QAV-PET: Quantitative Analysis and Visualization of PET Images

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Abstract— **Open source software advances research and allows for more application specific tuning in a very feasible and efficient manner. Chief among the open source platforms is the MATLAB programming environment which is very commonly used in research settings especially in the field of medical imaging. Although many scientists use MATLAB for analysis, there remains a significant lack of open source software platforms which allow for both the analysis and visualization of pathological regions within fused multi-modal medical images. There is a clear need for a MATLAB based software which allows for anatomical (i.e. CT or MRI) and functional (i.e. PET) joint visualization and quantification in an intuitive and efficient way. In particular, this software should focus on PET imaging which is being more widely used for small animal studies. We present here the structure, features, and potential applications of an open source software for the Quantitative Analysis and Visualization of PET Images (QAV-PET).**

I. INTRODUCTION

The development and use of novel medical image processing algorithms has furthered our understanding of complex diseases by allowing researchers to precisely quantify the severity of pathologies longitudinally. In order to further this research goal, open source software is integral for quickly optimizing and adjusting the image processing software for a particular research question or clinical application. Although a few open source softwares exist for medical image processing regarding PET imaging modality, most studies provide only visualization or PET/CT fusion, and there is a need for a software which provides visualization but also quantification. Many researchers use the MATLAB programming environment for analyzing medical images so, ideally, the open sourced software would be implemented in MATLAB. However, there is currently a lack of PET image analysis software, especially in the most commonly used framework for analyzing the images. Surprisingly, as of this writing there is only one PET image segmentation tool on the MATLAB file exchange (a software previously implemented by the authors of this article). Here, we present an open source software implemented in MATLAB for Quantitative Analysis and Visualization of PET images (QAV-PET). In addition, we also present a novel automated reporting system which generates a report based on imaging features to aid researchers in quickly and accurately quantifying disease

progression. In the following sections, we will outline the structure, features, and potential applications of the software.

II. SOFTWARE STRUCTURE

Visualization

First, our software loads the functional (PET) and the anatomical images (CT or MRI) in either Analyze or DICOM image format, the two most widely used for medical image analysis. The fused image is shown as the default view due to the necessity of anatomical information for interpreting and localizing the functional information. The fused image is constructed by combining the opacity-weighted sum of the anatomical and thresholded functional image. Note that PET-CT and MRI-PET scans are already in registration thanks to hybrid imaging technology.

For visualization, the functional, anatomical, or fused image can be shown rapidly using a user defined key or by a drop down menu at the top of the GUI. If the anatomical or functional image is shown, using solely the mouse movement and mouse buttons the contrast, brightness, zoom level, and pan can be easily manipulated giving the user intuitive control over the visualization of the images. Otherwise, if the fused image is shown the left mouse button plus dragging the mouse vertically changes the opacity of the fused images to quickly and intuitively change the type of information that is being presented in the fused images. This is especially usefully when segmenting and quantifying to efficiently view the information from multi types of imaging modalities together.

Quantification

Region of Interests (ROIs) must be defined before any type of quantification or analysis can take place. Essentially, the ROI tells the computer "where" the object of interest is on the image so the image properties of this region, such as the highest Standardized Uptake Value (SUV_{max}), can be computed. The software allows rough ROIs to be generated by the user followed by automatic refinement (segmentation), as described in the following subsection. For this initial rough ROI, the user first selects the label to assign the object of interest to such as Label 1, 2, etc. Then, the software tracks the position of the mouse cursor while the user manually draws the boundary of the object of interest. Once an ROI is created, the statistics of the region can be computed and displayed as a table or exported as a CSV file for further use in different statistical software. These statistics include the metabolic $volume$, SUV_{max}, and SUV_{mean} of all the slices for the given label. Note that these markers have been shown to be of particular importance for quantifying the
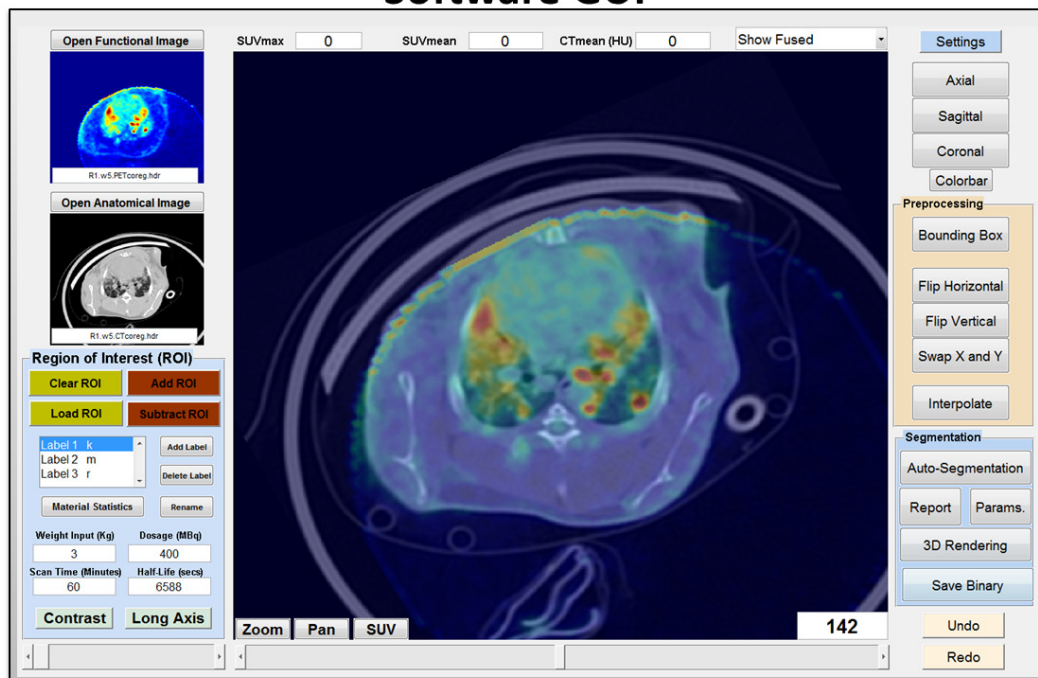
Software GUI

Fig. 1. The QAV-PET GUI with a PET-CT of a rabbit infected with tuberculosis shown.

pathologies in infectious lung diseases in longitudinal small animal models [1].

Segmentation

ROI labels can be easily added to have multiple ROI definitions thus giving the researcher the ability to separate and study pathological high uptake regions individually. Interpolation between slices of the ROI allows for quick and efficient ROI definition by the user. Once the rough ROI is created, the segmentation can be refined using an automatic segmentation algorithm named Affinity Propagation (AP) PET image segmentation [2], [3]. The automatic segmentation algorithm allows the user to refine the rough manual segmentations to the exact boundary of the high uptake region which increases accuracy and lowers variability while also decreasing total segmentation time. It was shown in [2] that the AP segmentation algorithm is more accurate than the current state-of-the-art PET image segmentation methods for diffuse, multi-focal uptake regions commonly seen in pulmonary infections such as tuberculosis. Very briefly, the segmentation method estimates and smoothes the histogram of the region of interest via kernel density estimation [4] to estimate and remove the points along the histogram that are most likely to be noise. Then, a novel similarity (affinity) function is applied to the histogram to estimate the similarity of the points along the histogram with the assumption that points that are most similar are more likely to belong to the same classification, i.e., image label. Lastly, the AP clustering algorithm [5] is applied to these similarities to automatically calculate the number and membership of the

classes within the image. All parameters of the AP image segmentation algorithm can be easily adjusted, if needed, in the software. This rough ROI definition with a fully automated segmentation algorithm dramatically decreases the total segmentation time and inter- and intra-observer variability while also increasing accuracy.

Auto-reporting

This software has a novel auto-reporting feature which, in an automated fashion, produces a report which includes the most important information needed for quantifying the disease and high uptake regions. To the best of our knowledge, this is the first auto-reporting system in MATLAB and PET imaging. In terms of a radiology perspective, auto-reporting is very important as it allows the researchers to create an unbiased and uniform interpretation of the medical images between various time points and subjects. It is meant to complement, not replace, the exported quantification as a .CSV file. After hitting the report button in the software, the user selects whether to create a report for each label individually or to create a single report for all the labels, essentially considering all the labels as one single label.

The report includes both quantitative and qualitative data. The quantitative data includes the SUV_{max}, SUV_{mean}, and the metabolic $volume$ of the current label, and, additionally, it provides the location of the SUV_{max} on the axial, sagittal, and coronal view of the PET image, the CT image, and the PET-CT fused image for a total of 9 images on the first page of the report. All of this information allows the user to get a quick view of the highest uptake lesion,
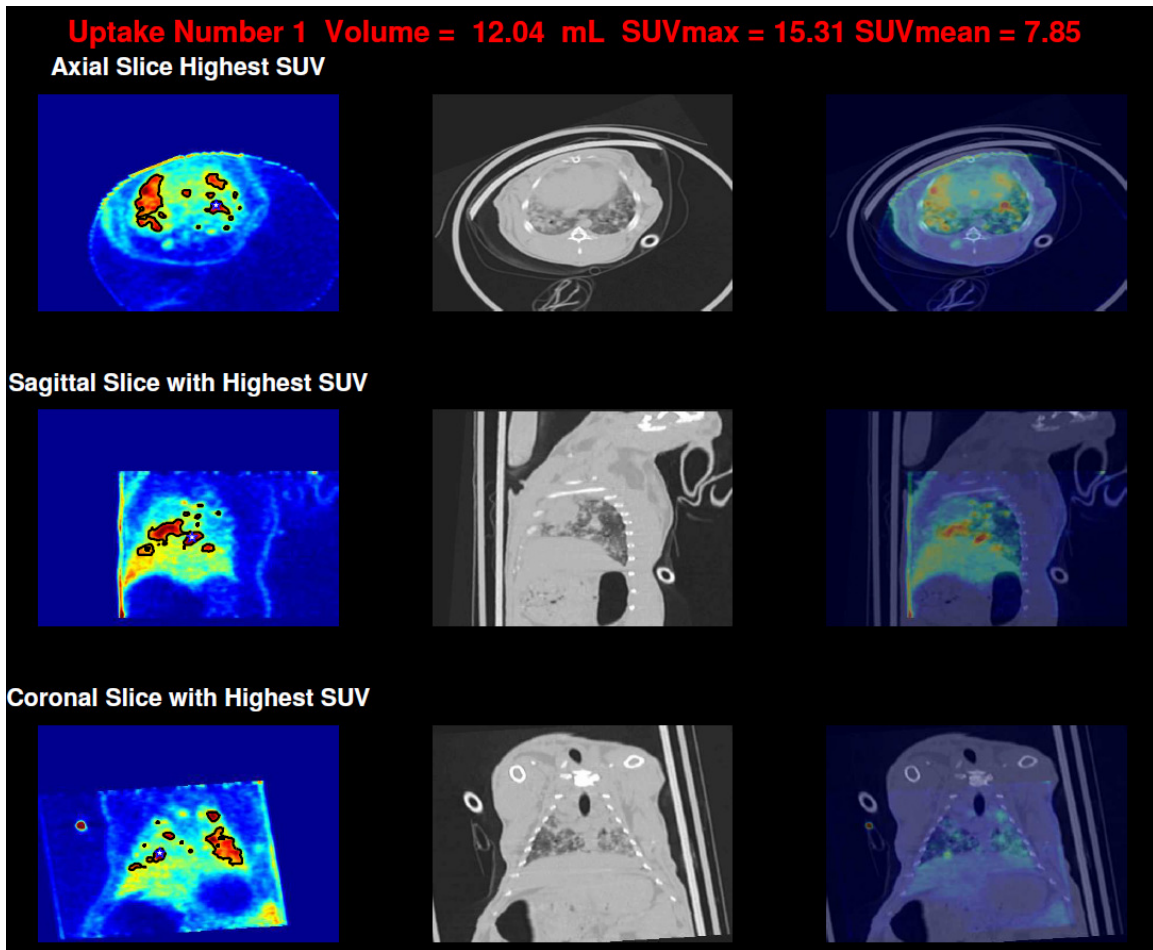
Fig. 2. Example page from the auto-generated report. On top, the title includes the lesion number along with the Volume, SUV_{max}, and SUV_{mean} for easy comparison between the various high uptake regions. The first row shows the location of the SUV_{max} with a star on the axial image while the second and third rows show the sagittal and coronal slices respectively. The PET image (first column), CT image (second column), and registered PET-CT image (third column) are provided in the first, second, and third column respectively.
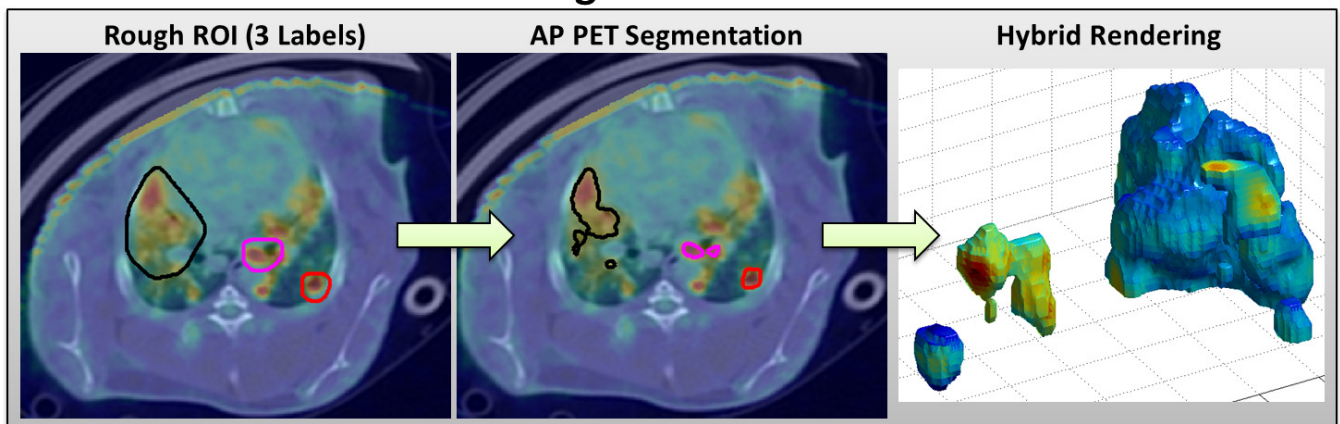

Fig. 3. Example of a segmentation involving 3 labels. **Left:** A rough ROI is created by the user. **Middle:** The AP PET segmentation is applied to the rough ROI for refinement of the boundary. **Right:** A hybrid rendering of the segmentations, with functional information overlaid, is provided. The redder areas correspond to higher radiotracer uptake areas while bluer areas have less uptake.
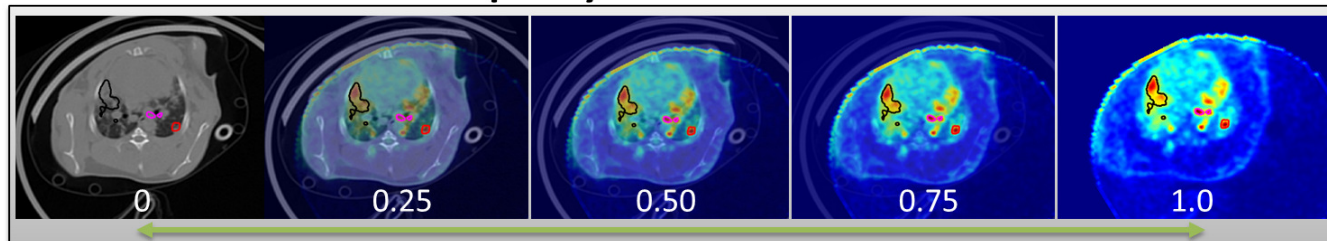
Opacity – Visualization

Fig. 4. Example of varying the opacity between PET and CT on the segmentations from Fig. 3. The opacity ranges from 0, fully anatomical (CT) information, to 1, fully functional (PET) information.

which is important for disease severity quantification. For an even better visualization, the boundary of the current uptake region is colored as the same color as the label the user used to create the segmentation for continuity between the segmentation creation and report generation. See Fig. 2 for an example of the first page of the report. It should be noted that other quantitative markers can be easily included into the report due to the open-source nature of our platform.

In addition to these views the software provides a three dimensional representation of the segmented high radiotracer uptake region by generating a rendering of the segmented lesions. First, it creates a rendering using the boundary and shape information from the labels. Then, the renderings are overlaid with the functional information from the PET image to give the distribution of the radiotracer uptake along the surface of the uptake region in order to visualize the information in a way that is simply not possible by only looking at 2D images. We refer to this type of rendering as a "hybrid rendering" since it contains information from different imaging modalities fused together, functional and anatomical. An example of this rendering from three different labels is shown in Fig. 3. The redder areas correspond to higher uptake areas (more severe disease) while bluer areas have less uptake. Notice how easily the distribution of the radiotracer uptake is visualized. Lastly, the report generates a rendering of all the various labels and colored using the same coloration and 3D coordinates as when the user was segmenting the regions. This allows the user to get a good sense of the spatial distribution of the various labels within the images.

III. APPLICATIONS

There are many potential applications for the QAV-PET open source software, and only a few will be highlighted here. Perhaps the most direct application is for the quantification and visualization of abnormalities on PET-CT images of small animal infectious disease studies. The segmentation algorithm that is implemented has been shown to be particularly well-suited for the segmentation of diffuse, multi-focal PET radiotracer uptakes that are commonly seen with infectious diseases, and the intuitive and efficient work flow of the software will aid researchers in analyzing these types of images since there is currently no software which

allows for easy segmentation of abnormalities on PET-CT images. Another potential application for this software is for visualization of the pathologies in three dimensions with the PET functional information overlaid for determining the optimal histology slice localization. When taking histology slices from a diseased organ, this three dimensional view of the distribution of the disease will aid researchers in determining the best location to take the histology slices from for the best characterization. Lastly, the open source nature of the software will allow researchers to quickly add features or modify existing features for novel applications. For instance, if the user needs to segment abnormalities based upon the fused PET and CT information a novel segmentation algorithm such as [6] can be easily added to the image analysis and quantification framework presented here.

IV. CONCLUSIONS

Our presented software and source code is freely available on the Matlab File Exchange, a popular and free-to-downloaded site for MATLAB software. This software allows researchers to easily and intuitively visualize, segment, render radiotracer uptake regions, and automatically generate a report that can be used in the analysis of medical images in routine clinics.

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