

# PAHPhysRAD: A Digital Imaging and Communications in Medicine Research Tool for Segmentation and Radiomic Feature Extraction

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## Abstract

**Introduction:** Segmentation and analysis of organs at risks (OARs) and tumor volumes are integral concepts in the development of radiotherapy treatment plans and prediction of patients' treatment outcomes. **Aims:** To develop a research tool, PAHPhysRAD, that can be used to semi- and fully automate segmentation of OARs. In addition, the proposed software seeks to extract 3214 radiomic features from tumor volumes and user-specified dose-volume parameters. **Materials and Methods:** Developed within MATLAB, PAHPhysRAD provides a comprehensive suite of segmentation tools, including manual, semi-automatic, and automatic options. For semi-autosegmentation, meta AI's Segment Anything Model was incorporated using the bounding box methods. Autosegmentation of OARs and tumor volume are implemented through a module that enables the addition of models in Open Neural Network Exchange format. To validate the radiomic feature extraction module in PAHPhysRAD, radiomic features extracted from gross tumor volume of 15 non-small cell lung carcinoma patients were compared against the features extracted from 3D Slicer™. The dose-volume parameters extraction module was validated using the dose volume data extracted from 28 tangential field-based breast treatment planning datasets. The volume receiving  $\geq 20$  Gy (V20) for ipsilateral lung and the mean doses received by the heart and ipsilateral lung, were compared against the parameters extracted from Eclipse. **Results:** The Wilcoxon signed-rank test revealed no significant difference between the majority of the radiomic features derived from PAHPhysRAD and 3D Slicer. The average mean lung and heart doses calculated in Eclipse were  $5.51 \pm 2.28$  Gy and  $1.64 \pm 1.98$  Gy, respectively. Similarly, the average mean lung and heart doses calculated in PAHPhysRAD were  $5.45 \pm 2.89$  Gy and  $1.67 \pm 2.08$  Gy, respectively. **Conclusion:** The MATLAB-based graphical user interface, PAHPhysRAD, offers a user-friendly platform for viewing and analyzing medical scans with options to extract radiomic features and dose-volume parameters. Its versatility, compatibility, and potential for further development make it an asset in medical image analysis.

**Keywords:** Matlab, radiomics, radiotherapy, segmentation, software

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## INTRODUCTION

Digital Imaging and Communications in Medicine (DICOM), developed by the National Electrical Manufacturers Association and the American College of Radiology, is the global standard for medical images.<sup>[1]</sup> Currently, it is the universal standard for storage, sharing, and interpretation of medical images and their associated data. Some of the most common medical images stored in DICOM format are X-ray radiography, mammography, fluoroscopy, computed tomography (CT), cone-beam CT, magnetic resonance imaging (MRI), positron emission computed tomography, single-photon emission CT, ultrasound images, electron microscopy, and optical coherence

tomography. With multiple vendors on the market, DICOM aids in the exchange of medical imaging information across the multiple systems.<sup>[2]</sup> DICOM images contain not only visual data but also essential patient metadata, providing a robust dataset for the analysis. With the rise of machine learning and artificial intelligence (AI), DICOM images have become vital for training predictive models. Radiomics, a process involving

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the high-throughput extraction of image features, is especially promising for predicting disease outcomes and responses to therapy.<sup>[3,4]</sup> DICOM images are also instrumental for tasks such as tumor classification, disease progression prediction, and image segmentation. Texture analysis of regions within these images offers insights into tissue nature, aiding in tumor classification and treatment efficacy assessments. Furthermore, DICOM images can be integrated with other patient data, such as genetic profiles or pathology results, to enhance disease prediction and classification models. These images also underpin numerous medical research endeavours, supporting the development and validation of new algorithms and fostering interdisciplinary collaborations, refining prediction and classification strategies. The standardized nature of DICOM is pivotal for maintaining consistency in imaging, a factor critical for the accuracy of prediction or classification models. To harness the full power of radiomics, there exists a need for precise segmentation of volumes of interest. Manual segmentation, while detailed, is time-consuming and might introduce inter-operator variability, which can adversely affect the integrity of the extracted radiomic features. Thus, auto-segmentation tools improve consistency in volume segmentation. Such auto-segmentation not only expedites analysis but ensures the standardization essential for extracting meaningful radiomic features. There are several tools available for extracting radiomic features, including 3D Slicer (which incorporates Pyradiomics),<sup>[5]</sup> TexRad,<sup>[6]</sup> RaCaT,<sup>[7]</sup> LifeX,<sup>[8]</sup> IBEX,<sup>[9]</sup> and CaPTK.<sup>[10]</sup> However, most of these radiomic feature extraction software tools either have limited segmentation capabilities or lack them entirely. In this study, we propose the development of a DICOM research tool that can manually segment volumes of interest, semi-automate organ delineation using the Segment Anything deep learning model, auto-segment organs at risk (OAR), extract radiomic features, and perform dose-volume extraction from DICOM radiation therapy (RT) datasets.

## MATERIALS AND METHODS

The DICOM Research Tool, PAHPhysRAD was developed in MATLAB 2023a with tools such as the Image Processing Toolbox, the Statistics and Machine Learning Toolbox, the Deep Learning Toolbox, and the Wavelet Toolbox. The former two toolboxes are essential for the program's functionality; the latter two are required only for auto-segmentation and radiomic processing. It actively uses many of the DICOM functions embedded within the Image Processing Toolbox, such as `dicomreadVolume`, `dicomreadInfo`, `dicomCollection`, and `dicomContours`. The development and testing of the application were conducted on a dual-core i5-6300U processor with a base clock speed of 2.6GHz, paired with 8GB of RAM and without a dedicated GPU. As the application has been optimized for a computer with the aforementioned specifications, it represents the minimum recommended hardware. Notably, due to the absence of parallel processing for most functions, the single-core central processing

unit (CPU) clock speed is paramount in ensuring optimal performance.

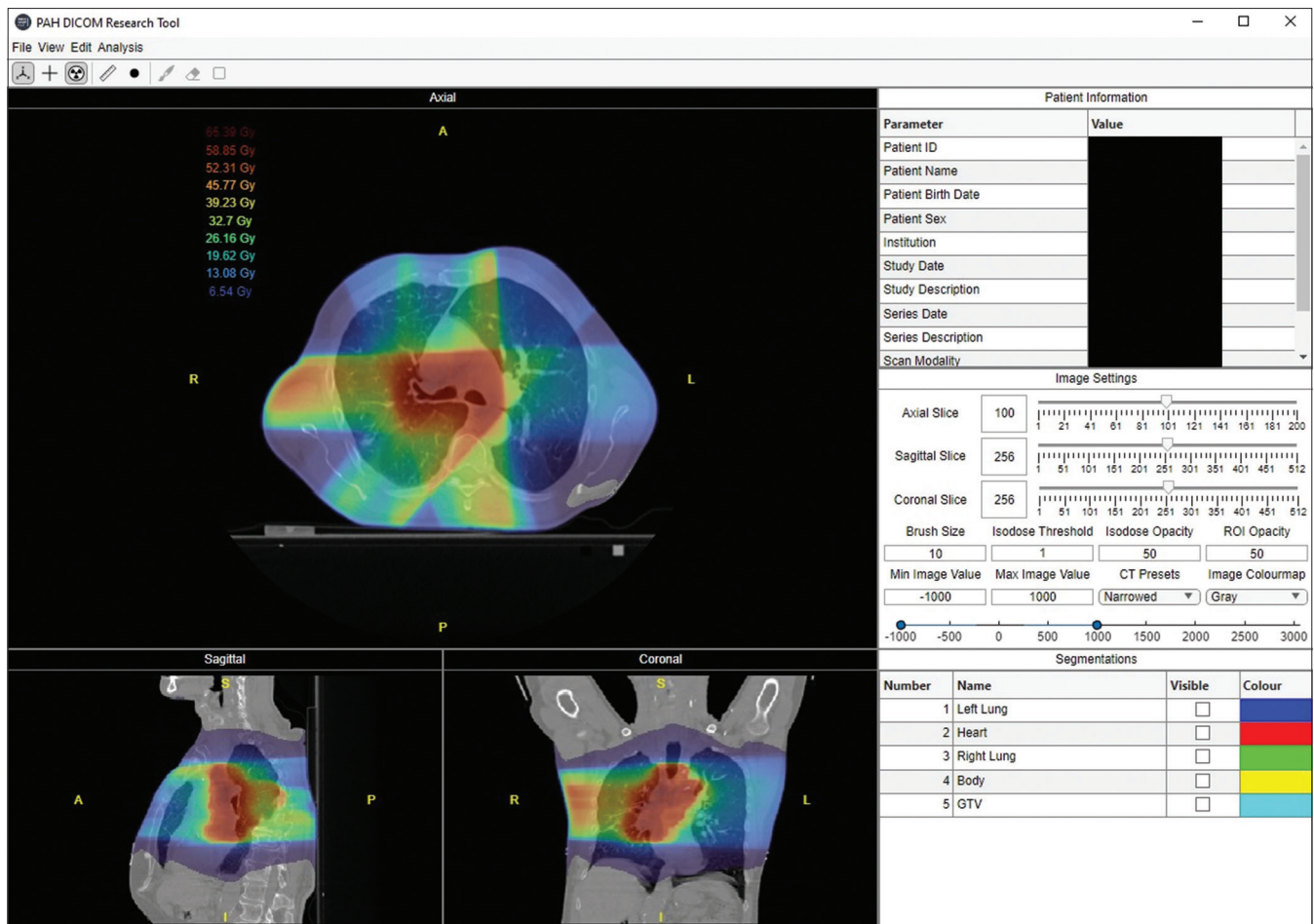
The graphical user interface (GUI) layout is designed for simplicity and user-friendliness, as shown in Figure 1. The design avoids an excessive number of sub-modules and pop-up user interface windows, aiming instead to cluster all relevant options cohesively. The layout's inspiration is drawn from Pinnacle, 3D Slicer, and Aliza MS, complemented by user experience feedback.

The right-hand module of the GUI is reserved for presenting workspace information, covering patient details, the display settings, and current segmentations. Patient information is gathered directly from the DICOM metadata. Options to manipulate the loaded images, such as adjusting the slice number or altering visibility, are accessible through the image setting panel. Furthermore, when hovering over the corresponding display panel, users can scroll through slices using the mouse wheel. The segmentations panel lists loaded or delineated structures, derived either from an imported DICOM-RT structure file or drawn manually with the available drawing tools. This panel also offers features allowing users to rename segmentations, toggle their visibility, and modify the representative color through a double-click.

Along the top section of the GUI, users have access to a variety of tools. To assist in determining the patient's orientation based on DICOM metadata, directional indicators can be superimposed on each display plane. The underlying code accounts for various combinations of biped patient positions, as defined by the DICOM patient position attribute, including head-first, feet-first, prone, supine, and decubitus orientations. Localization crosshairs are also available, which indicate the relative positioning of slices on each orientation plane. Users can select and move these crosshairs, offering an alternative method for slice scrolling. When a DICOM-RT Dose file is imported, the dose matrix can be visualized over the patient slices. The image settings panel provides controls to adjust the threshold at which the dose appears and to modify the transparency of the dose matrix. In addition, the GUI provides a measuring tool to calculate distances between voxels, with measurements hard-coded in millimeters (mm) based on patient-space units. The point tool enables users to pinpoint specific voxel intensities and/or dose values within any display plane. Finally, the application comes with drawing and erasing tools, simplifying the process of delineating selected segmentations.

### Digital Imaging and Communications in Medicine import

Upon launching the PAHPhysRAD, users are presented with two options: either scanning a directory containing DICOM files, or loading a previously saved database. The directory scan functionality is facilitated by the `dicomCollection` function, responsible for parsing DICOM files and aggregating metadata into a designated database variable. In scenarios involving batch radiomics exports, the process of parsing a substantial number of files can be time intensive. To address this, the



**Figure 1:** Overview of the PAHPhysRAD GUI layout with a loaded patient volume in the default view with a corresponding DICOM RT Dose overlayed

application offers the capability to save the aggregated database upon completion. This saved database can be reloaded at any time, mitigating the need to repeat the scanning process.

The application provides a simple GUI for visualizing the database and selectively loading desired files. Loading a medical volume, such as a CT or MRI dataset, is a prerequisite before loading a corresponding DICOM-RT Structure or Dose file. Once loaded, relevant GUI features will be enabled. Upon importing, the application retains the medical volume in the stored image-space, as opposed to patient-space. This design choice is to simplify code complexity within the MATLAB environment. To prevent conflicts in positioning relative to the DICOM-RT Structure, adjustments are made to the patient orientation and patient position DICOM tags. In cases where patient orientation includes rotation information, inverse matrix operations using the rotational matrix are applied. This approach is particularly significant for MRI volumes which often encompass rotated image data. Incorporating DICOM-RT dose files follows a methodology used in matRad, namely, trilinear resampling of the dose matrix to align with patient-space voxel specifications and extent. Regions outside the dose matrix are set as 0. The flexibility to import one or multiple DICOM-RT Dose files is also provided.

A notable feature of the application is its capability to load RT Structure or RT Dose files even when the Study Instance Unique Identifier (UID) DICOM tag does not match. This feature has been invaluable in ongoing research, especially when 3D Slicer faced difficulties loading and exporting RT Dose files.

### Segmentations

The segmentations are generated as 3D binary matrices using the built-in createMask function within MATLAB. This process utilizes the Dicom Contours object alongside spatial information from the medical volume, allowing for the mapping of vertex coordinates onto image-space voxels. Through MATLAB's matrix operations, any visible segmentation is fused into a display matrix. The color map for this matrix is established based on the stored contour color.

The PAHPhysRAD provides an array of tools accessible through the Edit drop-down menu, offering functionalities for segmentation creation, deletion, duplication, and modification. Bulk creation or deletion of segmentations is achievable, with the latter allowing users to select multiple items from the segmentations table. In addition, binary cleaning tools are available, with options to eliminate holes or small spots for a two-dimensional (2D) anatomical orientation or a 3D context.

Morphological operations can also be used to modify existing delineations, such as flipping along a specified axis, shifting it by a defined voxel count, and applying erosion or dilation either isotropically or in a specific axis.

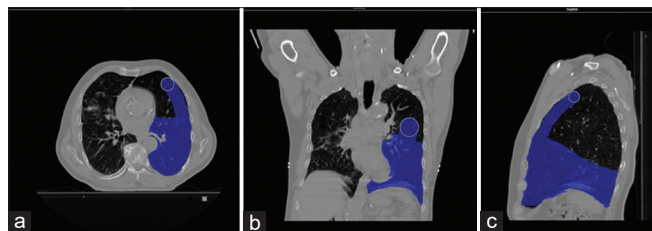
### Manual segmentation

The application also incorporates rudimentary drawing and erasing tools to alter stored or new segmentations. When activated, the display overlay isolates the selected segmentation, and a circular brush will track the cursor across the display panels, as depicted in Figure 2. The utilization of 3D logical matrices, instead of relying solely on stored DICOM contours, enables simple drawing in any orientation.

### Semi-automatic segmentation with segment anything

Meta's "Segment Anything Model" (SAM) represents a significant advancement in the field of image segmentation.<sup>[11]</sup> Introduced by Meta AI, SAM is designed to identify and segment various objects within images. The primary goal of this model is to create a foundational tool for image segmentation, allowing for zero-shot contouring of 2D images. SAM is a promptable segmentation model, which means it can be directed to "cut out" or segment any object in an image with a single command. This capability has vast applications in various domains, including medical computer vision. The model has been trained on the Segment Anything 1 Billion dataset of natural images. While medical images are underrepresented in this dataset, SAM has nonetheless demonstrated remarkable generalizability to the medical domain, even without fine-tuning.<sup>[12-15]</sup> The SAM model consists primarily of a large image encoder, followed by a lightweight mask decoder. The mask decoder is assisted by a prompt decoder which handles manual prompts provided by end users. There are three official SAM models, which in order of increasing parameter size are ViT-B, ViT-L, and ViT-H. In addition, MobileSAM has been independently developed to further enhance the efficiency of the SAM encoder.<sup>[16]</sup>

To integrate SAM into the PAHPhysRAD, the MobileSAM encoder and ViT-H decoder were converted to Open Neural Network eXchange (ONNX) models with MATLAB-compatible opset and IR versions. The ViT-H decoder was chosen since all the decoders are lightweight and there is therefore little benefit gained by using the smaller models. Once imported, bounding box prompting was implemented into the GUI. Users can enable this feature by clicking the square button



**Figure 2:** Drawing of a lung region on the axial (a), coronal (b) and sagittal (c) orientations. The brush will follow the cursor across the planes and will dynamically update the segmentation mask

in the ribbon menu, drawing a box to enclose the region to be contoured [Figure 3a and c], and then pressing ENTER to generate the contour [Figure 3b and d].

### Auto-segmentation

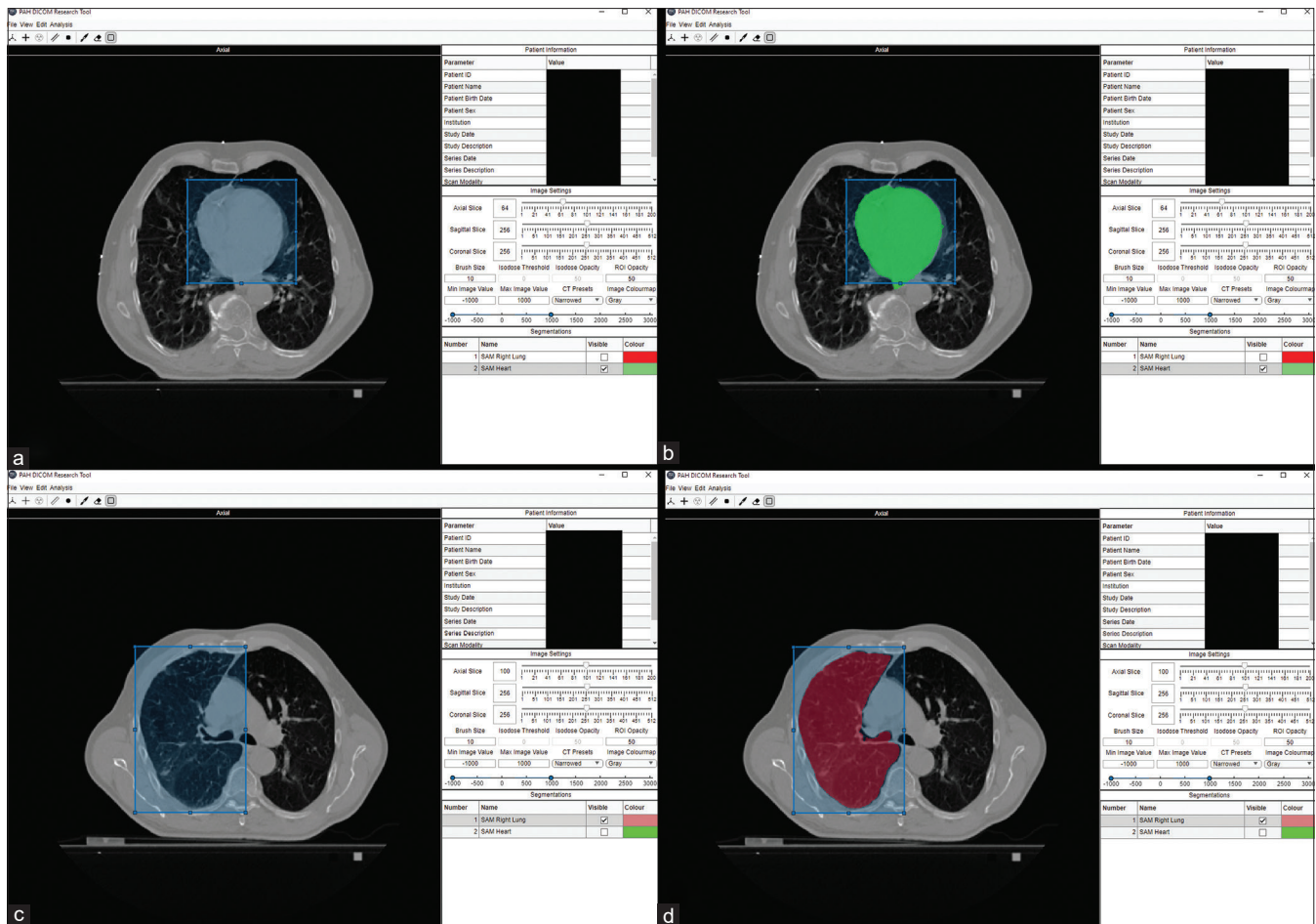
As of current development, the application has implemented the framework for auto-segmentation. Our team previously developed a state-of-the-art 3D U-Net model, optimized for multi-class auto-segmentation of thoracic CT scans.<sup>[17]</sup> This model, implemented in PyTorch, leverages a ResNet (2 + 1) D encoder whose parameters were kept constant during training. The model is capable of accurately delineating the contours of the breasts, lungs, and heart, as illustrated in Figure 4. Once auto-segmentation predictions are made within the PAHPhysRAD, they may be exported to patients' DICOM RTSS files. Once new models have been developed, it they can be simply merged into the application.

### Extraction of dose-volume parameters

Once a delineation has been established or imported within the application environment, it becomes possible to compute dose-volume histogram (DVH) statistics, as shown in Figure 5. This is achieved through the utilization of MATLAB's logical indexing capabilities. The logical segmentation mask serves as a direct means to access the dose matrix voxels situated within the region of interest. As a result, crucial statistics such as mean, median, minimum, and maximum dose can be accurately calculated.

The volume statistics are derived by multiplying the total number of voxels encompassed by the segmentation mask with the physical volume of an individual voxel, as defined by the spatial information in the DICOM metadata. Calculating the dose corresponding to a desired volume percentage involves the in-built percentile function. In addition, determining the volume percentage associated with a specific dose level is accomplished by computing the ratio of dose matrix voxels that are greater than or equal to the given dose to the overall number of indexed dose voxels.

A key advantage of this function lies in its flexibility to retrieve both volume and dose statistics at any point along the DVH curve as specified by the user. This has proven to be essential in ongoing research endeavours focused on assessing dose exposure to OAR. To test the functionality of extraction of dose-volume statistics from DICOM RT datasets, 28 Breast patients planned with standard tangential fields that include both 15 right and 13 left breasts were considered for this study. In this retrospective study, tangential treatment plans were generated in Eclipse with prescription dose varying from 42.5 Gy to 50 Gy. Three dosimetric parameters; volume receiving  $\geq 20$  Gy (V20) for ipsilateral lung, mean ipsilateral lung dose and mean heart dose were manually extracted from eclipse. The DICOM RT datasets that include CT images, RT Dose, RT Plan and RT structure sets were imported into the PAHPhysRad software and the above three dosimetric parameters were extracted for all patients using the batch processing module. The manually extracted dose-volume



**Figure 3:** Utilizing the Segment Anything Model (SAM). (Left) Using the bounding box method to draw around the desired region. (Right) The SAM output mask of the lung within the bounding box. DICOM: Digital Imaging and Communications in Medicine. (a) Bounding box enclosing the heart (b) Heart contoured by SAM (c) Bounding box enclosing Rt. Lung (d) Rt. Lung contoured by SAM

parameters were then compared against the values computed in eclipse.

**Digital Imaging and Communications in Medicine export**

The PAHPhysRAD allows users to export delineations into a DICOM-RT Structure format for utilization in alternative visualization or planning systems. The export script will align contour vertices to the patient spatial coordinates of the loaded medical volume and store the Service-Object Pair (SOP) Instance UIDs of the corresponding volume slices. Other DICOM metadata are preserved when editing a preexisting file. If creating a new DICOM-RT Structure file, the included metadata follows that as per matRad. The exported DICOM-RT Structure files have undergone validation against 3D Slicer and Aliza MS, confirming spatial and numerical alignment of delineations across slices [Figure 6]. The following images illustrate an example segmentation delineated within the DICOM Research Tool environment, and how the exported contours are depicted in Aliza MS and 3D Slicer, respectively. A strength of PAHPhysRAD is ability to reduce DICOM RT-structure file size by eliminating redundant points along a straight line by using Ramer-Douglas-Peucker algorithm, as

per MATLAB’s reducePoly function. This retains the spatial integrity of the stored contours by keeping only essential endpoints of lines, thereby reducing the required data to be stored.

**Radiomics**

With the analysis of radiomic features frequently being carried out using big datasets, the functionality to extract the features from a large patient cohort’s image requires prior time-intensive calculations on multiple patient datasets. Manually loading each dataset for feature extraction is a tedious process that risks inconsistencies between export settings. Thus, batch radiomic extraction was deemed a critical feature when designing the functionality of PAHPhysRAD’s radiomics module. This is achieved using the aggregated database produced by the dicomCollection function and importing into the radiomics module. Figure 7 shows the GUI for initiating the radiomic computation.

After being loaded into the GUI, patients’ DICOM datasets will be filtered based on whether they possess a CT or MRI volume along with a corresponding DICOM-RT structure file. The leftmost table enables specific patient selection for batch

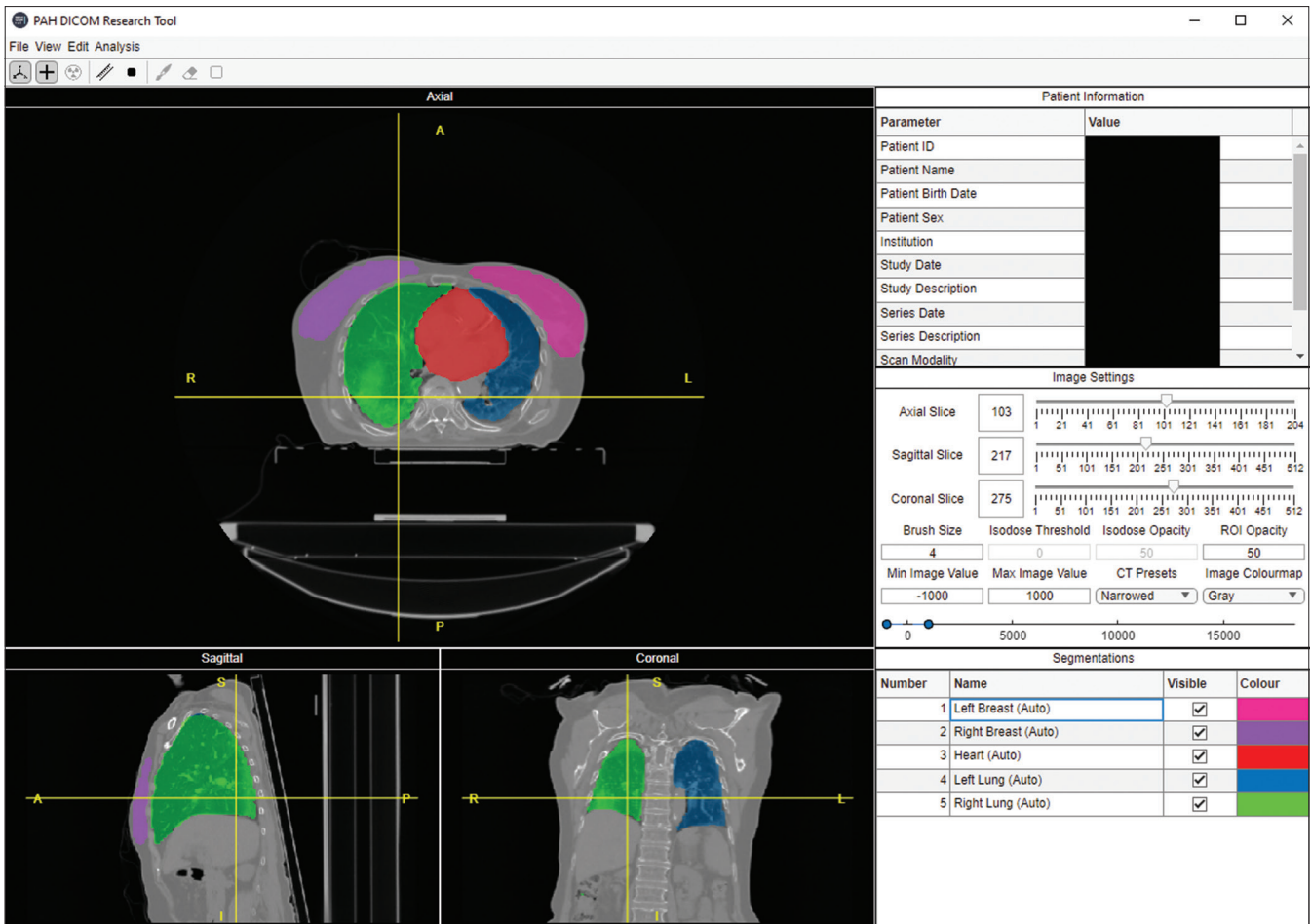


Figure 4: Automatic segmentation of thoracic OARs, including the heart, breasts, and lungs. PAH: Princess Alexandra Hospital

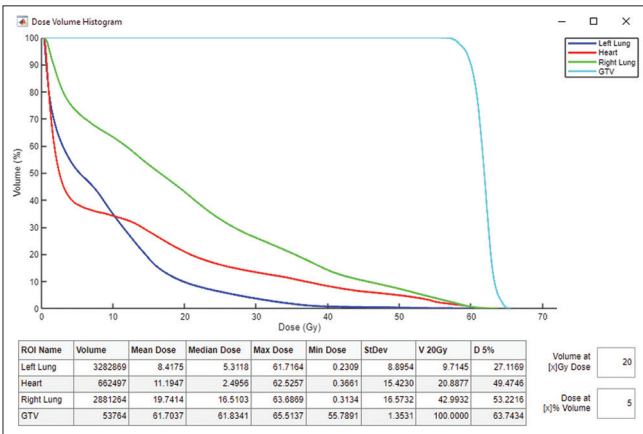


Figure 5: Dose Volume Histogram statistics of various segmentations, including the gross tumor volume and neighboring OARs. The volume has been calculated using the physical voxel size stored in the DICOM metadata

exporting, after which all segmentations within the relevant DICOM-RT files are aggregated into the second table. Similarly, users can select specific segmentations; when initiating batch processing, the application will filter each DICOM-RT file to retain only desired segmentations. Finally, users have the

flexibility to apply any of MATLAB’s supported wavelet types, including various types of 3D or 2D directional filters.

Utilizing all the categories of radiomic features without wavelet filtering amounts to 142 features; including one wavelet type with all combinations of 2D and 3D filters extends this to 3214 features. This extended number only includes one iteration of morphological statistics, as the segmentation matrix does not change during wavelet filtering. The First Order and 3D Shape features were computed using MATLAB’s built-in functions, following the methodology outlined in PyRadiomics’ documentation.<sup>[18]</sup> The gray level and neighboring gray tone matrices were generated through manual scripting, though the underlying logic aligns with PyRadiomics’ approach. To validate the radiomic feature extraction tool, the first order and 3D shape features generated in this software were compared against the features extracted for 15 non-small cell lung carcinoma patients. The DICOM-RT datasets of 15 patients, which include both CT images and DICOM-RT contours, were imported into 3D Slicer™. Using the pyRadiomics library encapsulated in slicer-radiomics, both first-order and 3D shape features were extracted for the gross tumour volumes. Even though, the PAHPhysRad can export up to 3214 features, for validation, we limited the comparison to first-order and 3D

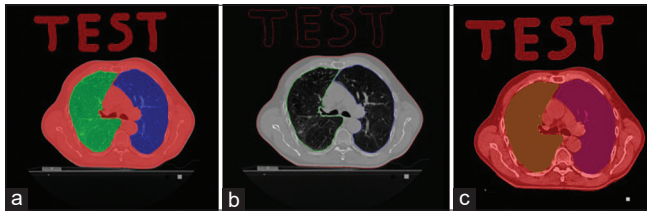
shaped features to ensure the comparative study used similar features. After applying the Shapiro–Wilk test on the extracted data, it was determined that most of the features did not follow a normal distribution, and hence, the Spearman correlation was used to assess the degree of correlation between the 3D slicer and PAHPhysRad extracted features sets. For texture-related radiomic feature formulae, we adapted previously published code<sup>[19-21]</sup> with modifications to ensure compatibility.

Wavelet filtering facilitates the transformation of the volume into low-frequency (approximations) and high-frequency (detailed) information, comprising the components of the original volume. This process yields multiple sets of sub-bands at a chosen decomposition level, corresponding to both volume approximations and details. For 3D filters, this encompasses the approximation sub-band (LLL) as well as the detail sub-bands (HLL, LHL, LLH, HHL, HLH, LHH, and HHH) – The latter of which relates to details along the X,

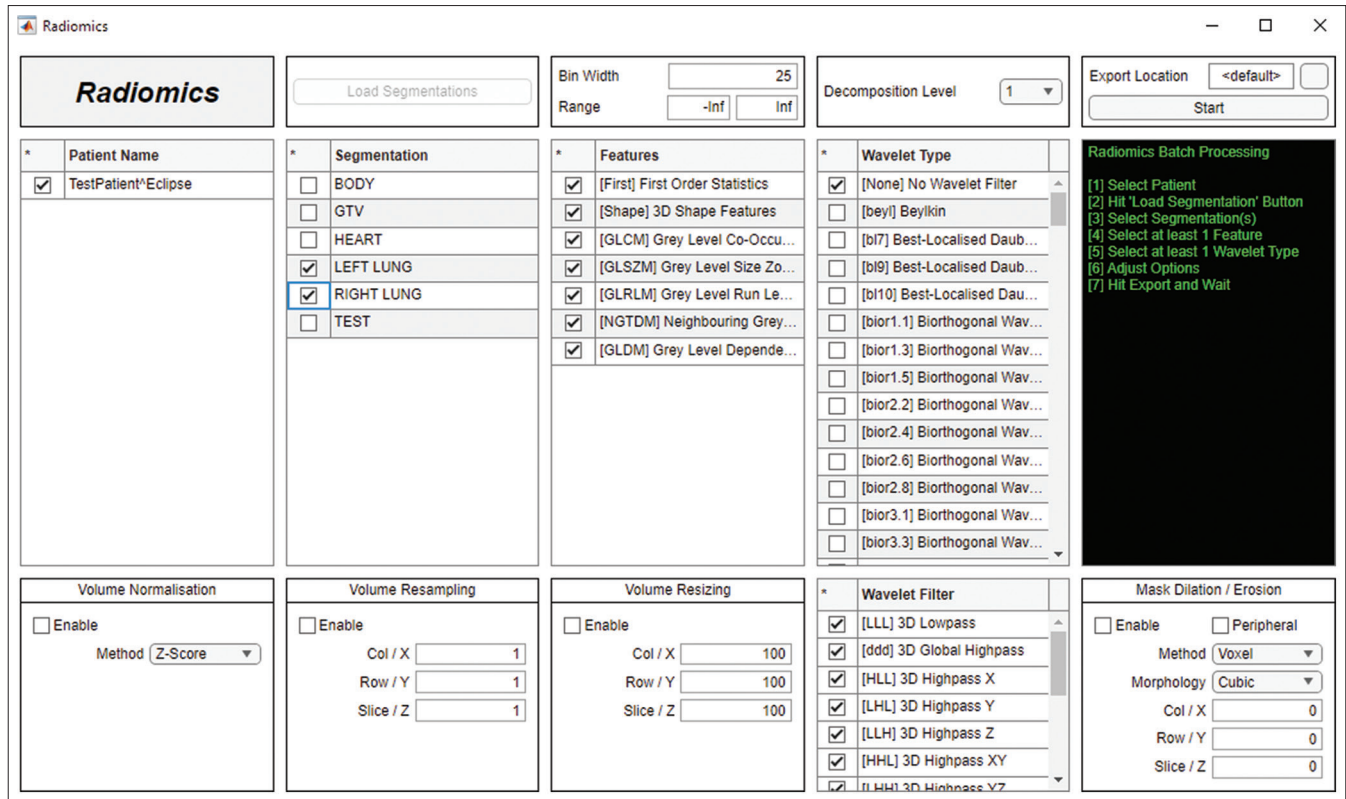
Y, and Z axes of the volume. The GUI also offers an option for a “global” highpass, referring to information outside the LLL approximation sub-band, or the cumulative sum of all detail sub-bands. In the context of 2D filters, these sub-bands are computed on a per-slice basis, resulting in LL, HL, LH, and HH sub-bands, along with the 2D “global” high pass. This can be accomplished for axial, sagittal, and coronal planes independently. Various wavelet types are available for selection, such as Daubechies, Symlets, Coiflets, and Biorthogonal wavelets.

In addition to the essential batch processing options, the GUI offers a range of choices for both image and morphological manipulation. The first order features, as outlined in PyRadiomics’ documentation, are the statistics derived from the distribution of voxel intensities within the defined delineations. Nevertheless, it is possible to impose a specific value range to eliminate the noise before computing the statistics. Furthermore, for texture-based statistics, an absolute bin width approach is employed for intensity discretization.

Other image manipulation options included involve the normalization of voxel intensities, image-space matrix dimensions, and patient-space voxel widths. Voxel intensities can be altered using Z-Score normalization, which centres the mean of the respective volume at 0 and aligns voxel values at standard deviations around the mean. This approach is currently favoured in the literature for MRI datasets. The



**Figure 6:** Comparison of contours stored in the Digital Imaging and Communications in Medicine-Radiation Therapy Structure files, drawn in (a) PAHPhysRAD (b) Aliza MS (c) 3D Slicer



**Figure 7:** The GUI for performing batch radiomic extraction on a cohort of patients. A wide range of options are available, including various wavelet types and filters, morphological operations for segmentations, and normalization

volumes can also be normalized with respect to patient-space and image-space sizes which involves resizing the volume to a specific matrix size or physical voxel size along the X, Y, and Z axes. This can either be applied to all dimensions or specific ones, such as resampling exclusively in the axial plane.

Finally, the segmentations can be dilated or eroded either isotropically or with respect to specific axes, employing a voxel-or physical-based approach. Thus, users have the option to expand or contract segmentations by a predetermined quantity to encompass critical information effectively. By enabling the peripheral feature, radiomic calculations will be performed on the regions between the original segmentation mask and the manipulated mask.

### RESULTS

With the validation of the radiomic feature extraction module, the Spearman correlation between radiomic features extracted by PAHPhysRAD and those extracted by 3D Slicer was 0.98, indicating strong alignment between the two methods. The Wilcoxon signed-rank test revealed no significant difference between the majority of shape-based and first-order radiomic features derived from PAHPhysRAD and 3D Slicer. This suggests that the radiomic features obtained through PAHPhysRADomics software agree well with those from 3D Slicer. For the batch processing-based dose-volume extraction module of PAHPhysRAD, the average V20 computed in Eclipse and PAHPhysRAD are  $9.39 \pm 5.59$  and  $9.52 \pm 5.59$ , respectively. Figure 8 presents side-by-side violin plots comparing Eclipse and PAHPhysRAD ipsilateral lung V20 volumes statistics for 28 patients. It provides a visual summary of the distribution, combining the elements of a box plot and a kernel density plot, for ipsilateral lung volumes receiving  $\geq 20$  Gy. Figure 9 demonstrates the mean lung and heart doses compared side-by-side. In both violin plots, the first half represents the mean doses manually extracted from Eclipse, while the second half corresponds to the data extracted by PAHPhysRad. The average mean lung dose and heart dose calculated in Eclipse are  $5.51 \pm 2.28$  and  $1.64 \pm 1.98$ , respectively. Similarly, the average mean lung dose and

heart dose calculated in PAHPhysRAD are  $5.45 \pm 2.89$  and  $1.67 \pm 2.08$ , respectively.

### DISCUSSION

This study introduces PAHPhysRAD, a DICOM Research Tool designed to streamline the processes of importing, delineating, and analyzing clinical DICOM datasets. In the market, there are several tools available, each with its own limitations. The software proposed in this study is a comprehensive tool capable of performing manual, semi-automated, and fully automated segmentation of regions of interest on DICOM images. It implements the recent SAM deep learning model for organ delineation in DICOM images. A standout feature of this software is its ability to batch process the extraction of 3214 Radiomic features, significantly reducing processing time. The ability to scan an entire patient cohort and batch compute radiomic features ensures consistency in image preprocessing and segmentation morphological operations, bypassing the risk of user error and fatigue of manually exporting radiomics on per-patient basis. In addition, we have incorporated dose volume extraction tools, which can also batch process multiple DICOM RT datasets in a short time, depending on the volume of data.

Figure 8 annotates the median and mean values in the violin plots for both Eclipse and PAHPhysRAD. The proximity of these values in the PAHPhysRAD plot indicates a symmetric distribution of data around the central value. In the Eclipse plot, the mean and median are very close as well, although not exactly the same, suggesting a nearly symmetric distribution with slight skewness in the tails. The area between the top (third quartile) and bottom (first quartile) dashed lines represents the interquartile range, which is the middle 50% of the data. In Figure 9, for the heart, the violin plot's wide base extends toward the lower end of the dose scale, suggests that a broader distribution of patients received lower doses.

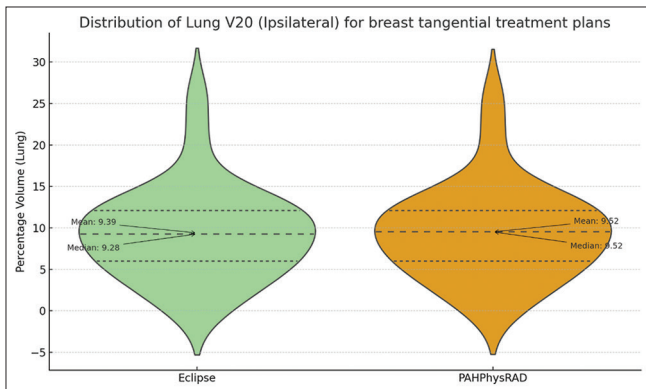


Figure 8: Comparison of Lung V20 volume for breast treatment plans

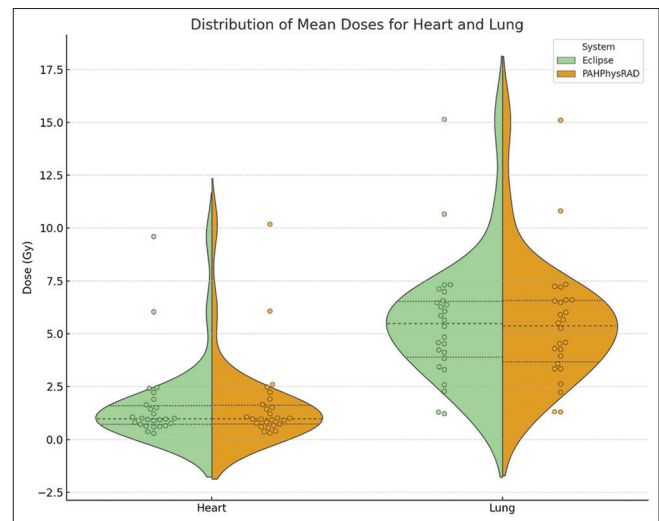


Figure 9: Side-by-side comparison of mean heart and lung doses computed in Eclipse and PAHPhysRad



The likely next step for the future development of PAHPhysRAD is to enable the data export in NIFTI and NRRD formats, which are well-suited for applications such as deep learning. One of the program's future objectives aligns with that of Computational Environment for Radiological Research (CERR), aiming to further utilize auto-segmentation models for delineating desired regions of interest. This goal, in conjunction with radiomic capabilities and the potential incorporation of classification-based machine learning models, could provide a simplified pipeline for importing any patient dataset, automatically generating segmentations (e.g., for tumor volumes), extracting radiomic features, and subsequently performing survival analysis, tumor recurrence and or predicting patient prognosis. The SAM incorporated into PAHPhysRAD is poised for ongoing development aligning with emerging AI research in medical imaging. Current studies indicate that bounding box prompts outperform point prompts in medical image segmentation.<sup>[12-15]</sup> As such, PAHPhysRAD integrates the bounding box method exclusively. While using multiple points per slice could potentially enhance accuracy, it compromises user experience by reducing simplicity and efficiency. Ideally, a single-point input method would be most user-friendly, allowing effortless segmentation across image slices. As advancements in SAM for medical applications evolve and become established, this can simply be implemented into PAHPhysRAD.

Although SAM and auto-segmentation models in PAHPhysRAD demonstrate considerable effectiveness, an inherent limitation arises from MATLAB's handling of ONNX file importation and execution. This necessitates the conversion of models to MATLAB-compatible opset and IR versions, with the MobileSAM encoder emerging as the only SAM encoder successfully converted. In addition, we observed that MATLAB execution times were greater compared to those in Python. Despite these constraints, integrating the ONNX models directly within the MATLAB framework offers a streamlined setup, eliminating the need for additional Python module installation and management. Thus, to maintain simplicity and user accessibility, we elected to retain the entire process within the MATLAB environment.

Another inherent MATLAB limitation is RAM usage when running the `dicomCollection` function. It was observed that for large datasets, MATLAB is at risk of using all available RAM, resulting in the `dicomCollection` function failing to complete. Whilst this issue can be avoided by scanning directories in chunks, users are likely to encounter this problem for radiomic studies involving hundreds of patient datasets. A future solution would be incorporate parsing script that manages RAM usage between loading DICOM metadata.

The issue with RAM usage is also one of the reasons why parallel processing is not currently implemented in PAHPhysRAD but will be considered for future versions. Many of the GUI functionalities can operate efficiently using a single CPU core, without significantly affecting the

user experience. However, for more demanding tasks such as batch radiomics export, incorporating parallel processing in future updates could significantly enhance the system's efficiency by allowing simultaneous processing of multiple patient datasets.

## CONCLUSION

The MATLAB-based GUI, PAHPhysRAD offers a user-friendly platform for viewing and analysing medical scans. Its versatility, compatibility, and potential for further development make it a valuable asset for medical image analysis.

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Project funded by SERTA.

## Conflicts of interest

There are no conflicts of interest.

## REFERENCES

1. Bidgood WD Jr., Horii SC. Introduction to the ACR-NEMA DICOM standard. *Radiographics* 1992;12:345-55.
2. Bidgood WD Jr., Horii SC, Prior FW, Van Syckle DE. Understanding and using DICOM, the data interchange standard for biomedical imaging. *J Am Med Inform Assoc* 1997;4:199-212.
3. Mayerhoefer ME, Materka A, Langs G, Häggström I, Szczyński P, Gibbs P, *et al.* Introduction to radiomics. *J Nucl Med* 2020;61:488-95.
4. Hatt M, Le Rest CC, Tixier F, Badic B, Schick U, Visvikis D. Radiomics: Data are also images. *J Nucl Med* 2019;60:38S-44S.
5. Wu S, Shen G, Mao J, Gao B. CT radiomics in predicting EGFR mutation in non-small cell lung cancer: A single institutional study. *Front Oncol* 2020;10:542957.
6. Ganeshan B, Miles KA, Young RC, Chatwin CR. Three-dimensional selective-scale texture analysis of computed tomography pulmonary angiograms. *Invest Radiol* 2008;43:382-94.
7. Davatzikos C, Rathore S, Bakas S, Pati S, Bergman M, Kalarot R, *et al.* Cancer imaging phenomics toolkit: Quantitative imaging analytics for precision diagnostics and predictive modeling of clinical outcome. *J Med Imaging (Bellingham)* 2018;5:011018.
8. Zhang L, Fried DV, Fave XJ, Hunter LA, Yang J, Court LE. IBEX: An open infrastructure software platform to facilitate collaborative work in radiomics. *Med Phys* 2015;42:1341-53.
9. Nioche C, Orhac F, Boughdad S, Reuzé S, Goya-Outi J, Robert C, *et al.* LIFEX: A freeware for radiomic feature calculation in multimodality imaging to accelerate advances in the characterization of tumor heterogeneity. *Cancer Res* 2018;78:4786-9.
10. Pfachler E, Zwanenburg A, de Jong JR, Boellaard R. RaCaT: An open source and easy to use radiomics calculator tool. *PLoS One* 2019;14:e0212223.
11. Kirillov A, Mintun E, Ravi N, Mao H, Rolland C, Gustafson L. Segment Anything. 2023. arXiv Preprint arXiv: 2304.02643.
12. Mattjie C, de Moura LV, Ravazio RC, Kupssinski LS, Parraga O, Delucis MM. Exploring the Zero-Shot Capabilities of the Segment Anything Model (SAM) in 2D Medical Imaging: A Comprehensive Evaluation and Practical Guideline. arXiv 2023. Preprint arXiv: 2305.00109.
13. Cheng D, Qin Z, Jiang Z, Zhang S, Lao Q, Li K. Sam on Medical Images: A Comprehensive Study on Three Prompt Modes. arXiv 2023. Preprint arXiv:2305.00035.
14. Roy S, Wald T, Koehler G, Rokuss MR, Disch N, Holzschuh J. Sam. Md: Zero-Shot Medical Image Segmentation Capabilities of the Segment Anything Model. arXiv 2023. Preprint arXiv:2304.05396.
15. Ma J, Wang B. Segment Anything in Medical Images. arXiv 2023. Preprint arXiv:2304.12306.
16. Zhang C, Han D, Qiao Y, Kim JU, Bae SH, Lee S. Faster Segment Anything: Towards lightweight SAM for Mobile Applications. arXiv

- preprint arXiv:2306.14289.
17. Colbert ZM, Ramachandran P. Auto-segmentation of thoracic organs in CT scans of breast cancer patients using a 3D U-net cascaded into 2D patchGANs. *Biomed Phys Eng Express* 2023;9:055011. [doi: 10.1088/2057-1976/ace631].
  18. Pyradiomics. Available from: <https://pyradiomics.readthedocs.io/en/latest/index.html>. [Last accessed on 2023 Aug 10].
  19. Vallières M, Freeman CR, Skamene SR, El Naqa I. A radiomics model from joint FDG-PET and MRI texture features for the prediction of lung metastases in soft-tissue sarcomas of the extremities. *Phys Med Biol* 2015;60:5471-96.
  20. Zhou H, Vallières M, Bai HX, Su C, Tang H, Oldridge D, *et al.* MRI features predict survival and molecular markers in diffuse lower-grade gliomas. *Neuro Oncol* 2017;19:862-70.
  21. Vallières M, Kay-Rivest E, Perrin LJ, Liem X, Furstoss C, Aerts HJ, *et al.* Radiomics strategies for risk assessment of tumour failure in head-and-neck cancer. *Sci Rep* 2017;7:10117.