Diagnostic, prognostic and predictive capabilities of radiomic analysis in oncology

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Introduction

Radiotherapy (RT) is known to lead to both immune stimulatory and suppressive effects, the latter of which can cause such side effects as radiation-induced lymphopenia (RIL). RIL can lead to a worse response to cancer treatment and was therefore reported as a negative prognostic factor in patients treated with RT for variety of tumors. This line of research is a continuation of my work on prediction of RT side effects, but it is more challenging than prediction of Radiation Induced Hypothyroidism (RIHT) that I worked on during previous year. RIL, contrary to RIHT, is not associated with any single anatomic region, so any commonly used state-of-art normal tissue complication probability (NTCP) model, would not perform satisfactorily. In consequence, my research must incorporate anatomic regions rich in immune cells and identification of the most relevant ones for RIL prediction.

In order to extend the spectrum of information that can be obtained through investigation of affected patients, I employ a method called radiomics. It aims at deriving biomarkers from medical images, which are typically features describing shape, intensity or texture of specific Region(s) of Interest (ROI), typically organs at risk. The radiomic approach provides the ability to efficiently mine features, which are imperceptible to the human eye, but may provide crucial data about the patient's condition.

One of the steps in the pipeline of data preparation before radiomic features extraction, that could benefit the most from automatization, is the segmentation of ROIs. Currently such segmentation is performed by doctors and requires specialized knowledge to delineate each of the organs by hand. Moreover, prediction of RIL may require analysis of regions that are typically not segmented during RT planning, e.g. ribs or sternum, so manual delineation would generate considerable workload for radiotherapist or radiologist.

Methods

For development of a pipeline for automized segmentation and assessing its reliability, I collected a preliminary set of CT images, together with matching RT plans. The population for my study consisted of patients, who have undergone radical RT for non-small cell lung cancer. After the preselection of patients based on the inclusion criteria (age, tumor location, RT type) I managed to collect image scans, with required modalities, for 30 of them, half of them with RIL that developed during or after RT. All images and organ segmentations were stored in DICOM format in CT and RTSTRUCT modalities.

In order to compare manual and automatic segmentation methods, I prepared 2 separate pipelines, beginning with the same CT scans. For performing automatic segmentation, a tool, based on a machine learning model adapted to CT images, called TotalSegmentator [1] was incorporated into the pipeline. The first organ to be investigated was chosen to be a heart, because it is always delineated manually for lung cancer RT as is it is considered organ at risk that should receive the lowest possible radiation dose. The concordance of volumes (3D shapes) resulting from both investigated segmentation methods was quantified by the Dice similarity coefficient (DSC) [2].
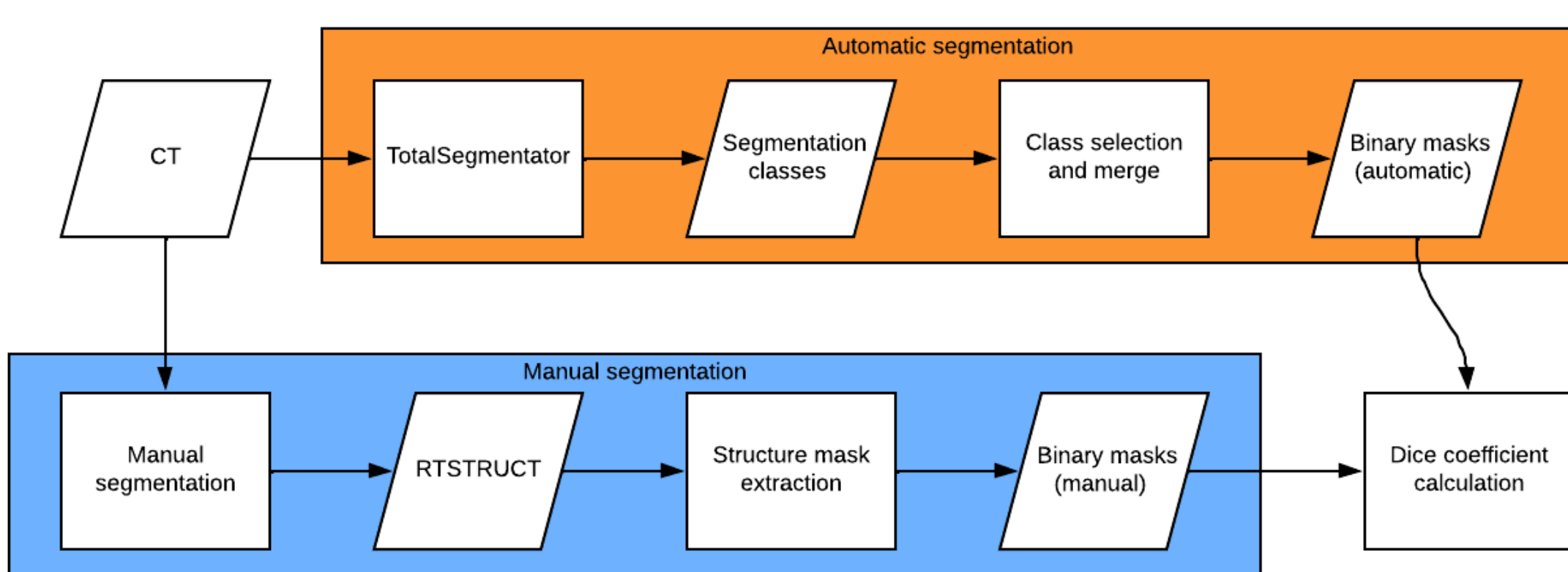

Figure 1. Comparison of steps between automatic and manual pipelines for organ segmentation into binary organ masks

Results

Currently, images collected from 11 patients have sufficient image metadata and manual organ delineations to complete both pipelines. The average DSC value for the included patients was equal to 0.835 (±0.027), indicating a relatively high similarity between volumes across both approaches. However, simply by looking at the raw value of DSC, it is not possible to determine which approach is superior. In general, I observed that the understanding of how an organ should be delineated varies between those two approaches. During a manual segmentation, a heart is considered as the entire region, which encompasses all of the heart's structures and sometimes even fragments of blood vessels coming to/from the heart. On the other hand, automatic algorithm performs segmentation of various heart structures (ventricles, atria, myocardium) separately and treats a heart as a volumetric sum of these structures.
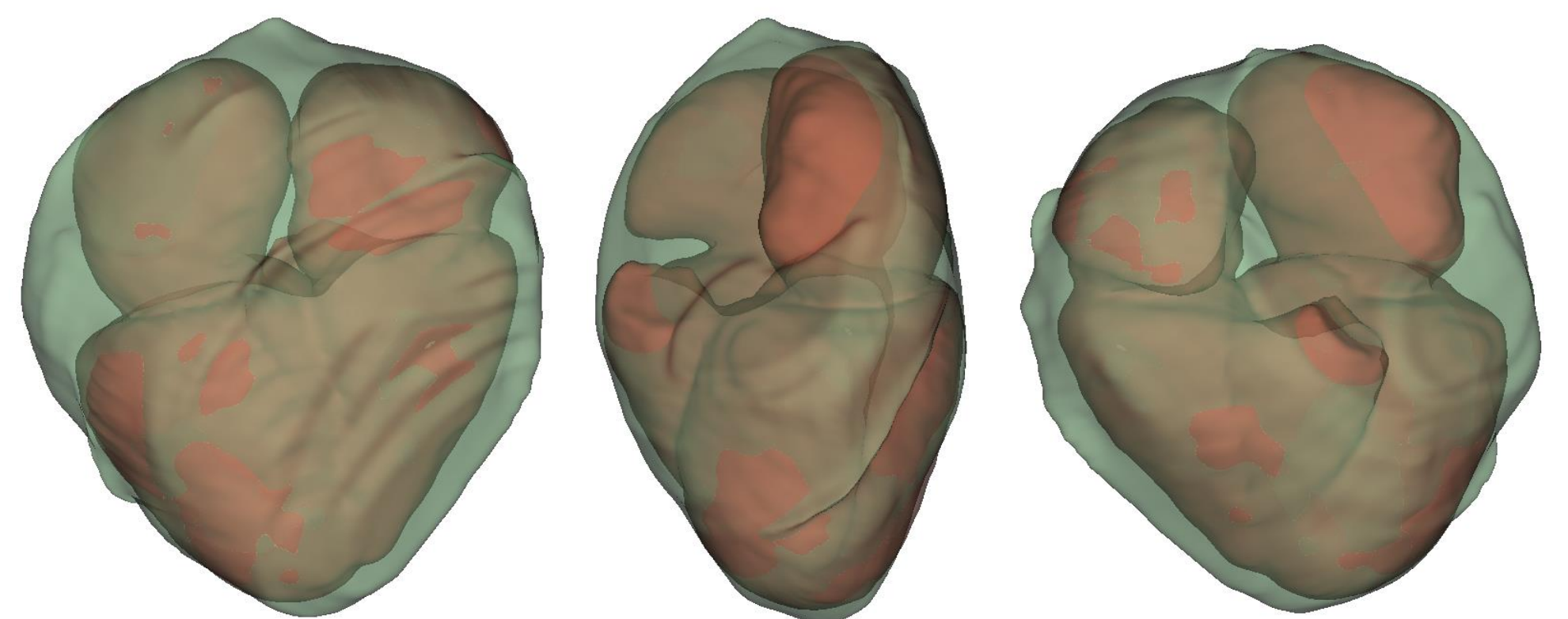

Figure 2. Manual (green) and automatic (red) segmentation volumes of a heart

Conclusions

After successful creation of pipelines for extraction of binary organ masks for a heart, I was able to calculate a coefficient of similarity between manual and automatic segmentation. Even though the raw values of this coefficient seem to indicate that the automatic approach could be a viable replacement for manual segmentation, examining the differences in shapes revealed that this problem requires further investigation and consultation with specialists.

An important step in improving the applicability of my pipeline to a wider range of imaging files is to extend its ability to deal with different DICOM tag values and formats and thus being able to process more images. In the future, I plan to analyze other immune-system-related structures, including bones, which are a reservoir of bone marrow containing stem, as well as large blood vessels, where mature blood cells are concentrated, similarly as in the heart. Furthermore, I will continue to collect DICOM CT files from patients fulfilling the inclusion criteria.

The ultimate goal of this line of investigation would be the analysis of a similarity index for extracted radiomic features from manually and automatically segmented ROIs related with immune system. The entirety of over 1300 radiomic features (including those extracted from filtered images) for each of CT and RTDOSE modalities would sufficiently cover the spectrum of information that can be obtained from medical scans. Any potential differences in their values could influence the quality of machine learning models, which would be created for the purpose of outcome prediction.

References

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