Technical Note

Radiomics integration into a picture archiving and communication system

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\textbf{ABSTRACT}

Radiomics is referred to as quantitative imaging of biomarkers used for clinical outcome prognosis or tumor characterization. In order to bridge radiomics and its clinical application, we aimed to build an integrated solution of radiomics extraction with an open-source Picture Archiving and Communication System (PACS). The integrated SQLite4Radiomics software was tested in three different imaging modalities and its performance was...
1. Introduction

Radiological images have been acquired routinely for decades in the process of radiation treatment. Commonly used imaging modalities are (cone beam) computed tomography (CT), magnetic resonance imaging (MRI), and positron emission tomography (PET). The aim of these imaging modalities is to give either anatomical (CT and MRI) or functional (MRI and PET) information. Generally, the interpretation of medical images is performed by visual inspection. With the advent of advanced computer vision, it was hypothesized that algorithms could add quantitative and objective measurements to visual interpretation, as for example, in Computer-aided diagnosis (CAD) systems [1].

Recently, radiomics, where properties of the image, such as local textures, can be used as imaging biomarkers was proposed. Radiomics has been extensively applied to quantify biological properties of the tumor for better prognostication or treatment response predictions [2]. However, many studies have shown that radiomic values can be influenced by specific acquisition settings [3], leading to a poor generalizability of radiomic signatures on multi-center data.

Radiomic feature computations need to be combined with the corresponding image acquisition settings (Digital Imaging and Communications in Medicine, DICOM, metadata) so that the feature values can be harmonized against these settings using appropriately calibrated algorithms [3,4]. Conquest is an open-source Picture Archiving and Communication System (PACS) that stores DICOM metadata as database tables, opening the possibility of combining imaging data and metadata hosted on a PACS with radiomics. There are several radiomics extraction solutions available [5–8], however, from the best of our knowledge, current existing radiomics extraction software solutions do not support direct PACS integration and database-centered radiometric feature storage.

So far, the calculation of radiomic features required some knowledge of programming. As all the imaging data is already stored in a PACS, we viewed radiomics-PACS integration as a logical step to facilitate the introduction of radiomics in a clinical environment. We believe that due to the DICOM connectivity of Conquest, SQLite4Radiomics can be used to form a pipeline within the hospital wide PACS system, enabling routine analysis of the data.

The aim of this study was to develop a solution for wider radiomics adoption in radiation oncology by integrating a publicly available library, pyradiomics, with the open-source Conquest DICOM PACS software. In this technical note, we described the architecture, workflow, and benchmarking of SQLite4Radiomics – an integration software for pyradiomics and Conquest DICOM. The code and the user manual are available as open-source.

2. Materials and methods

2.1. SQLite4Radiomics

Conquest (or Conquest DICOM) is open-source PACS software (https://ingenium.home.xs4all.nl/dicom.html) that stores imaging data as DICOM files and the DICOM metadata in a SQL database. It runs a DICOM server and has full DICOM functionality, which makes it suitable for integration in a radiation oncology department. Pyradiomics is an open-source Python package (https://github.com/Radiomics/pyradiomics) for radiomics extraction [5] from medical images as defined in the Image Biomarker Standardization Initiative (IBSI) [9]. SQLite4Radiomics further broadens Conquest’s functionality by integrating pyradiomics feature extraction into the PACS. The supplementary materials describe SQLite4Radiomics application customization, pipeline, graphical user interface (GUI) frontend and backend.

2.2. Case study: Datasets

Open data from the Maastro LUNG1 cohort [10,11] was used to develop and test the software. These data included CT scans with manual delineations stored in the RTSTRUCT format. The LUNG1 dataset with the detailed cohort description is publicly available at the XNAT repository (https://xnat.bmia.nl/). Individual users collected their internal CT, MR, and PET data with RTSTRUCT delineations to test SQLite4Radiomics application in those modalities.

To benchmark SQLite4Radiomics performance, two open lung cancer cohorts were selected: Interobserver MMD PET-CT dataset and RIDER CT dataset, both available at the XNAT repository (https://xnat.bmia.nl/). The former consists of 22 unique PET-CT lung cancer images with multiple gross tumor volume delineations, and it was originally described and used in Aerts et al [10]. The latter, consists of 32 pairs of test–retest scans of lung cancer patients. The ROI delineations in both datasets were provided as DICOM RTSTRUCT files suitable for SQLite4Radiomics. These data were previously used to benchmark the performance of the O-RAW software, which we compared SQLite4Radiomics performance to [6].

2.3. Case study: Benchmarking and performance evaluation

The MMD PET-CT and RIDER CT datasets were used to evaluate the performance of SQLite4Radiomics including the pyradiomics parameter file corresponds to the default parameter file of SQLite4Radiomics stored on GitHub. With this file, 107 features including shape, first order statistics, and texture (GLCM, GLRLM, GLDM, GLSZM, NGTDM) categories were extracted from each of two ROIs per DICOMSeries. For instance, an MMD patient instance contains two series (PET and CT) – for both of those two, we extracted radiomics from two ROIs – the total of four extractions per patient.

Three system configurations were used to evaluate the performance of SQLite4Radiomics including SQLite query, plasmatch conversion, pyradiomics feature extraction, feature storage in the Conquest database. The first system configuration was represented with a HP EliteDesk 800 G2 TWR workstation (Windows 7 Enterprise, 16 GB RAM, Processor Intel(R) Core(TM) i7-6700). The second configuration was represented with HP EliteBook 840 G4 laptop (Windows 10 Enterprise, 8 GB RAM, Processor Intel(R) Core(TM) i5-7200U). The third configuration was represented by a Lenovo ThinkPad L480 laptop (Windows 10 Pro, 16 GB RAM, Processor Intel(R) Core(TM) i5-8250U). All the three system configurations were benchmarked using Novabench System Benchmarking Software (version 4.0.9 – January 2021).

A total of 107 features were extracted from two ROIs per DICOMSeries (either CT or PET) with the default parameter and configuration files listed on SQLite4Radiomics repository. The extraction time in seconds per ROI was chosen as a performance benchmarking metric in our study. There is, however, the possibility to customize the SQLite4Radiomics performance evaluation by, for instance, extraction time per voxel of ROI – this might be beneficial when there is a high ROI volume variation in a dataset.

2.4. User testing

In addition to the developers, two users independently tested the standalone pipeline application, while five users tested the GUI version. Two of the users are clinical physicists, one is a radiobiologist, and two are researchers. The user tests were performed by observation (a user performs a set of tasks, while a developer observes the process without interfering and takes notes) and in a remote fashion (a user freely tested
and used SQLite4Radiomics tool in their own time). In both cases, feedback was given by the users at the end of each test.

3. Results

In system configuration I, it took 4057, 4074, and 4204 s to process the RIDER dataset with a median extraction time per ROI of 10.1 s and it took 1592, 1537, and 1547 s to run the MMD dataset with a median extraction time per ROI of 6.3 s. In system configuration II, it took 7492, 7527, and 8745 s to run the RIDER dataset with a median extraction time per ROI of 20.5 s and it took 3472, 3843, and 3727 s to run the MMD dataset with a median extraction time per ROI of 17.4 s. In system configuration III, it took 4687, 4817, and 4776 s to run the RIDER dataset with a median extraction time per ROI of 9.7 s and it took 1632, 1596, and 1696 s to run the MMD dataset with a median extraction time per ROI of 6.2 s. All three configurations resulted in the total of 18 successful runs of SQLite4Radiomics. The results are represented in Fig. 1.

Each of the three configurations were benchmarked with the Nova-bench System Benchmarking Software. The configuration I received a total score of 1264 (CPU 920, RAM 257, Disk 87, GPU unavailable); the configuration II received 766 points (CPU 395, RAM 169, Disk 55, GPU 147), and the configuration III received 1330 (CPU 821, RAM 254, Disk 52, GPU 203). The GPU score was irrelevant for this specific study because the radiomics calculation and SQLite4Radiomics operation were CPU-based.

4. Discussion

Radiomics currently lacks integration in clinical pipelines. At the same time, we routinely generate, archive, and store images routinely in hospital PACS systems. In order to bridge radiomics and its clinical application, we presented SQLite4Radiomics – an integration software of pyradiomics and Conquest DICOM – two popular open-source tools of both worlds of radiomic analysis imaging and clinical imaging. SQLite4Radiomics can receive data through the standard DICOM frameworks – two popular open-source tools of both worlds of radiomic analysis imaging and clinical imaging. SQLite4Radiomics can receive data through the standard DICOM frameworks.

Fig. 1. Performance letter-value plot (generalization of the boxplot [15]). The graph shows the performance in seconds per region-of-interest in both MMD PET-CT and RIDER CT datasets for the three system configurations we used to benchmark SQLite4Radiomics’ performance in. The letter-value plot generalizes the classical boxplot by visualizing more percentiles (in %): {3.125, 96.875}, (6.25, 93.75), (12.5, 87.5), (25.0, 75.0)). The box area is proportional to the percentage of covered data. Each system configuration contains its Nova-bench score for reference.
Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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