

M-Protein 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 professionalism. 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 build. Plus, they are probably already preoccupied.

M-protein can be detected by immunofixation electrophoresis(IFE) images, and different categories of results may indicate MGUS, multiple myeloma, etc.

Active learning and GAN

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. asldfklfklfdjfkadf;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

References

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