

Exploring XNAT to Foster Development and Testing of Image Processing Methods for Clinical Settings: Preliminary Results

Samuel Silva¹, João Abrantes¹

¹*IEETA – Institute of Electronics and Informatics of Aveiro,
DETI – Department of Electronics, Telecommunications and Informatics, University of Aveiro
Campus Universitário de Santiago, 3810-193, Aveiro, Portugal
sss@ua.pt, jabrantes@ua.pt*

Abstract. Medical imaging has evolved greatly in the past two decades and provides a rich set of data on the anatomy and function of important organs such as the heart. In this regard, medical image processing has also evolved to take advantage of these data and provide clinicians with methods supporting, for instance, (semi-) automatic identification of regions of interest and objective measures that can inform diagnosis. Recently, methods have also been proposed to perform haemodynamic simulations based on anatomic structures extracted from this data, which substantiate a noninvasive alternative to obtain important descriptors, such as the fractional flow reserve (FFR). The development of such methods is best served by working closely with clinicians, and, after a first validation, if these methods can be experimented with in a wide range of cases, they can more closely inform their evolution and an assessment of their performance.

Clinicians often have their diagnosis workflow supported on dedicated workstations, often proprietary, that not only integrate the processing and analysis of the imaging data but also provide visualization features that allow, for instance, visualizing the data from specific angles so as to conform with standard practice. Therefore, when developing new methods, it is important to comply with these basic features to promote easier use and evaluation. However, integrating novel methods in existing workstations is mostly out of question and developing a new framework from scratch to support all the workflow is a major effort.

In this work, we argue for a novel approach to supporting the research workflow in image processing and analysis methods and explored the XNAT framework, designed to support clinical studies pipelines, to assess how it can be used to deploy these methods, particularly by its integration with image viewers such as the one provided by the Open Health Image Foundation (OHIF). After its deployment in a virtualized environment and exploration of its main features, a proof-of-concept pipeline developed in Python was successfully integrated to smooth the images and return the processing results to the framework. Overall, mastering the integration with XNAT is complex at first, but the framework provided a promising response to the intended use.

Keywords: XNAT, OHIF Viewer, Image Processing, user-centered research workflow

1 Introduction

Cardiovascular diseases (CVDs) exact a heavy toll, causing approximately 17.9 million deaths annually, representing about 32% of global mortality according to the World Health Organization (a recent analysis of the data can be found in [1]). To counter this staggering statistic, enhancing clinical diagnostic capabilities remains paramount [1, 2]. Detecting CVDs early significantly improves treatment success rates. Recent years have witnessed remarkable technological strides, especially in medical imaging and software-driven diagnostic solutions, yielding increased precision, efficiency, and non-invasiveness. These advances extend to cardiac health, enabling analysis of three-dimensional heart images and simulating reconstructive and invasive procedures using computed tomography (CT) and magnetic resonance imaging (MRI) data. These innovations also offer temporal image data, enabling assessment of cardiac function, such as myocardial contractility and perfusion.

Yet, managing the vast and complex data generated by imaging technologies while embracing quantitative diagnostic frameworks demands computer-assisted diagnosis (CAD) tools [3]. Researchers are actively developing advanced diagnostic techniques, including methods like quantitative characterization such as calcium scoring [4]. However, validating and integrating these methods pose challenges.

To improve CAD tools for cardiac diagnosis using heart CT imaging [5, 6], our team is working on innovative methods to assess coronary artery function [7, 8]. Understanding how the coronary arteries work, providing the myocardium with blood, is an important source of information to judge heart function and inform, for example,

intervention. In this regard, based on the anatomic structure of the coronary tree, extracted from the CT data, mesh representations are built, and hemodynamic simulations are computed, providing a noninvasive method to estimate important coronary function descriptors, such as the fractional flow reserve (FFR), which would otherwise have to be determined by invasive coronary angiography. Having a method that can estimate the important parameters from the imaging data – often the first step taken to assess the patient’s condition – is thus valuable to inform diagnosis and future action.

Cardiac CT scans produce substantial data and require a significant amount of computational resources for processing. And the challenges extend to the integration of novel approaches into existing cardiac workstations, which are often proprietary and not designed to integrate third-party solutions. This hinders comprehensive evaluation by clinicians for multiple reasons: first of all, developers must establish a base platform that aligns with clinicians’ familiarity and training, making manipulation and visualization of imaging data similar to what they use in other tools; next, obtaining feedback about the proposed methods becomes complex due to nonintegration with the clinical systems, limiting the data (e.g., low number of patients) over which the methods can be explored and tested; additionally, introducing and updating features, e.g., when a method is improved based on clinician feedback, is troublesome; and finally, current approaches to these tools are not compatible with mobile platforms, which could expand the range of use contexts.

Recognizing these challenges, we advocate for a more structured approach and have been exploring several alternatives that could provide a versatile platform for long-term support to this research context. In this work, as part of that effort, we explore XNAT to assess its suitability to provide the integration of novel processing methods and make them available through a web-based interface. To this effect, we start by settling on the scenarios and requirements envisaged and summarize our previous efforts [9] in this topic (Section 2); then, we move on to describing the deployment and configuration of XNAT along with a discussion regarding its ability to respond to the requirements. Finally, Section 4 provides some concluding insights and potential future directions.

2 Background Work

In this section, we start by describing the overall scenario that is being targeted, establish overall requirements, and briefly discuss earlier steps of our work leading to the current stage.

2.1 Desired Scenario

In our envisioned scenario (refer to Figure 1 for an illustrative representation), researchers are actively developing innovative tools to aid in diagnostics within their laboratory, using a limited set of anonymized imaging data for initial tests. As these methods progress and offer a set of potential useful and meaningful features, the researchers recognize the need for clinical validation and feedback to guide further refinement. At this point, researchers introduce the method into the research infrastructure, making it available for testing by clinicians.

Within the cardiology service, at Hospital Center A, a clinician accesses the research infrastructure through a normal computer, in the office, and tests the methods made available by the researchers, applying them to the data already on the platform (the test data also used by the researchers). He then remembers a few other cases that could be interesting to test the method, accesses the Hospital’s PACS server, retrieves them, and uploads them into the research infrastructure. Although a direct connection from the research infrastructure to the PACS server is possible, our initial vision approaches it this way to ensure full privacy of clinical data and full control of the clinician regarding which exams are uploaded.

The clinician continues to test the methods with the new data, goes back and forth between examining the anatomy and outcomes of the methods, and even uses a tablet to discuss one of the cases with a colleague. They conclude that something is not right with the results obtained for one of the exams and send feedback on it to the researchers. In the research lab, the method is tested with that specific exam (since it is available in the research infrastructure), and they improve the method to correct the issue.

At the same time, Hospital Center B can also participate in providing feedback and contributing data. This serves to highlight that a multicenter scenario can also be very common and can be advantageous for a wide range of reasons, e.g., access to more data, availability of a wider range of clinician experience, and data coming from different equipment (particularly important to ensure method robustness).

In this overall scenario, we argue that the flow of data and method improvements is facilitated among all parties, making it easier to advance the research and more strongly involving the clinicians, in line with a user-centered methodology for design and development [10].

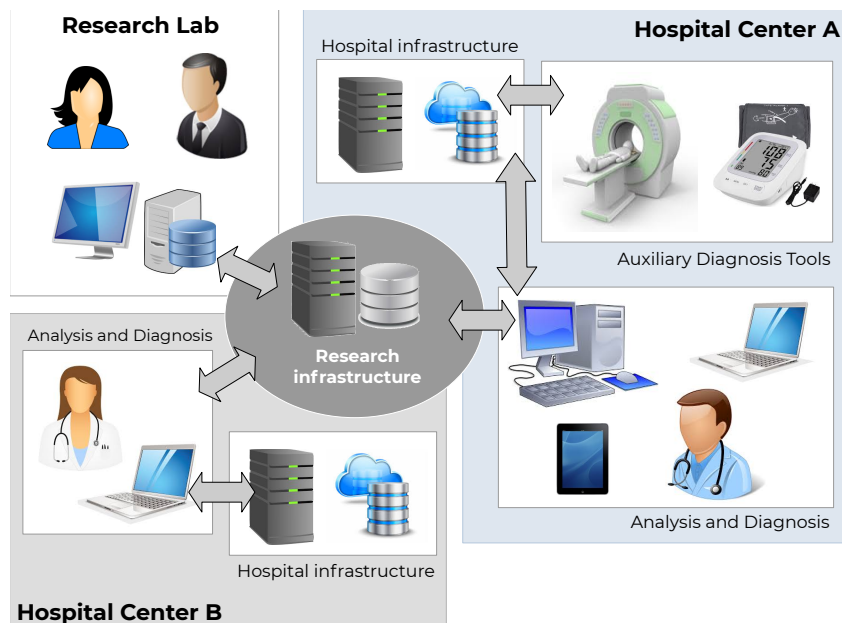


Figure 1. Diagram depicting the overall vision of a research infrastructure handling the research workflow of novel methods to support diagnosis.

2.2 Requirements

Analyzing the overall scenario described above, there are several requirements that can be identified. Without the pretense of completeness, Table 1 lists a set of features that should be made available.

Table 1. Overall requirements for the main features that should be available to support research on novel methods to aid diagnosis by including the clinicians more closely into the process.

RESEARCHER

Image Viewing: multiplanar view; access to clinician-set views

Exam data: image data retrieval; image annotation; easy integration of novel data into the development and test workflow; access to clinician submitted exam data

Development: agile refinement and deployment of processing and analysis methods; abstraction from the image viewer complexity; complete decoupling from the remaining components; version control

CLINICIAN

Image Viewing: multi-planar views; viewer layout customization; measurement tools; window/level adjustment; image annotation;

Exam data: DICOM data uploading; exam annotation; study and series browser; DICOM metadata access

Testing and validation: run methods on-demand; use multiple platforms; provide feedback; provide ground truth data (e.g., obtained from other modalities)

An important aspect that needs to be highlighted is that the aim is to support these features in a completely centralized form, in what we call the research infrastructure. At this point, for these features to be possible involves continuous back and forth with transferring exams, updating software on workstations, or even providing the clinicians a test version during a few minutes, working on the researcher's laptop.

2.3 The OHIF Viewer

Considering the central role of the image viewer in the analysis of cardiac CT image volumes, as made evident, also, by the requirements, our first step was to explore existing open-source viewers such as Weasis [11] and the OHIF viewer [12]. In [9] we have explored the latter and the possibility of integrating the processing methods within this tool.

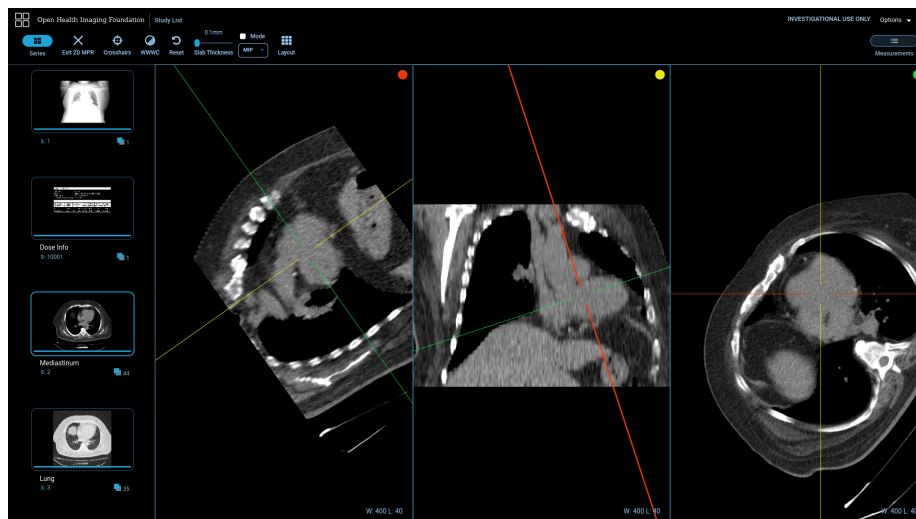


Figure 2. OHIF viewer showing different image planes for a cardiac CT angiography exam.

From this first effort around the OHIF viewer, some relevant conclusions could be drawn. First, the viewer is very versatile, allows the desired multiplanar view of the image volumes (see Figure 2 for an example), can be easily integrated with PACS servers, and has strong potential to be expanded with a wide range of features (e.g., analysis reports). However, integration of processing methods faced some challenges. While it was possible to do it, it required modifying core parts of the viewer, and deploying multiple processing methods was not easy. Furthermore, the solution was not completely decoupled, meaning that adding or modifying a custom processing method would always entail modifying the core code of the viewer rendering it a potential 'quick' solution for the short-term, but impractical to support the long-term research effort, as required.

So, at this point, we considered alternatives that might tackle the integration of processing and analysis methods, eventually keeping the advantages of using the OHIF viewer. This led to the exploration of XNAT as described below.

3 Infrastructure Deployment

When studying XNAT and how to perform the integration of novel processing methods, it is important to note that the first option that seemed viable was XNAT pipelines. However, and while this was not clear from the documentation, this option is deprecated and has been replaced by the container service, allowing for methods to be deployed in a docker server and then run from XNAT. Figure 3 shows the overall diagram of the main aspects concerning this first deployment and testing of XNAT.

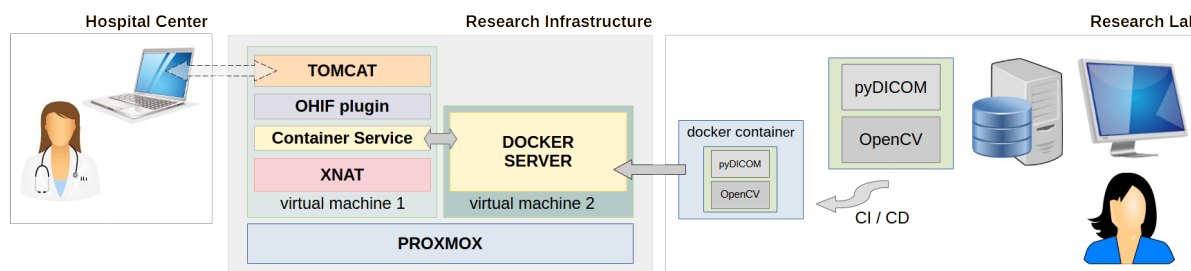


Figure 3. Diagram depicting main components deployed and tested for a research infrastructure supported on XNAT.

To start with, we opt for a virtualized environment based on Proxmox. Two virtual machines were provisioned, one running the XNAT core logic and a webserver (Tomcat¹), and the other running a docker server. The latter machine could be replaced by using DockerHub, but this approach gave us more control over the process of managing the different container images. On the XNAT side, two other elements needed to be added: the **container service** plugin, responsible for managing the containers that provide the processing and analysis methods; and the **OHIF viewer plugin**², which supports browsing and viewing image data.

3.1 Preliminary Testing

After provisioning the main infrastructure, the next step was to test the integration of a new image processing method within the platform, the task that will probably be the most common when researching and improving new image processing and analysis methods. For the sake of a proof-of-concept, we opted to implement a simple method that, given an image volume, would apply Gaussian smoothing. A first advantage of the overall proposal of this work is that, by decoupling the processing methods from the remaining pieces of the research infrastructure, one is not limited by any programming language or library. For our case, we opt to use Python together with the pyDICOM³ package and the OpenCV⁴ library. After the method was developed, it was integrated into a docker container and sent to the docker server. On the XNAT side, a new processing method was configured, based on the added container, and could be applied to any exam already uploaded. When a container is run, the container service makes all the data available in a specific folder from which the method can retrieve it, and sets a default results folder where the method needs to store the results. Then, these new data are added to the XNAT project, along with the source exam data. All this was achieved successfully.

4 Conclusions

The deployment and testing of image processing and analysis methods in clinical settings is challenging, but a step that must be performed to promote testing over a wide range of data and to take the most out of clinician experience and feedback. In an effort to devise an approach that can support this goal, we have been exploring different open source tools and frameworks. In this context, this article presents preliminary results of the use of XNAT to create the overall supporting infrastructure and tests the integration of a simple image processing method. Overall, despite the complexity of instantiating the base XNAT framework, the deployment of novel processing methods follows a completely decoupled approach, something that was missing in our previous effort using the OHIF viewer, making it clearer to manage and expand. The deployment of a novel processing method into the XNAT platform follows a straightforward process based on docker containers, and we were able to fully test it by implementing a simple image smoothing method using Python and OpenCV. Nevertheless, and while all the generated data are present in the XNAT data tree, it still cannot be visualized as a full image set.

At this point, we are concentrating our efforts in understanding how the output data of the processing method need to be configured to be readily available to the OHIF viewer plugin. From preliminary analysis, this will probably involve building a DICOM series for it to be interpretable by the viewer.

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¹Tomcat: <https://tomcat.apache.org/>

²OHIF viewer plugin: <https://wiki.xnat.org/documentation/xnat-ohif-viewer>

³pyDICOM package: <https://pydicom.github.io/>

⁴OpenCV: <https://opencv.org/>

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