Detecting brain hemorrhage/colorectal neoplasia in CT images

Predicting colorectal malignancy from CT Colonography

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1. Motivation and Related Work

A computerized tomography (CT) scan is the most widespread imaging examination worldwide for diagnosis and screening many disorders, including adenomas, neoplasma and hemorrhages Hara et al. (2018a). Automated CT image interpretation could provide many benefits in medical settings, such as workflow prioritization and clinical decision support, especially for time-sensitive cerebral hemorrhages where immediate diagnosis is crucial Hamidian et al. (2017). Recently, rapid CTC detection of colorectal neoplasia is being assessed as a population screening tool. Here, our aim is to develop a deep learning algorithm that detects colorectal neoplasia using CT images.

2. Dataset

The dataset was obtained from the Cancer Imaging Archive CT Colonography dataset.K et al. (2015) It was ready-to-use and contained prone and supine DICOM images from same-day validated images- 243 negative cases, 69 cases with 6 to 9 mm polyps, and 35 cases which have at least one ¿ 10 mm polyp and their histological type(836 patients). There are 3,451 series and 941,771 image from this end data. Samples which did not have the Supine identification were discarded, resulting in negative cases, z cases with 6 to 9 mm polyps and AAAAAAAA cases with at least 1 polyp¿10mm in size. Separate files were available for download containing the labels for each patient data. The initial resolution was 512 x 512 which was scaled down to 112 x 112 pixel resolution.The images were appended in order to create input into 3D CNN models.

3. Methodology

Our goal is to predict polyps caused by brain hemorrhages/colorectal neoplasms, from CT scans.

3.1 Label extraction from radiology reports

We will set up a labeler to extract the mentions from radiology reports, then make classification to positive or negative interpreting from the mentions. For the TCIA CT colongraphy dataset, the dicom files are labelled into 2 categories based on the polyp of presence(0 for no polyp and 1 for polyps exist).

3.2 Initial Approach

Originally, our approach was to convert the image volumes into numpy arrays. However, even the most popular 3D Convolutional Neural Networks that use this approach found difficulties. Converting into the same dimensions has been limited to only 20 slices here Jiandanjinxin (2017) for hundreds of patients for a decent accuracy of 70 percent. We propose that our model will somehow do better.

3.3 Select the best model using validation set

We plan to use a 3D Convolutional Neural Network (3D CNN) architecture.

We compare performance of different approaches on a validation set. We used a pre-trained weights from the ResNet-18 model. Due to the similarity in domain and size of 3D dicom volumes and action recognition from video data. We hypothesize that the pre-trained weights are sufficient enough to accurately predict the presence of polyps in our data Hara et al. (2018b).

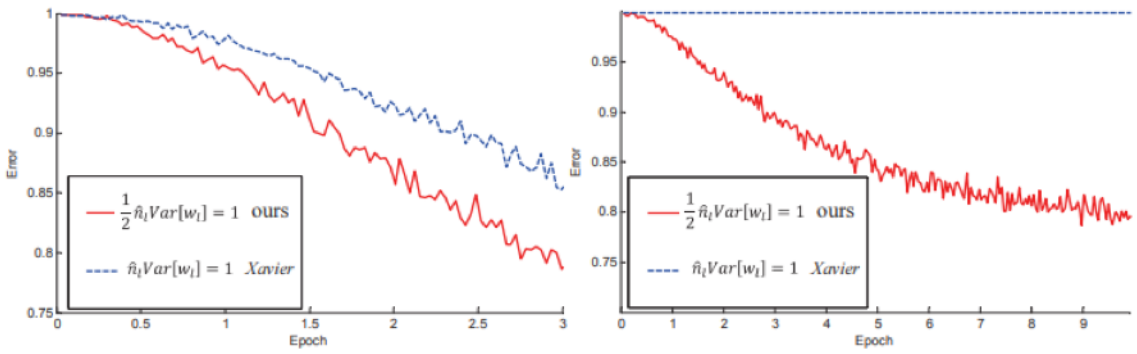
3.4 Optimization

We observe the performance and generalization errors of our model, and optimize to resolve potential issues of under/overfitting. We also report AUC/ROC and learning curves.

3.5 He Normal Initialization

We used He Normal Initialization for initialization for weights as the error rates while using ReLU function for activation is less than in the case of Xavier initialization, which assumes linearity, and initialization with zeros due to the vanishing gradient problem He et al. (2015). This allows for deep models to converge, which the Xavier initialization cannot. This can be seen in the figure below as well.

The weights are distributed with a mean of zero and a standard deviation which is (2/n) where n is the receptive field size*number of output feature maps. This is when mode-fanout, which maintains the magnitude of variance of weights in back-propagation. The figure below shows validation error in He initialized(Red) and Xavier initialized(blue) 22- layer(Left) and 30-layer(Right) models with ReLu used as activation functions.



¡return¿

4. Evaluation Metrics

We propose that the model will successfully classify negative/positive cases of polyps. After reporting AUCs, accuracy, and precision, we plan to improve the performance of the model by optimizing the hyper-parameters and through regularization.

5. Results

We utilized a log-softmax function with the criterion as Negative Log Likelihood Loss.

5.1 Loss curves

References

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