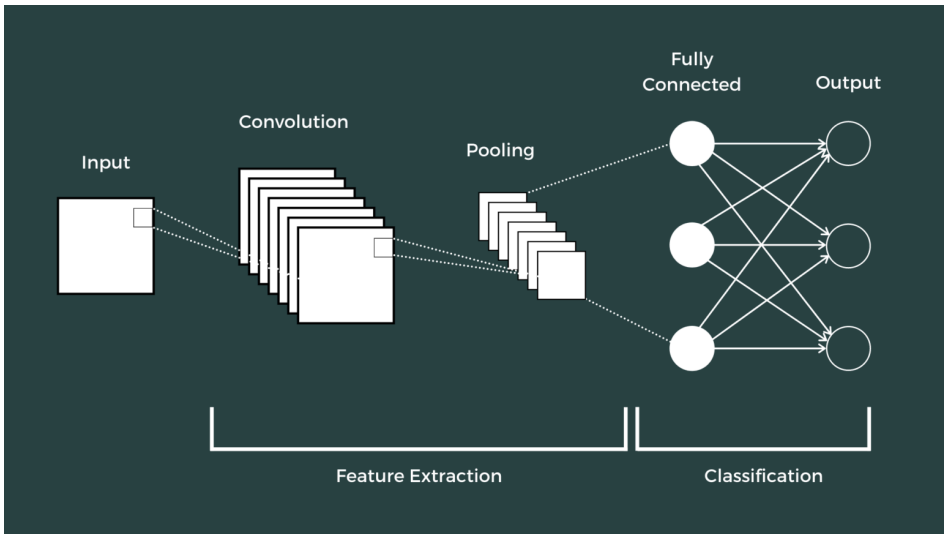

Figure 2 Basic Convolutional Neural Network architecture

Image taken from
https://akhiltvsn.medium.com/cnn-notes-1-the-convolution-operation-e2a47be1d890

Methodology

For data preparation, the KVAIR-SEG dataset was imported into Kaggle's coding environment, with file paths created for both the image and mask folders. After visualizing the image sets to check functionality, a data block was created for image processing. A train-test split was created in the dataset, with 80% of the images being used for training and 20% for testing. Fastai image augmentations were also added to diversify the data the model would be trained on. The rand transform augmentation was used to apply a random transformation on each image. The flip item augmentation was also applied to transform images horizontally from left to right. Due to the fact that the images from a colonoscopy will never all be from the same angle, the augmentations were added to adjust to this problem. The images were also turned into tensors as a batch transformation for the computer to be able to interpret. After initializing the data block, the data would fit with a U-Net model with different Resnet models to find which depth was most effective. The four models used were Resnet-18, Resnet-34, Resnet-50, and Resnet 101. The utilization of these models follow the principle of transfer learning where pretrained models are finetuned to successfully function for specific data. Mean_dice was used as a metric in order to compare to other published papers regarding image segmentation of gastrointestinal polyps.

$$\text{Dice} = \frac{2 \times \text{Intersection}}{\text{Predicted Area} + \text{True Area}}$$

Equation 1 *Mean Dice metric equation*
created by student researcher

Results

The four Resnet models were trained until accuracy rates plateaued and no further improvement was deemed to be possible. Resnet-34 was found to outscore its counterparts with a peak accuracy of 96.8% at epoch 10. Resnet-50 reached a peak accuracy of 94.6% at epoch 18. Resnet-18 reached a peak accuracy of 94.4% at epoch 38. Resnet-101 reached a peak accuracy of 85.1% at epoch 2. A confusion matrix was also constructed with total pixels correctly identified as the metric for the best-performing resnet-34 model.

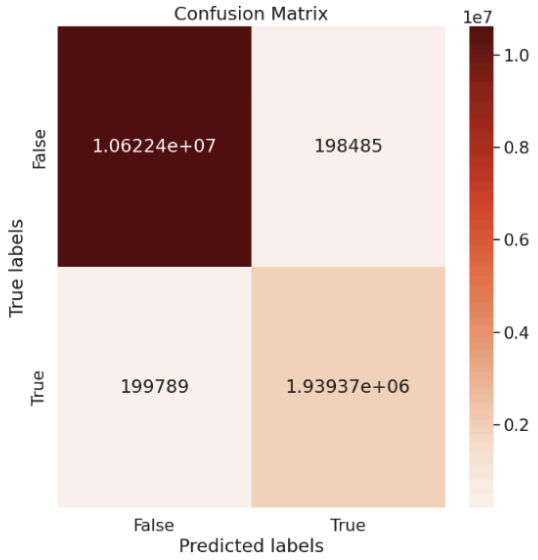

Figure 2 Confusion Matrix for CNN model results
created by student researcher

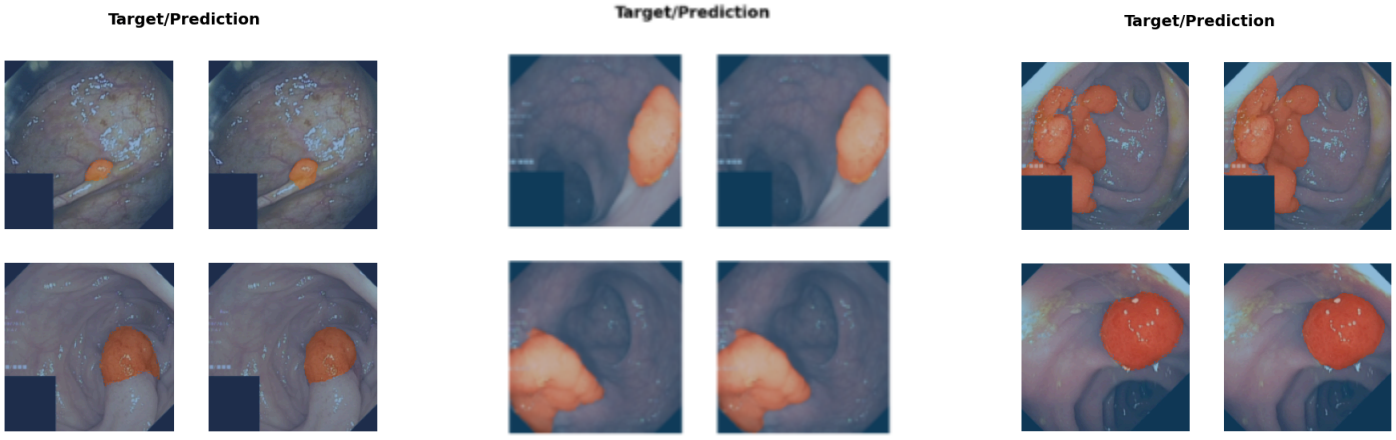

Figure 3 Visualization of Resnet − 34 polyp segmentation
created by student researcher

Resnet-34

epoch	train_loss	valid_loss	mean_dice	time
0	0.059460	0.065257	0.954558	01:14
1	0.064649	0.073017	0.948483	01:14
2	0.061626	0.070139	0.951402	01:14
3	0.072153	0.068931	0.958250	01:14
4	0.063590	0.065696	0.958298	01:14
5	0.075393	0.067000	0.960881	01:14
6	0.044795	0.059867	0.960731	01:14
7	0.054024	0.053280	0.963930	01:14
8	0.038856	0.055592	0.960715	01:14
9	0.038050	0.059006	0.965203	01:14
10	0.032290	0.046765	0.968119	01:14
11	0.025737	0.050668	0.965787	01:13
12	0.021100	0.058360	0.966686	01:13
13	0.021940	0.052843	0.967037	01:12
14	0.023991	0.053437	0.967075	01:12

Resnet-50

epoch	train_loss	valid_loss	mean_dice	time
0	0.030394	0.114185	0.941384	08:07
1	0.026451	0.098261	0.943355	08:07
2	0.022527	0.168819	0.928072	08:07
3	0.019981	0.138018	0.941492	08:07
4	0.019053	0.136969	0.945242	08:07
5	0.020287	0.195827	0.933161	08:07
6	0.025024	0.098842	0.943685	08:07
7	0.032423	0.444879	0.933178	08:07
8	0.032599	0.087466	0.942761	08:07
9	0.023274	0.134041	0.939417	08:07
10	0.039573	0.096274	0.923833	08:07
11	0.027097	0.161013	0.934684	08:07
12	0.028655	0.163098	0.942253	08:07
13	0.035989	0.101690	0.943703	08:07
14	0.038088	0.111080	0.938676	08:07
15	0.019351	0.138620	0.946634	08:07
16	0.025821	0.158246	0.942325	08:07
17	0.018922	0.151490	0.940825	08:07
18	0.027499	0.133210	0.946970	08:07

Resnet-18

21	0.019329	0.140703	0.940170	01:04
22	0.017881	0.175597	0.940984	01:03
23	0.016805	0.208092	0.941461	01:03
24	0.017640	0.165196	0.935932	01:03
25	0.015827	0.188999	0.943227	01:03
26	0.014929	0.207196	0.941863	01:03
27	0.013952	0.171355	0.940456	01:03
28	0.014159	0.189469	0.941649	01:03
29	0.013535	0.208670	0.942233	01:03
30	0.014886	0.187104	0.943579	01:03
31	0.013351	0.196529	0.941204	01:03
32	0.014528	0.193717	0.943835	01:03
33	0.014906	0.222240	0.944691	01:03
34	0.013338	0.215827	0.943345	01:03
35	0.012774	0.214535	0.943606	01:03
36	0.013005	0.220246	0.943750	01:03
37	0.013770	0.230772	0.943278	01:03
38	0.013119	0.227392	0.943575	01:03
39	0.012825	0.230557	0.944129	01:03

Resnet-101

epoch	train_loss	valid_loss	mean_dice	time
0	0.455469	0.600333	0.526531	09:07
1	0.297318	0.279309	0.762758	09:13
2	0.246050	0.203780	0.791961	09:16
3	0.218264	0.185689	0.824496	09:13
4	0.228186	0.176094	0.837615	09:12
5	0.186675	0.174271	0.841171	09:12
6	0.234144	0.165405	0.851022	09:11
7	0.183468	0.168111	0.851106	09:11

Figure 4 Training results for all 4 Resnet models
created by student researcher

Conclusion and Future Works

Gastrointestinal polyps highlight the efficiency of machine learning approaches in healthcare, which have rapidly evolved. The significance of accurate polyp detection cannot be overstated, given its direct impact on preventing and managing colorectal cancer, a major contributor to global cancer morbidity and mortality. This image segmentation model will serve as an excellent checking tool for doctors and other healthcare professionals to compensate for the possibility of human error during the process of detecting polyps in colonoscopies. Implementing this new method would not impact hospitals' finances as it is solely software-based, with no new hardware changes needed. For future works, this project would benefit from creating a user friendly desktop application making usage as convenient as possible for healthcare professionals to utilize. Furthermore, collaboration with medical professionals and institutions for extensive validation studies on diverse patient populations would validate the robustness of the model. Continuous refinement and fine-tuning based on feedback from these studies would contribute to the model's adaptability to different clinical scenarios and ensure its reliability in real-world applications. The Resnet-34 model achieved a state-of-the-art accuracy of 96.8% in identifying gastrointestinal polyps, allowing for thorough segmentation with polyp sizes of different sizes.

Simplified snippet of code utilized:

```
import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import os
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))
import os
import shutil
from fastai.basics import *
from fastai.vision.all import *
from fastai.callback.all import *
path_im = Path('/kaggle/input/kvair-seg/Kvasir-SEG/images')
path_lbl = Path('/kaggle/input/kvair-seg/Kvasir-SEG/masks')
fnames = get_image_files(path_im)   #images
label_names = get_image_files(path_lbl)    #masks
get_msk = lambda o: path_lbl/f'{o.stem}{o.suffix}' #o is the filename of the mask
img_fn = fnames[4]
img= PILImage.create(img_fn)
Fnames[0]
Label_names[0]
img_fn = fnames[4]
img= PILImage.create(img_fn)
img.show()
mask = PILMask.create(get_msk(img_fn))
mask.show(alpha=1)
print(tensor(mask))
codes = ['n','y']
sz= mask.shape; sz
half = tuple(int(x/2) for x in sz); half\
#ORIGINAL

from PIL import Image
cancer = DataBlock(
    blocks=(ImageBlock, MaskBlock(codes)),
    get_items=get_image_files,
    splitter=RandomSplitter(valid_pct=0.2),
    get_y=get_msk,
    item_tfms=[Resize(180),FlipItem(p=0.5),RandTransform(p=1)],
```

```
    # Resize images to 800x800
    batch_tfms=[
        Normalize.from_stats(*imagenet_stats),
        IntToFloatTensor(div_mask=255)
    ]
)
source_p=Path('/kaggle/input/kvair-seg/Kvasir-SEG')
dls =  cancer.dataloaders(source_p,bs=2)
dls.show_batch()
name2id = {v:k for k,v in enumerate(codes)}
name2id
opt=Adam
learn = unet_learner(dls, resnet34 , metrics=[mean_dice])
def binary_dice_coef(preds, targets, cls_idx):
    # Convert to binary format
    preds_bin = (preds == cls_idx).float()
    targets_bin = (targets == cls_idx).float()

    # Calculate intersection and union
    intersection = (preds_bin * targets_bin).sum()
    union = preds_bin.sum() + targets_bin.sum()

    # Dice coefficient
    dice = 2. * intersection / (union + 1e-8)  # Epsilon to avoid division by zero
    return dice

learn.summary()
learn.freeze()
learn.fit_one_cycle(3,lr_max=1e-7)
learn.unfreeze()
learn.fit_one_cycle(20,lr_max=slice(1e-7,1e-3))
import matplotlib.pyplot as plt
import seaborn as sns

def plot_confusion_matrix(confusion_matrix, class_names):
    fig, ax = plt.subplots(figsize=(8, 8))
    sns.heatmap(confusion_matrix, annot=True, fmt='g', cmap='Reds', ax=ax)

    ax.set_xlabel('Predicted labels')
    ax.set_ylabel('True labels')
```

```
    ax.set_title('Confusion Matrix')
    ax.xaxis.set_ticklabels(class_names)
    ax.yaxis.set_ticklabels(class_names)

# Call the function with your confusion matrix
class_names = ['False', 'True']
plot_confusion_matrix(total_confusion_matrix, class_names)
plt.show()
```

References

1. “Worldwide Cancer Data: World Cancer Research Fund International.” *WCRF International*, 14 Apr. 2022, www.wcrf.org/cancer-trends/worldwide-cancer-data/.
2. Lee J, Park SW, Kim YS, Lee KJ, Sung H, Song PH, Yoon WJ, Moon JS. Risk factors of missed colorectal lesions after colonoscopy. Medicine (Baltimore). 2017 Jul;96(27):e7468. doi: 10.1097/MD.0000000000007468. PMID: 28682916; PMCID: PMC5502189.
3. Rijn, Jeroen C. van et al. “Polyp Miss Rate Determined by Tandem Colonoscopy: A Systematic Review.” *The American Journal of Gastroenterology* 101 (2006): 343-350.
4. SimulaMet, Debesh Jha, et al. “Kvasir-SEG: A Segmented Polyp Dataset: Multimedia Modeling.” *Guide Proceedings*, 1 Jan. 2020, dl.acm.org/doi/10.1007/978-3-030-37734-2_37.
5. “Colon Cancer.” *Mayo Clinic*, Mayo Foundation for Medical Education and Research, 27 July 2023, www.mayoclinic.org/diseases-conditions/colon-cancer/symptoms-causes/syc-20353669.
6. Ronneberger, Olaf, Philipp Fischer, and Thomas Brox. "U-net: Convolutional networks for biomedical image segmentation." *Medical Image Computing and Computer-Assisted Intervention–MICCAI 2015: 18th International Conference, Munich, Germany, October 5-9, 2015, Proceedings, Part III 18*. Springer International Publishing, 2015.