A Transfer Learning Approach to Aggregated DICOM Lung Tumor Classification

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Abstract

1. Introduction

Transfer Learning is a technique that offers a unique approach to problems that require

1.1. Problem Definition

2. Related Works

3. Datasets

For this research we needed to obtain two separate datasets to fit two distinct roles. ImageNet, 3.1, was needed to train the classifier on general image data to fit the convolution segment of the network to recognize underlying image Structure. This is our source domain, D_s.

LIDC-IDRI, 3.2, is used to train the output segment of the the network. This is our target domain, D_t.

3.1. ImageNet Dataset

3.2. LIDC-IDRI Dataset

The Lung Image Database Consortium image collection (LIDC-IDRI) dataset is a very popular cancer classification dataset that focuses on tumors located in the lungs. The lung scans are CT images of the upper torso. The entire dataset consists of 1018 cases that each contain thoracic radiologists annotations of tumor segments These tumors annotations each contain 9 different descriptors such as malignancy, calcification, and lobulation. The descriptor this paper is interested in is the malignancy of each nodule.

The malignancy is rated on a 1-5 scale. 1 being 'Highly Unlikely' of malignancy and 5 being 'Highly Suspicious' of malignancy. Using these ratings each slice in a chest CT was rated as either malignant, benign, or non-nodule. A slice was considered non-nodule if there was no nodule annotations found within the slice. To split nodules into malignant and benign labels, the annotations performed on a specific node were averaged and for malignancy values ≥ 3, the node was considered malignant and for malignancy values < 3, the node was considered benign, based upon the 4 radiologists predictions.

3.2.1 PyLIDC

To assist in the extraction of data from the DICOM image files, a python library was utilized to read to XML files which contained the annotation information for each nodule. [1]

4. Network Structure

4.1. Convolutional Neural Network

4.2. Aggregation SVM

5. Experiments

6. Results

7. Conclusion

References

[1] M. Hancock. Pylidc. https://github.com/notmatthancock/pylidc, 2018.