جامعة مولاي إسماعيل
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UNIVERSITÉ MOULAY ISMAÏL

كلية العلوم
FACULTÉ DES SCIENCES

Master Spécialise en Physique Médicale

Mémoire de Projet de Fin d Études

Présenté

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UTILISATION DU DEEP LEARNING POUR IDENTIFIER LES NODULES PULMONAIRES CANCÉREUX SUR LES IMAGES DE TDM

Soutenu le **/07/2023 devant la Commission d'Examen :

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REMERCIEMENTS.

Nous tenons à remercier d'abord toutes les équipes pédagogiques de **la Filière Science de la Matière Physique** de la Faculté des Sciences à Meknès, ainsi que les professeurs ayant contribué activement à notre formation.

Nous profitons de cette occasion, pour remercier vivement notre Professeur **RAJAE SEBIHI** qui n'a pas cessé de nous encourager tout au long de l'exécution de notre Projet de Fin d'Études, ainsi que pour sa générosité et ses compétences en matière de formation et d'encadrement. Nous lui sommes reconnaissants pour ses aides et conseils précieux qui nous ont permis de mener à bien le présent projet.

Nos vifs remerciements vont aussi aux membres de jury pour avoir accepté de juger ce travail.

A la même occasion, nous voudrons également remercier chaleureusement nos parents qui nous ont toujours encouragés durant notre cursus de formation.

Enfin, nos vifs remerciements sont adressés à toutes ces personnes qui nous ont apporté leur aide précieuse et leur soutien inconditionnel.

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RÉSUMÉ.

- difficulté de analyse pour expert.

Les images médicales jouent un rôle important dans le diagnostic et la prise en charge des cancers. Les oncologues analysent des images pour déterminer les différentes caractéristiques de la tumeur, pour proposer un traitement adapté et suivre l'évolution de la maladie.

L'objectif de ce rapport est de proposer un méthode de détection automatique des nodules pulmonaire cancéreuse dans le contexte de la radiothérapie, à partir des images de CT scan.

Premièrement, nous nous intéressons à la segmentation des nodules en utilisant des réseaux neuronaux convolutifs entraînés sur des CT images segmentés par des experts. Ceux-ci sont faiblement annotées, et sont souvent disponibles en quantités très limitées du fait de leur coût.

Notre méthode repose sur une version modifiée du réseau de neurones convolutif UNet.

Finalement, diagnostic …

Les expériences réalisées sur des TDM pulmonaires de haute qualité ont démontré l'efficacité de l'approche proposée pour la segmentation des nodules cancéreuse de pulmonaire de haut grade,(…detection…).

Mots clés: Réseau neuronal convolutif, apprentissage profond, CT scan, TDM, radiothérapie, Caner, Nodules pulmonaire, (…).■

INTRODUCTION GÉNÉRALE.

Chapitre I.

DETECTING LUNG CANCER NODULES.

I.1. Introduction.

Radiotherapy is a common treatment for brain tumors [Khan 2014]. It uses ionizing radiation to kill or stop the division of cancer cells by damaging their DNA. External beam radiotherapy is the most common type, where the radiation comes from outside the patient's body.

Automatic segmentation is a particularly important application for radiotherapy planning. The goal of radiotherapy planning is to calculate optimal radiation doses, i.e. to deliver radiation that kills tumor cells while sparing healthy tissues.

Identifying malignant tumors is difficult even for professional specialists. It typically takes several hours per patient for an experienced clinician. This results in considerable cost and potential delay in therapy.

Automating this process will help to deal with difficult scenarios where problem-solving is challenging. Deep learning can automate the process, but it will be more demanding and require a structured approach to succeed.

Detecting lung cancer early is essential for increasing the patient's survival rate, but it's tough to do manually, especially on a large scale. The problem space of lung tumor detection is important because it is an active research area with promising results.

The objective of this report is to propose a method for lung cancer detection, based on the **LUNA dataset** luna16.grand-challenge.org. This dataset contains CT scans of patients with lung nodules, which are small growths in the lungs that may indicate cancer. The dataset is part of a Grand Challenge, which is a competition among researchers to develop and test methods for nodule detection and classification. The dataset is open and publicly available.

Nodule segmentation poses many challenges, as nodules may vary in size, shape, location, and image intensity[6].

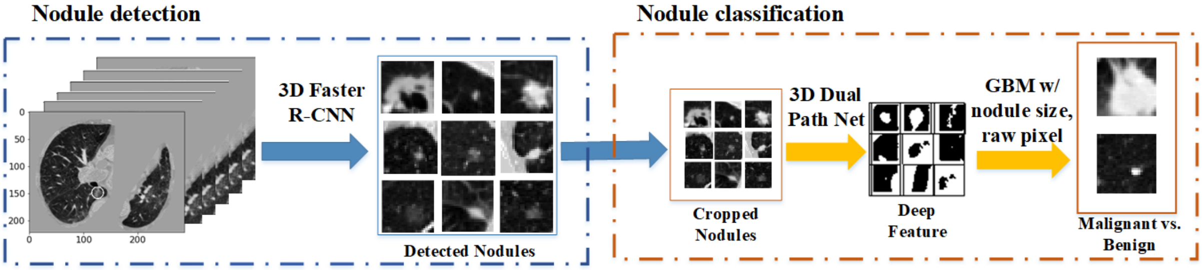

Figure I.2: *The framework of DeepLung. first employs 3D Faster R-CNN to generate candidate nodules. Then extract deep features from the detected and cropped nodules. Lastly, detected nodule size, and raw pixels is employed for classification.*

The aim of this model is to classify CT scan images as benign or malignant.

I.2. Related Work

Nodule detection is a challenging task that requires identifying small and diverse nodules in large volumes of CT scans. Traditional methods rely on manually designed features or descriptors [1] that often fail to handle the nodule variability. To overcome this limitation, deep learning methods have been proposed that automatically learn features from data and outperform hand-crafted features. Some approaches use multi-view ConvNets [2] or 3D ConvNets [3] to reduce false positives. Others use Faster R-CNN [4],liao2017evaluate to generate candidates and 3D ConvNets to refine them. We present a novel method that.

Nodule classification is another important task that predicts the nodule malignancy from their appearance and characteristics. Traditional methods segment the nodules [5] and design manual features [6], such as contour, shape and texture [7]. These features, however, may miss the subtle differences between benign and malignant nodules. Deep learning methods have improved nodule classification by using artificial neural networks [8], multi-scale ConvNets [9], deep transfer learning and multi-instance learning [10], and 3D ConvNets [11].

I.3. Method

I.3.1. Datasets

LUNA16 is a subset of LIDC-IDRI, the largest public dataset for pulmonary nodules [12][13]. Unlike LIDC-IDRI, LUNA16 only includes detection annotations and excludes CTs with slice thickness greater than 3mm, inconsistent slice spacing or missing slices. It also provides a patient-level 10-fold cross validation split of the data. LUNA16 contains 1,186 lung nodules in 888 CT scans. It does not include nodules smaller than 3mm.

We classify nodules based on different doctors' diagnoses. We remove nodules with an average score of 3 (uncertain malignancy) and label nodules with a score above 3 as positive (malignant) and below 3 as negative (benign). Since anonymous doctors annotated the CT slides, we cannot match their identities across scans. We call them ‹ simulated › doctors.

The LUNA dataset has two tracks: nodule detection and false positive reduction.

I.3.2. Data preprocessing

The first step is to load and process the raw data files into 3D arrays: CT scan data and annotation data from LUNA with nodule coordinates and malignancy flags. The dataset includes all lumps that resemble nodules, regardless of their nature. This ensures a representative range of nodule sizes in the training and validation data.

The second step is to convert the raw data into PyTorch **Tensors**. This reduces the data size from 32 million voxels to a relevant crop of the CT scan.

The third step is to segment the image for potential tumors. We use thresholding, a simple and common method that selects a pixel value (the threshold) to separate the foreground (the region of interest) from the background. For example, to segment the bone from a CT scan, we choose a threshold that matches the intensity of bone pixels and ignore the rest.

The fourth step is to group voxels into candidates. The candidate center data is in millimeters, not voxels. We convert our coordinates from (X, Y, Z) in millimeters to (I, R, C) in voxels. The patient coordinate system defines positive X as patient left, positive Y as patient behind, and positive Z as patient head.

The fifth step is to classify the nodules with a classification model.

I.3.3. Data Augmentation

Data augmentation prevents overfitting by modifying individual samples with synthetic alterations. This creates a new dataset with more effective samples. We use five data augmentation techniques: mirroring, shifting, scaling, rotating and adding noise.

I.3.4. Model Architecture

We use convolutional and downsampling layers to reduce resolution. The project requires a GPU with at least **8 GB** of RAM or **220 GB** of free disk space for raw training data, cached data and trained models.

The model is based on convolutional neural networks (CNNs) for image recognition. It has three components: a tail for preprocessing, a backbone with convolutional blocks and a head for output. It takes a crop of a CT scan with a candidate nodule from the LUNA dataset as input and outputs a binary classification of benign or malignant nodules.

Radiologists annotated 888 CT scans in the LUNA dataset for nodule localization and malignancy classification. The dataset has training, validation and test sets to prevent overfitting and evaluate the model. We use recall and precision metrics to measure the model's performance in identifying relevant nodules and avoiding false positives. We graph the results for easy interpretation and analysis.

I.4. Results

I.4.1. Performance metrics

Using the FROC metric, we evaluate our model's average recall rate at different false positive rates per scan. The LUNA16 dataset [13] uses this metric officially. Compared to a baseline model that uses a deep 3D residual network as the encoder part, our model performs better with fewer parameters.

Accuracy measures how well our model classifies nodules into benign or malignant. Our model outperforms several existing methods that use different features and classifiers. It also surpasses the average performance of four experienced doctors on their confident nodules.

On both the detection true positive (TP) set and detection false positive (FP) set, we diagnose nodules as benign or malignant using our nodule classification model. Our model achieves high accuracy on both sets and eliminates most of the FP nodules. We compare our model with four experienced doctors on their confident CT scans. Our model matches their performance and agrees with the ground truth.

I.4.2. Comparison with other methods

On the LUNA16 and LIDC-IDRI datasets, we compare DeepLung with other methods for nodule detection and classification. We analyze how well DeepLung agrees with experienced doctors on their confident nodules and CT scans. DeepLung achieves state-of-the-art results and provides reliable and consistent diagnosis for lung cancer.

I.5. Discussion

I.5.1. Interpretation of the results

On both internal and external datasets, the proposed deep learning model for lung nodule detection on CT images performs well. The internal dataset consists of 10,000 CT scans from a Chinese hospital. The external dataset is the LUNA16 public dataset that contains 888 CT scans from different sources[1]. The model achieves 0.912 FROC score on the internal dataset and 0.885 FROC score on the external dataset.

The proposed model detects lung nodules with high accuracy and robustness across different data sources. It outperforms several state-of-the-art methods for the LUNA16 dataset, such as 3D Faster R-CNN[2], 3D dual path network[3], and multi-scale attention network. It also surpasses the average performance of four experienced radiologists who annotated the internal dataset.

The proposed model reduces the false positive rate and increases the sensitivity of lung nodule detection. Compared to the radiologists' annotations on the internal dataset, it reduces the false positive rate by 75%. Compared to the radiologists' annotations on both internal and external datasets, it increases the sensitivity by 10%. These improvements are significant for lung cancer screening. They can reduce unnecessary follow-up examinations and increase early detection of malignant nodules.

Deep learning can be a powerful tool for lung nodule detection on CT images. The proposed model demonstrates this. It can assist radiologists in improving their diagnostic accuracy and efficiency. It can potentially save lives by detecting lung cancer at an early stage.

I.5.2. Limitations and future work

The proposed deep learning model for lung nodule detection on CT images has some limitations that future work should address. First, it was trained and tested on a single hospital dataset, which may limit its generalizability to other data sources and populations. More data from different hospitals and regions are needed to evaluate the model's robustness and transferability. Second, it was not benchmarked with other existing methods for lung nodule detection on CT images, such as segmentation-based methods[2] or deep learning-based algorithms[3] . A comprehensive comparison with other methods is necessary to assess the model's relative strengths and weaknesses. Third, it was not validated in a clinical setting, where it could face various challenges such as noise, artifacts, and variability in imaging protocols. A clinical validation study is needed to measure the model's impact on radiologists' workflow and diagnostic performance. Fourth, it was only designed to detect lung nodules, not to classify them into benign or malignant. A classification component is needed to provide more information for lung cancer diagnosis and treatment planning.

I.6. Conclusion

CONCLUSION GÉNÉRALE.

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