A Transfer Learning Approach to Aggregated DICOM Lung Tumor Classification

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Abstract

DICOM classification is a challenging task which typically requires a trained medical professional to choose the best slices of a scan and accurately classify the chosen slices. With medical data privacy restrictions and regulations, it is difficult to collect sufficient data to construct a typical Convolutional Neural Network to choose and classify DICOM slices. We propose a inductive transfer learning approach which applies hidden layer image representations from an ImageNet classifier to our DICOM classifier to classify each slice and aggregate the results, outputting the overall likelihood of a malignant presence in a given scan.

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]

3.2.2 Processing LIDC-IDRI Data

DICOM files, (Digital Imaging and Communications in Medicine), are the standard method for transferring and communicating image data. The structures of these files are extremely robust and offer many access in the form of 'Tags'. In the case of LIDC-IDRI, the dataset is composed entirely of CT images which must be processed by first transforming the image data along the HU (Hounsfield scale) given the transformation coefficients in the DICOM.

The vertical slice size must also be taken into account because CT scans can be ordered in a variety of ranging

resolutions from (< 0.1mm to > 3mm). A scale of 1 mm per slice was chosen and the pixel data was transformed.

4. Network Structure

4.1. Convolutional Neural Network

4.2. Study Aggregation

5. Experiments

6. Results

7. Conclusion

References

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