Radiomic Medical Data Transformation for Radiologists Support

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Abstract

We present a process of transforming medical data into a system that supports radiologists' interpretation and understanding of Computed Tomography (CT) images. The system is based on a pipeline that includes image conversion, organ segmentation, feature extraction, and report rendering. The final report presents organ visualisations and information about organ measurements, with marked outliers, to the radiologist. The system was created using data from the database containing over 40,000 CT scans and a pre-trained Swin UNETR architecture. The system obtained 89.09% DICE for five segmented organs. The created solution can go through the process in less than five and a half minutes, and its usability was confirmed by radiologists.

Keywords: Radiomics, Data processing, Segmentation, Visualisation, Reference values.

1. Introduction

Diagnostic imaging in radiology can be taken as an example of digital transformation, as the radiologists analyse digital images, such as Computed Tomography (CT) scans and the process can be supported by IT solutions, including software using AI solutions. However, many commercial solutions cannot guarantee that the proposed digital innovation is effective, as they lack peer-reviewed evidence of efficacy [4]. On the other hand, some solutions that came through the scientific review process, i.e. [5],[10], are distributed as libraries, without an efficient workflow.

To fill this gap, we propose a streamlined pipeline that replaces the manual tasks of taking the measurements of organs on CT scans with AI and transfers DICOM data into a readable report, improving the user's experience.

Because the proposed solution is based on a massive database of 40 thousand CT scans, it was possible to calculate reference values and use to highlight outlier values in the final report. Thanks to size of the dataset it was more feasible to create robust references than using smaller data sets. i.e. [5],[7]. Performed tests answered the research questions, whether the proposed automation will perform high-quality organ segmentation in a reasonable time and improve the radiologists' experience of working with digital data.

2. State of the art

The commercial market of AI software in radiology was summarised in [4]. The authors analysed 100 CE-marked AI products from 54 different vendors. However, 64% of products had no peer-reviewed evidence of their efficacy, and only 18% AI products have demonstrated clinical impact. Therefore, the authors concluded that the sector is still in its infancy.

Several applications of deep learning for organ segmentation already exist. The architecture of the applied network is similar, and the solutions differ according to the used learning dataset. Using a dataset of 140 CT scans, a deep neural network was trained, which requires only 4.3 s to simultaneously segment six organs [5]. The same dataset was used to create an improved U-Net-based solution, obtaining the average DICE of 80.46% [7].

In work [6], a Res-UNET model was trained and tested on a dataset of 3106 CT images to generate segmentation masks of 15 common organs. The obtained average DICE coefficient before and after post-processing was at the level of 84.28% and 83.26%, respectively, with an inference time of 1.67 seconds per case per organ for a total-body CT image. A lightweight medical image segmentation network named LCOV-Net was proposed in [10]. Experiments on two public CT datasets for multiple organ segmentation showed that LCOV-Net obtained an average DICE of up to 85.91%. Work presented in [8] used pediatric CT examinations, which differ from adult data sets. Using 1731 CT examinations and various architectures (SegResNet, DynUNet, and SwinUNETR), the obtained DICE reached 95% on the three examined organs.

3. Methodology

3.1. Data

The largest and most diverse source of lung data used in the project was the Polish Lung Cancer Group (PLCG) database[1]. The database consists of 40,000 CT scans of people participating in a nationwide lung cancer screening trial between 2010 and 2018. It makes the data set more extensive than the biggest public CT data set - The National Lung Screening Trial (NLST).

The data copying process took four months. An average of 450 discs per hour were copied, which was made possible by using a system consisting of two laptops with twenty DVD readers connected and four external drives with a total capacity of more than 10 TB.

To aid the interpretation of radiomic organ parametrisations by end users of our solution, observations from the PLCG database were used to create reference value distributions. In order to do so first, we processed CT images from the entire database using the presented data processing pipeline. Next, for each organ and each radiomic feature, we computed a set of

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[1] `https://www.polgrp.org.pl`

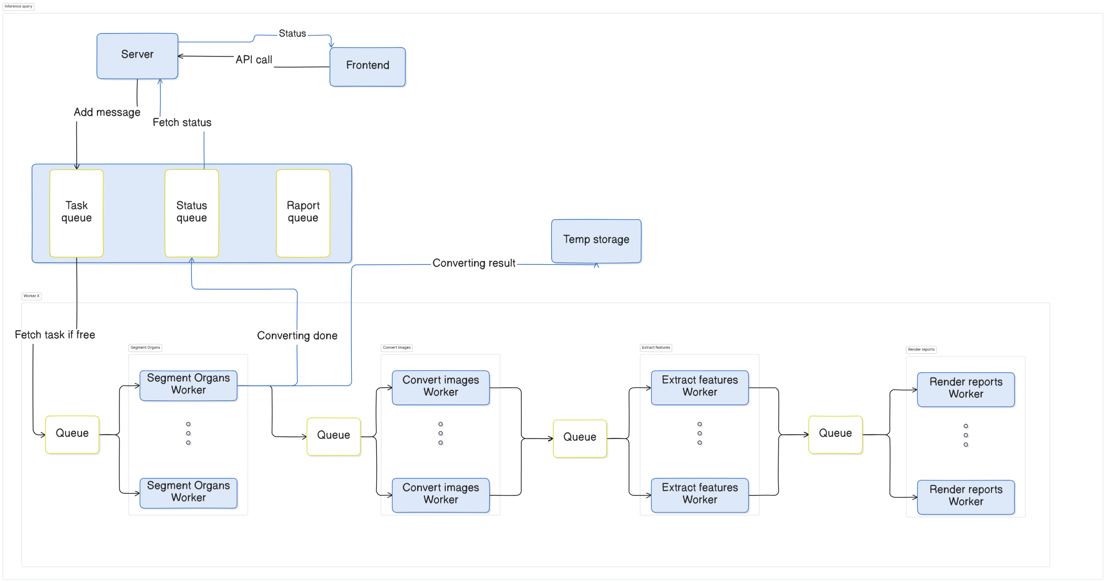


Fig. 1. Schema of the system with task processing components

percentiles. These percentile tables enable end users to quickly assess whether all radiomic feature values for a given organ fall within the typical range or to identify any outlying values. Our references may be replaced with data from any other dataset. However, we recommend a minimum size of 1,000 records.

3.2. System

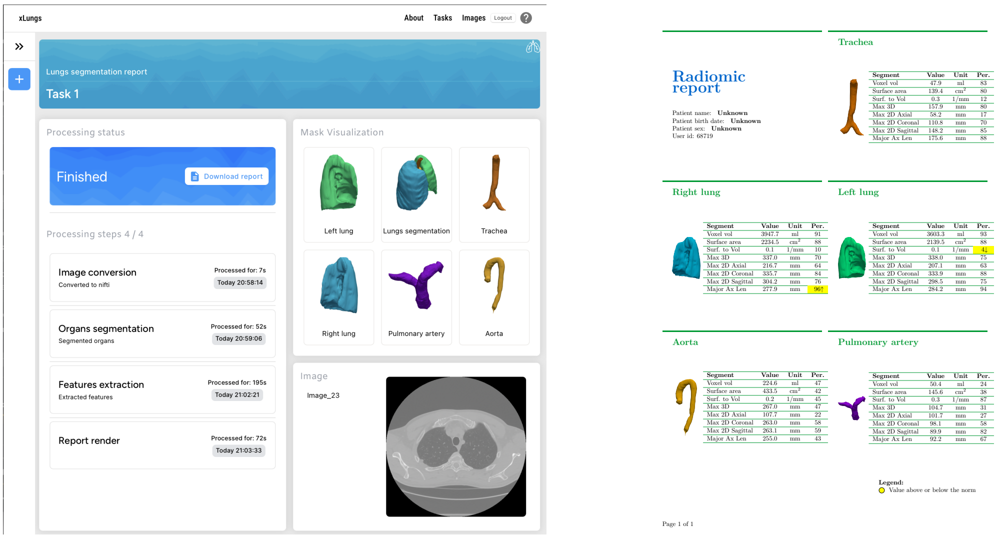
As presented in Fig. 1, the computation server consists of four types of horizontally scalable workers, communicating with different RabbitMQ queues. The user interface presented in Fig. 2a was implemented using React. Further communication with the server is performed using API calls. The web backend sends a message to the first queue. Workers sequentially process the data, and the task is moved to the next queue when finished.

The image conversion converts data from DICOM format to NIfTI (Neuroimaging Informatics Technology Initiative), which is necessary to prepare numerical data for organ segmentation.

The GPU-accelerated segmentation model is based on a pre-trained Swin UNETR architecture [2]. It is an improved version of the TotalSegmentator model [9] that is based on the older nnUNet [3] architecture and can segment over one hundred anatomical structures in CT images. More information about the created model can be found in [1].

The radiomic feature extraction is performed using the PyRadiomics library. The utilisation of the CPU by this worker is the highest in the whole pipeline. The most resource-consuming part of the extraction is the computation of spatial shape, which is the base for the feature calculation. The selection of radiomic metrics for further presentation was consulted with radiologists and includes: Mesh volume, Voxel Volume, Surface area, Surface Area to Volume ratio, Maximum 3D diameter, Maximum 2D diameter (Slice), Maximum 2D diameter (Column), Maximum 2D diameter (Row), and Major Axis Length.

The features are compared with the reference values, computed outside the main pipeline, and updated only if the reference dataset has been extended or modified. After feature values are compared with references to detect outliers, an automated LaTeX-based reporting service assembles interactive dashboards and PDF summaries. To create the PDF file, the report render uses Jinja to fill out the template and compile the file using Latexmk. Fig. 2b presents the final report, with the outliers marked in yellow.



Lungs segmentation report

Task 1

Processing status

Finished

Processing steps 4 / 4

Image conversion
Converted to nifti
Processed for: 7s
Today 20:58:14

Organs segmentation
Segmented organs
Processed for: 52s
Today 20:59:06

Features extraction
Extracted features
Processed for: 195s
Today 21:02:21

Report render
Processed for: 72s
Today 21:03:33

Mask Visualization

Image
Image_23

(a) Web application

Radiomic report

Patient name: **Unknown**
Patient birth date: **Unknown**
Patient sex: **Unknown**
User id: 68719

Trachea

Segment	**Value**	**Unit**	**Per.**
Voxel vol	47.9	ml	83
Surface area	139.4	cm^2	80
Surf. to Vol	0.3	1/mm	12
Max 3D	157.9	mm	80
Max 2D Axial	58.2	mm	17
Max 2D Coronal	110.8	mm	70
Max 2D Sagittal	148.2	mm	85
Major Ax Len	175.6	mm	88

Right lung

Segment	**Value**	**Unit**	**Per.**
Voxel vol	3947.7	ml	91
Surface area	2234.5	cm^2	88
Surf. to Vol	0.1	1/mm	10
Max 3D	337.0	mm	70
Max 2D Axial	216.7	mm	64
Max 2D Coronal	335.7	mm	84
Max 2D Sagittal	304.2	mm	76
Major Ax Len	277.9	mm	96↑

Left lung

Segment	**Value**	**Unit**	**Per.**
Voxel vol	3603.3	ml	93
Surface area	2139.5	cm^2	88
Surf. to Vol	0.1	1/mm	4↓
Max 3D	338.0	mm	75
Max 2D Axial	207.1	mm	63
Max 2D Coronal	333.9	mm	88
Max 2D Sagittal	298.5	mm	75
Major Ax Len	284.2	mm	94

Aorta

Segment	**Value**	**Unit**	**Per.**
Voxel vol	224.6	ml	47
Surface area	433.5	cm^2	42
Surf. to Vol	0.2	1/mm	45
Max 3D	267.0	mm	47
Max 2D Axial	107.7	mm	22
Max 2D Coronal	263.0	mm	58
Max 2D Sagittal	263.1	mm	59
Major Ax Len	255.0	mm	43

Pulmonary artery

Segment	**Value**	**Unit**	**Per.**
Voxel vol	50.4	ml	24
Surface area	145.6	cm^2	38
Surf. to Vol	0.3	1/mm	87
Max 3D	104.7	mm	31
Max 2D Axial	101.7	mm	27
Max 2D Coronal	98.1	mm	58
Max 2D Sagittal	89.9	mm	82
Major Ax Len	92.2	mm	67

Legend:
● Value above or below the norm

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(b) Report with radiomic features

Fig. 2. Example of processing for a single CT scan (DCIM format)

4. Tests

The segmentation results were evaluated using a holdout dataset with masks prepared by the radiologists. The DICE, a volume of the common part of the mask and prediction to the union of both elements, was used to evaluate the segmentation quality. The average DICE for all organs reached 89.09. The best scores were obtained for lungs, 92.80 and 90.34 for left and right, respectively. Smaller organs like the aorta and trachea obtained results slightly over 89. The lower results of 84 were obtained for the pulmonary artery.

The obtained result is better than presented in works [7] (U-Net, 80.46%), [6] (Res-UNET, 84.28%), and [10] (LCOV-Net, 85.91%), but smaller than in [8] (SwinUNETR, 95%). However, the results were obtained from various data sets and various organs. Therefore, the obtained result can be taken as satisfactory.

The median time for processing a single DICOM was 5 minutes and 24 seconds. The median time of the segmentation was 55 seconds, which is a longer time than reported in [5] (4.3 seconds to segment six organs) and in [6] (1.67 seconds to segment a single organ). However, the reconstruction of a three-dimensional organ involves several inferences.

The application was also tested in user study by 15 physicians specialised in radiology. The average satisfaction with the system was 4.3/5 (SD = 0.62).

5. Conclusions

We have presented an end-to-end system that transforms a DICOM CT into a report that points out standout measures. Its creation was possible due to the conversion and analysis of a massive CT data set.

The performed tests showed that the system can segment the selected organs with a DICE of 89.09%, which is similar to the best existing solutions, analysing a single DICOM in time close to 5 minutes. Therefore, the proposed workflow of medical image analysis can improve radiologists' experience in interaction with digital data, which was confirmed by usability tests.

In the current form, an application started a customer-driven innovation, where, after a good reception of the introduction of AI in a lower-risk but challenging process of describing a typical human organ, the workflow can be extended to model and visualise various lung conditions, like fluid in the pleural cavity and nodules.

Acknowledgements

This work was financially supported by the Polish National Center for Research and Development grant number INFOSTRATEG-I/0022/2021-00, and carried out with the support of the Laboratory of Bioinformatics and Computational Genomics and the High Performance Computing Center of the Faculty of Mathematics and Information Science, Warsaw University of Technology.

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