M-Protain Diagnostics Using Generative Active Learning

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Abstract

With comparatively less labeled data and high labeling cost, most of the medical involved tasks can not be directly tackled by state of art machine learning approaches for their demand of large carefully labeled datasets.

Introduction

As deep models achieve astonishing results in almost every machine learning tasks, some unavoidable problems such as the need for large carefully labeled dataset has troubled researchers from the start. Part of the reason behind the tremendous success in deep learning is the availability of large-scale labeled data(Sun et al. 2017). Although data labeling companies and platforms claim that they can provide inexpensive yet high quality data(Buhrmester, Kwang, and Gosling 2011), achieving such datasets can be extremely costly or even unrealistic in the scenarios where labeling requires high professionality. For instance, some medical image tasks can not be labeled by people without systematic training. However, the small number of these experts has determined that large-scale dataset is difficult to biuld. Plus, they are probably already preoccupied.

M-protain stands for Myeloma protein, which can be identified by applying immunofixation electrophoresis(IFE) because its sharp monoclonal band in the image. Different categories of results may indicate MGUS, smouldering myeloma(sMM), or multiple myeloma(MM). It usually takes three doctors to examine the IFE image and reach the final conclusion. Therefore the process is highly time consuming. In real world scenarios, more than half of the electrophoresis results are obviously normal which do not need further concern. Although final decision should be made by doctors, if a classifier can give an indicating result, then time can be greatly saved. Every IFE image consists of five columns of one dimensional signal. According to these columns, a 12 dimensional 0/1 vector will be computed as output. Part of the proposed method can be implemented by manually constructed rules, so in the end, machine learning involved section is narrowed down to a binary classification(normal or abnormal) of one dimensional signal.

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A large dataset of IFE images is accessible, but each of them comes with a diagnostics report instead of the binary output of each column. Thus, due to the lack of explicit label, this is a classic semi-supervised situation. Our paper tries to utilize the combination of active learning and generative model to tackle with this unlabeled dataset. Active learning is that a machine learning algorithm that can achieve greater accuracy with fewer labeled training instances if it is allowed to choose the training data from an unlabeled dataset(Settles 2009). When using same amount of labeled data, active learning tends to achieve better results. Thus, active learning techniques significantly reduce the amount of labor required compared to manually label all existing data. Generative models including GAN and

Our paper try to

Related Work

Multiple techniques were used to tackle with small datasets and partially labeled datasets including active learning(Settles 2009), generative models(Goodfellow et al. 2014)(Kingma and Welling 2013), data augmentation(Tanner and Wong 1987), and domain transfer(Pan and Yang 2009) etc. asdlfdklflkdjflkadf;asdafsdjklfajfkjadf(Zhu and Bento 2017)

Preliminaries

The problem is defined as below

Proposed Method

Our method make use of

Experiments

I did such experiments

Discussion

After I did these experiments

Conclusion

To sum up

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