How transferable are the deep features from false positive reduction network for lung nodule detection in CT to malignancy prediction?

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Abstract

Achieving highly generalizable deep features from data is a fundamentally important problem in various tasks. This work presents experimental results that we can use features from a false positive reduction network for lung nodule detection as generalizable nodule features. Feature visualization with t-SNE and nodule feature based similar nodule search results show that these features have discriminative malignancy and shape information even though the network was only trained to classify nodules from non-nodules.

1 Introduction

Many of the recent success of various general vision tasks (e.g. detection, segmentation, classification) can be achieved by transfer learning with highly generalizable deep features which is pre-trained on the IMAGENET classification task. These pre-trained, highly generalizable, deep features can be applied on different problems and make possible for us to solve problems which have small datasets.

The domain that we will be discussing is lung nodules in CTs, where it is challenging to collect a comprehensive dataset with nodule characteristic labels (e.g. malignancy, spiculation). If you consider heterogeneity of labeled data from multiple datasets, the problem only gets harder. Because every dataset has different labeling policies and formats for documenting nodule characteristics, merging different datasets for nodule characteristic classification is nearly impossible. Hence, in many medical imaging domains like the nodule characteristic classification task, it is very hard to build a large dataset like IMAGENET to achieve highly generalizable deep features. However, if we just consider the nodule center coordinate labels, we can easily merge several datasets.

We can train a false positive reduction network for lung nodule detection by nodule coordinate labels. And if this network's features contain highly generalizable nodule features, we can implemented on various tasks. For example, nodule based CBIR and transfer learning for various small dataset problems.

2 Methods

2.1 Network Structure

We use an encoder-decoder style fully convolutional 3D false positive reduction network. It is trained by curriculum learning with hard example mining and on-line sample filtering[2]. We use mid-feature (See figure 1) for our experiments.

1st Conference on Medical Imaging with Deep Learning (MIDL 2018), Amsterdam, The Netherlands.

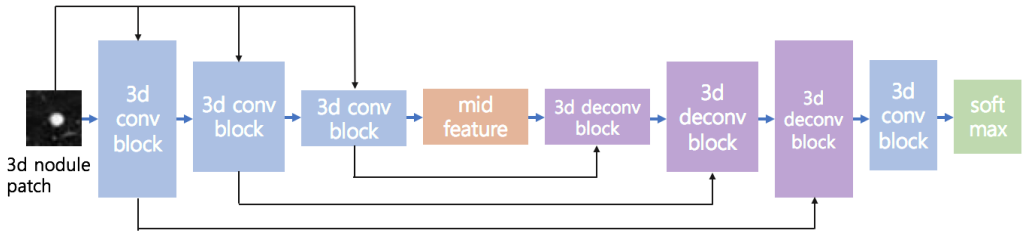

Figure 1: encoder-decoder style fully convolutional 3D false positive reduction network structure

2.2 Dataset

For false positive reduction network training, we used the LIDC dataset[1]. And for feature visualization with t-SNE and feature based similar nodule search, we used nodules, which have consensus of three or more radiologists, from the LUNA16 dataset. We also used the mean of the malignancy likelihood label from LIDC. The malignancy label is given as a value between 1 and 5 where larger values mean higher probability. We exclude nodules that have malignancy value 3 due to ambiguity. The setting is also used in other works[3].

3 Result

3.1 Feature Visualization with t-SNE

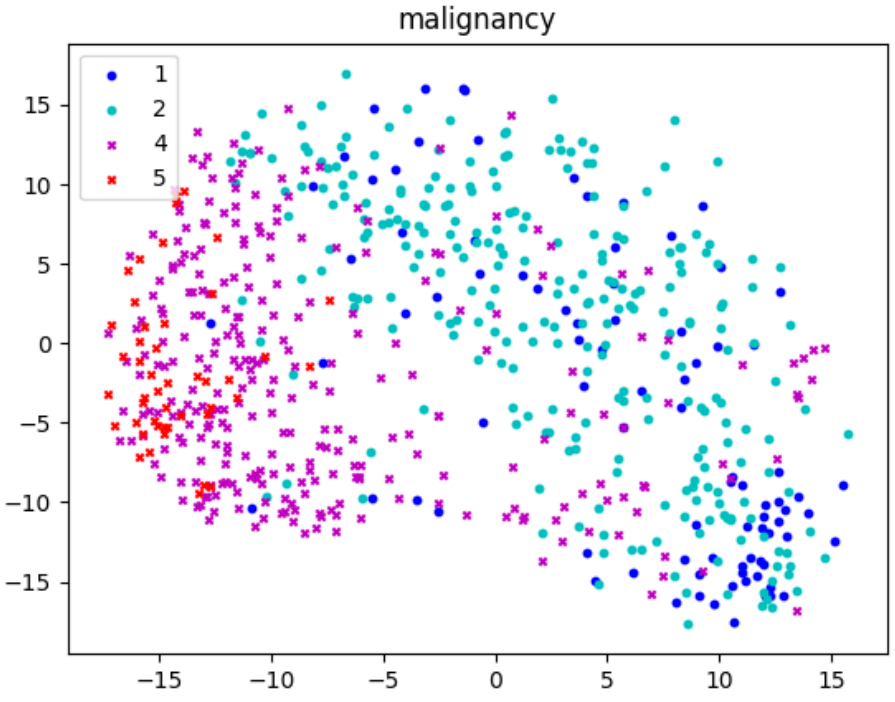

Figure 2: t-SNE feature(mid-feature in figure 1) visualization with malignancy label from lidc. We uses 679 LUNA16 nodules. Each marker means nodule.

In figure 2, we can see nodule feature which achieved by false positive reduction network that only trained with nodule coordinate label has discriminative information in malignancy label perspective.

3.2 Nodule Feature based Similar Nodule Search

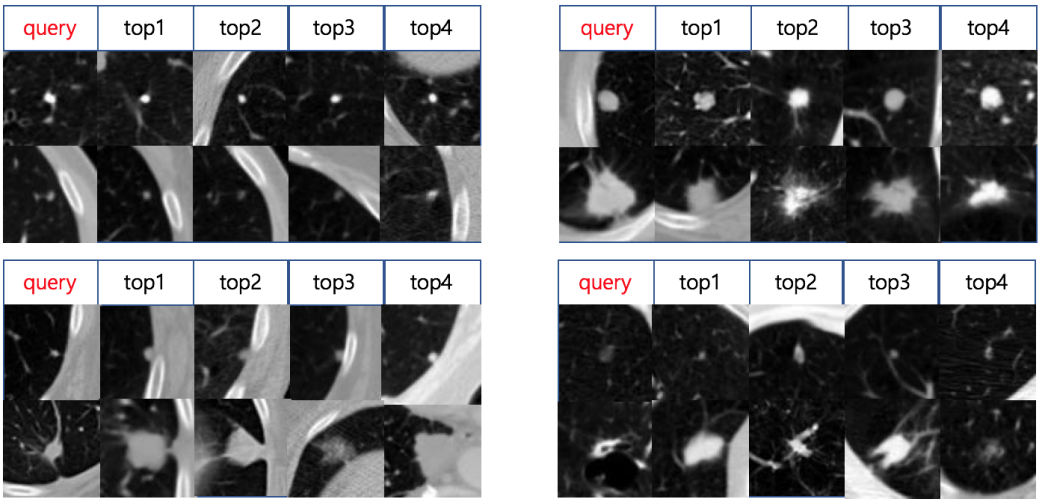

Figure 3: Nodule feature based similar nodule search top-4 result images and query image.(qualitative result)

malignancy label	Recall@1	Recall@2	Recall@3	Recall@4
(1, 2) / (4, 5)	0.844 (573/679)	0.909 (617/679)	0.946 (642/679)	0.954 (648/679)
1 / 2 / 4 / 5	0.627 (426/679)	0.784 (532/679)	0.850 (577/679)	0.884 (600/679)

Table 1: Nodule malignancy prediction by feature based similar nodule search (quantitative result). "(1, 2) / (4, 5)" means regarding 1, 2 as same label and 4, 5 as same label. "1 / 2/ 4 / 5" means regard 1, 2, 4, 5 as different labels.

Figure 3 illustrates that similar nodule search based on our proposed method works qualitatively well. Our approach is able to find nodules that have similar shape given a query nodule. This means that nodule features taken from a false positive reduction network contains generalizable information useful for other tasks. In table 1, we quantitatively show that the generated nodule features are well clustered with nodules with similar malignancy labels. This shows that our features can also be used for nodule malignancy prediction by similar nodule search.

4 Conclusion and Future Work

We show that taking generalizable nodule features from a false positive reduction network for lung nodule detection ,which trained by nodule coordinate labels, is a feasible approach. We also show that the taken nodule features can be used for similar nodule search. In future work, we will attempt further validation on various datasets and transfer learning for small dataset problems.

References

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