DicomDoodle: A Comprehensive MRI 3D DICOM Image Annotation and Visualization Tool

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1. Introduction

DicomDoodle is a Python-based, user-friendly graphical user interface (GUI) tool designed to streamline the annotation, segmentation, and visualization of DICOM medical images, with a particular focus on MRI data. Developed to assist researchers, radiologists, and medical professionals, DicomDoodle integrates state-of-the-art deep learning models—such as YOLO (You Only Look Once) for object detection and SAM (Segment Anything Model) for precise segmentation—to automate and enhance the process of identifying and annotating regions of interest, such as tumors, in MRI images.

The tool provides a robust suite of features for both automated and manual segmentation, along with advanced 2D and 3D visualization capabilities. It ensures compatibility with other medical imaging software by saving annotations as standard DICOM segmentation files (_seg.dcm). DicomDoodle aims to assist users in efficiently and accurately performing medical image analysis tasks, from diagnostic annotations to preparing datasets for AI training.

2. System Requirements and Installation

To ensure optimal performance and functionality, DicomDoodle requires the following:

Operating System:

- Windows 7/8/8.1/10/11
- Linux (Recommended for better speed and performance)
- macOS (Recommended for better speed and performance)

Python Environment:

- Python 3.10 or higher

Required Libraries (will be installed automatically if using pip and requirements.txt):

- PyQt5 (for the graphical user interface)
- numpy (for numerical operations)
- pydicom (for DICOM file reading and writing)
- opencv-python (for image processing tasks)
- Pillow (PIL fork, for image manipulation)
- ultralytics (for YOLO and SAM models)
- highdicom (for creating DICOM Segmentation objects)
- SimpleITK (for advanced image processing and resampling in 3D viewer)
- vtk (for 3D visualization, including vtk.qt.QVTKRenderWindowInteractor)
- ontoportal-client (for BioPortal ontology integration)
- scikit-image (optional, for texture analysis in 3D viewer; will run without it but features will be "N/A")

GPU (Highly Recommended for Performance):

- An NVIDIA GPU with CUDA support is highly recommended for faster inference with YOLO and SAM models. Without a GPU, processing times, especially for batch operations, will be significantly longer.

Installation (from source):

1. **Clone the repository (if applicable):** git clone <repository_url> cd DicomDoodle
- **Create a virtual environment (recommended):** python -m venv venv
- **On Windows:** .\venv\Scripts\activate
- **On Linux/macOS:** source venv/bin/activate
- **Install dependencies:** pip install -r requirements.txt (requirements.txt is provided) Alternatively, install individually: pip install PyQt5 numpy pydicom opencv-python pillow ultralytics highdicom SimpleITK vtk ontoportal-client scikit-image*Note:* vtk can be complex to install. If you encounter issues, refer to VTK documentation or consider using a pre-compiled distribution.

Running as an Executable:

- If a bundled executable (.exe for Windows, or similar for other OS) is provided, simply run it directly. All dependencies will be packaged within.

3. Getting Started: Launching and Understanding the Interface

3.1. Launching DicomDoodle

- **From Source:** Navigate to the main directory of the tool in your terminal/command prompt and run: python main_app_script_name.py (replace main_app_script_name.py with the actual name of the main Python script, e.g., main.py if present).
- **From Executable:** Double-click the DicomDoodle.exe (or equivalent) file.

Upon successful launch, a window titled "DICOM Viewer and Annotator" will appear, displaying the main interface.

3.2. Understanding the Main Interface

The main window of DicomDoodle is intuitively designed to facilitate efficient DICOM image handling and annotation. It comprises several key areas:

- **Menu Bar (Top-Left, "☰" icon):** This provides access to various utility functions and specialized viewers.
- **Horizontal Scrollbar (Top):** Located beneath the menu bar, this scrollbar enables seamless navigation through loaded DICOM slices.
- **Graphics View (Central Area):** This is the primary display area where the current DICOM slice is rendered. All annotations, segmentations, and bounding boxes are visualized here.
- **Message Labels (Within Graphics View):"Mask already saved for this slice" (Yellow background):** Appears when a segmentation file (_seg.dcm) corresponding to the current slice has been saved.
- **Progress Label (Green background):** Displays real-time status updates during batch processing operations (e.g., "Processing X/Y slices"). This label appears temporarily and provides feedback on the background tasks.
- **Button Rows (Below Graphics View):** Organized into three distinct rows, these buttons provide access to the tool's core functionalities:
- **Row 1 (General Actions):** Includes buttons for Load DICOM Folder, Auto Detect (single slice), Plot Results, Save Results, and Refresh.
- **Row 2 (Batch Processing & Manual Drawing):** Contains controls for setting blank mask ranges (Set Blank Mask Range 1 Start/End, Set Blank Mask Range 2 Start/End), Save Blank Masks, Set Auto Detect Range Start/End, Save Auto Detected Masks, and Manual Draw.
- **Row 3 (Color Selection):** Provides buttons to select different colors for manual and automated segmentations, each pre-assigned to a specific biological label.
- **Window Title:** Dynamically updates to display the current slice number and total number of slices (e.g., "DICOM Viewer - Slice 1/100").

3.3. Menu Bar Options

Clicking the "☰" icon in the top-left corner of the main window reveals a dropdown menu with the following options:

- **About:** Opens a dialog providing information about the DicomDoodle tool, its purpose, features, and the author's contact details.
- **How to Use:** Launches a detailed guide (this documentation) explaining all features and functionalities of the tool.
- **Citations:** Displays a list of academic citations for the key open-source libraries and modules utilized in DicomDoodle's development (e.g., PyQt5, NumPy, Ultralytics, PyDICOM).
- **Annotated Dicom Viewer:** Opens a separate window designed specifically for reviewing DICOM files with existing segmentation overlays. This viewer allows loading folders containing both original DICOMs and their _seg.dcm counterparts.
- **View 3D Model:** Launches an advanced 3D visualization window, allowing users to generate and interact with 3D renderings of the anatomy and segmented tumors from loaded DICOM series.
- **Convert Multi Frame Dicom to Single Dicom:** Opens a utility window to convert multi-frame DICOM files into individual single-frame DICOM files.
- **Lesion Volume Calculator:** Opens a dedicated application for calculating the volume of segmented lesions/tumors from DICOM series across different anatomical planes.

4. Loading DICOM Files

To begin, you need to load a series of DICOM images:

1. **Click the "Load DICOM Folder" Button:** This is the first button in the top row, typically colored red.
2. **Select a Folder:** A file dialog will appear. Navigate to a directory containing your DICOM files (.dcm extension).
- **Important:** Ensure the folder contains only the original DICOM image files and *not* any existing segmentation files (which typically have _seg.dcm in their names) at this initial loading stage for the main viewer. Segmentation files will be loaded automatically by the "Annotated DICOM Viewer" later.
1. **Confirm Selection:** Select the desired folder and click "Open."
2. **Loading Process:** The tool will read all valid DICOM files within the selected folder, sort them by InstanceNumber, and display the first slice in the central graphics view.
- **Verification:**The window title will update to reflect the currently displayed slice and the total number of slices (e.g., "DICOM Viewer - Slice 1/50").
- The horizontal scrollbar at the top will adjust its range to correspond to the total number of loaded slices, enabling navigation.
- If no valid DICOM files are found, an error message will be displayed.

5. Navigating Through Slices

DicomDoodle provides two convenient methods for moving through DICOM slices:

- **Using the Mouse Wheel:Scroll Up:** Move the mouse wheel upwards to go to the *previous* slice (e.g., from slice 10 to slice 9).
- **Scroll Down:** Move the mouse wheel downwards to advance to the *next* slice (e.g., from slice 10 to slice 11).
- The window title and the horizontal scrollbar will automatically update to indicate the new current slice.
- **Using the Horizontal Scrollbar:Drag the Slider:** Click and drag the slider on the horizontal scrollbar located at the top of the window. This allows for rapid navigation to any specific slice within the loaded series.
- The scrollbar's range is dynamically set to 0 (first slice) to N-1 (last slice) where N is the total number of slices.

6. Automatic Segmentation with YOLO and SAM

DicomDoodle integrates YOLO for initial tumor detection and SAM for subsequent precise segmentation. This powerful combination can be applied to individual slices or entire ranges.

6.1. Single Slice Auto-Detection

1. **Select a Slice:** Navigate to the specific DICOM slice you wish to segment using the mouse wheel or the scrollbar.
2. **Run Auto-Detection:** Click the **"Auto Detect"** button (blue, first row, second button).
- **Process and Display:**The tool will utilize the YOLO model to identify and draw a green bounding box around any detected tumor regions on the current slice.
- If a bounding box is successfully detected, the SAM model will then perform a detailed segmentation within that bounding box.
- The segmentation result is overlaid on the DICOM slice as a colored edge, with the default color being red.
- **Verify Results:**If YOLO does not detect a bounding box, a message "No bounding box detected by YOLO" will be printed to the console (and potentially a pop-up warning).
- The color of the segmentation edge can be customized using the color selection buttons (see Section 9).

6.2. Batch Auto-Detection for a Range of Slices

This feature allows for automatic segmentation of multiple slices sequentially.

- **Set the Range Start:**Navigate to the first slice of your desired batch processing range.
- Click **"Set Auto Detect Range Start"** (purple, second row, sixth button).
- A confirmation message will appear in the console (e.g., "YOLO Range Start set to slice 10").
- **Set the Range End:**Navigate to the last slice of your desired batch processing range.
- Click **"Set Auto Detect Range End"** (magenta, second row, seventh button).
- A confirmation message will appear in the console (e.g., "YOLO Range End set to slice 20").
- **Run Batch Auto-Detection:**Click **"Save Auto Detected Masks"** (bright magenta, second row, eighth button).
- A splash screen with a progress bar will appear, showing the real-time processing status (e.g., "Processing 5/11 slices").
- For each slice within the defined range:
- YOLO attempts to detect a bounding box.
- If a bounding box is found, SAM performs segmentation within it.
- The resulting segmentation (or a blank mask if no detection) is saved as a DICOM segmentation file (<original_filename>_seg.dcm) in the same directory as the original DICOM file.
- If no bounding box is detected by YOLO, a blank mask (all zeros) is saved for that slice.
- Upon completion, a "Finished" dialog will display the total time taken for the batch operation (e.g., "Finished - Total time: 15s"). Click "OK" to close it.

7. Manual Segmentation

DicomDoodle provides flexible options for manual annotation, allowing users to define regions for SAM segmentation or draw freehand.

7.1. Manual Bounding Box for SAM Segmentation

This method allows users to guide SAM segmentation by manually drawing a region of interest.

1. **Select a Slice:** Navigate to the desired slice.
- **Draw a Bounding Box:Left-click and Drag:** Click and hold the left mouse button on the graphics view at the starting point of your desired region.
- **Drag:** Drag the mouse to define the rectangular region. A red rectangle will dynamically appear as you drag.
- **Release:** Release the mouse button to finalize the bounding box.
- **Adjust:** The drawn bounding box can be interactively resized by dragging its corner handles (blue dots) or moved by dragging its center.
- **Run SAM Segmentation:Right-click "Detect":** Right-click *inside* the finalized bounding box. A context menu will appear.
- Select **"Detect"** from the context menu.
- The SAM model will then segment the region precisely within the drawn box. The segmentation result is overlaid as a colored edge (using the currently selected color from the color palette).
- The bounding box and its handles will disappear after detection, and the segmentation will be displayed.

7.2. Freehand Drawing Tool

For more detailed or irregular annotations, use the manual drawing tool:

1. **Open the Manual Drawing Tool:** Click the **"Manual Draw"** button (orange-red, second row, ninth button).
- A new, separate window titled "Manual Drawing Tool" will open, displaying the current slice from the main viewer.
- **Drawing Annotations:Select a Color:** Use the color buttons located at the bottom of the "Manual Drawing Tool" window (e.g., Red, Green, Blue, Yellow). The selected button will highlight in its chosen color, indicating the active drawing color. This color will correspond to a specific label in the saved DICOM segmentation file (see Section 9).
- **Draw:** Left-click and drag the mouse on the image to draw freehand annotations. The drawing will appear in the selected color.
- **Erase:** Click the **"Eraser"** button (blue) to toggle eraser mode. In this mode, left-click and drag will erase annotations by setting the drawn area to black. Click the button again to return to drawing mode.
- **Zoom:** Use the mouse wheel to zoom in or out on the image for more precise drawing or erasing.

- **Refresh:** Click the **"Refresh"** button (yellow) to clear all annotations and revert the slice to its original state (without annotations). This also resets contrast and brightness.
- **Load Annotation:** Click the **"Load Annotation"** button to load any existing _seg.dcm file for the current slice into the manual drawing canvas, allowing for further editing.
- **Adjust Image Appearance (within Manual Drawing Tool):Contrast Slider:** Adjusts the contrast of the underlying DICOM image to aid visibility during manual drawing.
- **Brightness Slider:** Adjusts the brightness of the underlying DICOM image.
- **Slice Slider:** Allows navigation to other slices directly within the manual drawing window.
1. **Save the Annotation:** Click the **"Save Mask"** button (pink).
- The freehand annotations will be saved as a DICOM segmentation file (<original_filename>_seg.dcm) in the same folder as the original DICOM file.
- The "Manual Drawing Tool" window will then close, and the main viewer will refresh to display the newly saved mask. The "Mask already saved" message will appear.
1. **Close Without Saving:** Click the **"Close"** button (red) to discard any unsaved changes and return to the main viewer.

8. Saving Segmentations

DicomDoodle allows saving single slice segmentations and batch saving blank masks or auto-detected masks.

8.1. Saving a Single Slice Segmentation

After performing auto-detection (Section 6.1) or manual segmentation (Section 7.1 or 7.2) on a single slice:

1. Click the **"Save Results"** button (pink, first row, fourth button).
2. The current segmentation mask will be saved as a DICOM segmentation file (<original_filename>_seg.dcm) in the same directory as its corresponding original DICOM file.
3. The "Mask already saved for this slice" message will appear in the graphics view, indicating successful saving.

8.2. Saving Blank Masks for a Range of Slices

This feature is useful for efficiently creating _seg.dcm files for slices that contain no tumors or require no annotations, maintaining consistent file structure.

- **Set Range 1 (Mandatory for first batch):**Navigate to the *start* slice of your first desired range and click **"Set Blank Mask Range 1 Start"** (light sea green, second row, first button).
- Navigate to the *end* slice of this range and click **"Set Blank Mask Range 1 End"** (medium sea green, second row, second button).
- **Set Range 2 (Optional):**If you have a second, non-contiguous range of slices for which you want to save blank masks, repeat the process using **"Set Blank Mask Range 2 Start"** (dark turquoise, second row, third button) and **"Set Blank Mask Range 2 End"** (medium turquoise, second row, fourth button).
- **Save Blank Masks:**Click **"Save Blank Masks"** (yellow-green, second row, fifth button).
- A splash screen with a progress bar will appear, indicating the number of slices being processed.
- For each slice within the specified ranges, a blank DICOM segmentation file (all zeros in the pixel array) will be created and saved as <original_filename>_seg.dcm.
- A "Finished" dialog will confirm completion, showing the total processing time.

9. Changing Segmentation Colors and Labeling

DicomDoodle allows users to choose different colors for their segmentations, which also correspond to specific semantic labels in the output DICOM segmentation files.

1. **Select a Color:**
- Use the color buttons located in the **third row** of the main interface (e.g., Red, Green, Blue, Yellow, Cyan, Magenta).
- Clicking a color button will set it as the active color for subsequent manual and automatic segmentations.
- The selected button will highlight in its chosen color, and a confirmation message will appear in the console (e.g., "Drawing color set to: [255, 0, 0]").
1. **Apply the Color:**
- The chosen color will be used for displaying the segmentation edge in the main viewer and in the "Plot Results" window.
- **Crucially, each color is mapped to a specific SegmentLabel and SegmentedPropertyTypeCodeSequence within the DICOM segmentation file (HighDICOM standard).** This provides semantic meaning to your annotations:
- **Red (255, 0, 0):** SegmentLabel: "Tumor & Brain Boundary" (Category: Tissue, Type: Connective Tissue)
- **Green (0, 255, 0):** SegmentLabel: "Tumor & Dura Boundary" (Category: Tissue, Type: Connective Tissue)
- **Blue (0, 0, 255):** SegmentLabel: "Tumor & Necrosis Boundary" (Category: Tissue, Type: Connective Tissue)
- **Yellow (255, 255, 0):** SegmentLabel: "Edema & Brain Boundary" (Category: Tissue, Type: Connective Tissue)
- **Cyan (0, 255, 255):** SegmentLabel: "Tumor & Edema Boundary" (Category: Tissue, Type: Connective Tissue)
- **Magenta (255, 0, 255):** SegmentLabel: "Magenta Boundary" (Category: Tissue, Type: Connective Tissue)
1. *Note: The actual CodedConcept values for SegmentedPropertyCategoryCodeSequence and SegmentedPropertyTypeCodeSequence default to general "Tissue" and "Connective Tissue" if not explicitly set via the Ontology Integration (Section 11). For blank masks, they default to "Organ" and "Brain".*

10. Visualizing Results

DicomDoodle offers several ways to visualize your segmentation results, from 2D overlays to full 3D models and quantitative volume calculations.

10.1. Plotting Segmentation Results (2D Overlay)

To see a detailed 2D visualization of a segmented slice:

1. After segmenting a slice (either automatically or manually), click the **"Plot Results"** button (lime green, first row, third button).
2. A new window titled "Segmentation Results" will open, displaying two synchronized views:
● **Left View:** Shows the original DICOM image with the segmented tumor region overlaid and blended for context.
● **Right View:** Displays the original image with only the *boundary* (edge) of the segmented tumor highlighted, providing a clear outline.
1. You can resize this window to adjust the display; the images will automatically scale to fit while maintaining their aspect ratio.

10.2. Viewing Annotated DICOMs (Overlay Viewer)

This dedicated viewer is for reviewing entire DICOM series with their corresponding segmentation files.

1. From the main menu bar, select **"Annotated Dicom Viewer"**.
2. A new window titled "DICOM Annotated Image Viewer" will open.
3. Click **"Load DICOM Folder"** within this viewer. Select the folder containing both your original DICOM files and the _seg.dcm segmentation files generated by DicomDoodle.
4. Navigate through the slices using the mouse wheel.
5. For slices that have a corresponding segmentation file, the annotations will be overlaid on the original image in their respective assigned colors (e.g., red for "Tumor & Brain Boundary", green for "Tumor & Dura Boundary").
6. Labels for "Segment Category" and "Segment Type" will be displayed in the top-left corner of the image, derived from the SegmentSequence in the _seg.dcm file.

10.3. Viewing 3D Models (3D Volume Viewer)

For a comprehensive spatial understanding of the anatomy and tumor:

1. From the main menu bar, select **"View 3D Model"**.
2. A new window titled "DICOM 3D Volume Viewer" will open, with two VTK rendering panels.
3. Click the **"≡" icon (menu bar) -> "Load"** in this 3D viewer window to select a DICOM folder (this folder should contain original DICOM files and their _seg.dcm files if you want tumor visualization).
4. The viewer will process the DICOM series and render two 3D visualizations:

- **Left Panel (Anatomy/Tumor):** Displays the anatomical structures (e.g., brain tissue) as a translucent volume, with the segmented tumor overlaid as an opaque red object.
- **Right Panel (Full Volume):** Displays the full anatomical volume without specific tumor overlay, allowing for general anatomical exploration.
1. **Interaction:** Use the mouse to interact with the 3D models:
- **Left-click and drag:** Rotate the model.
- **Right-click and drag:** Zoom in/out.
- **Middle-click (or Ctrl+Left-click) and drag:** Pan the model.
- **Customization (Anatomy & Volume Visualization Dialogs):**The "View 3D Model" menu offers "Anatomy Visualization" and "Volume Visualization" options. Clicking these opens dedicated dialogs with extensive controls:
- **Basic Controls:** Adjust Contrast, Ambience, Opacity Threshold, Gradient Opacity, Specular Power, Scalar Min/Max, and Colormap (e.g., Grayscale, Bone, Hot, Jet, BrainTumorSpecific).
- **Advanced Controls for Surgery Planning:** Toggle Advanced Shading, Edge Enhancement, Tissue Density, Tumor Annotations (for the anatomy view), and Measurement Tool.
- **Clipping Planes:** Enable X-Axis, Y-Axis, and Z-Axis clipping planes and adjust their positions to virtually "slice" through the 3D volume, revealing internal structures.
- **Lighting Controls:** Adjust Light Azimuth, Light Elevation, and Light Intensity to optimize the illumination of the 3D model for better perception of depth and surface details.
- **Tumor Metrics:** The 3D viewer also calculates and displays key tumor metrics (Volume, Surface Area, Sphericity, and Texture properties like Contrast and Homogeneity if scikit-image is available) in the left panel when Show Tumor Annotations is enabled in the Anatomy Visualization dialog.

10.4. Lesion Volume Calculator

This utility provides a direct quantitative measurement of tumor volumes.

1. From the main menu bar, select **"Lesion Volume Calculator"**.
2. A new window titled "DICOM Tumor Volume Calculator" will open.
3. **Select Folders:** Click "Browse Axial Folder," "Browse Coronal Folder," and/or "Browse Sagittal Folder" to select the respective DICOM series folders. You can select one or multiple orientations.
4. **Calculate:** Click **"Calculate Tumor Volumes"**.
5. The tool will read the DICOM series (and corresponding _seg.dcm files if present), calculate the tumor volume in cm³ for each selected orientation, and display an average volume. A message box will present these results.

11. Ontology Integration for Semantic Labeling

DicomDoodle allows you to enhance the semantic labeling of your segmentations by integrating with external ontologies via BioPortal. This ensures that your segmentation files contain standardized, machine-readable information about the segmented anatomy or pathology.

1. **Open Ontology Search:** In the "DICOM Annotated Image Viewer" (opened via Menu Bar -> Annotated Dicom Viewer), click the **"Add Ontology"** button.
- A new "BioPortal Ontology Search" window will open.
- **Search for Concepts:** Enter a search term (e.g., "brain", "tumor", "glioma") in the search bar and click **"Get Labels"**.
- The results list will populate with matching concepts from various ontologies available on BioPortal.
- If there are more than 10 results, a "Show All Results" button will appear, allowing you to view the full list.
- **Select Category and Type:Right-click** on a concept in the results list to bring up a context menu.
- Select **"Add Segment Category"**: This assigns the chosen concept as the broad category for your segmentations (e.g., "Organ", "Tissue").
- Select **"Add Segment Type"**: This assigns the chosen concept as the specific type within the category (e.g., "Brain", "Tumor", "Glioma").
- You can also select "Definition And Synonyms" to view more details about a concept.
- **Apply to DICOM Segmentation Files:** Once both a "Segment Category" and "Segment Type" have been selected in the BioPortal Search window, the DICOMOverlayViewer (Annotated DICOM Viewer) will automatically attempt to update the SegmentSequence within *all existing* _seg.dcm files in the currently loaded folder.
- For _seg.dcm files that contain actual segmented data (non-zero pixel arrays), the chosen BioPortal concepts will be applied to their SegmentedPropertyCategoryCodeSequence and SegmentedPropertyTypeCodeSequence.
- For _seg.dcm files that are blank (all zeros), the system will automatically assign default concepts for "Organ" (SCT value: 91772007) and "Brain" (SCT value: 12738006). This ensures that even blank masks have some basic semantic context.
- A success message will confirm the update, and the DICOMOverlayViewer will reload to reflect the new labels.

12. Undoing and Refreshing Actions

DicomDoodle provides options to revert changes or reset the current view:

- **Undo Last Segmentation (Ctrl+Z):**Press Ctrl+Z on your keyboard to undo the last segmentation action performed on the current slice (e.g., after an auto-detection or manual bounding box segmentation).
- This will restore the previous visual state of the slice.
- **Refresh the Current Slice (Refresh button):**Click the **"Refresh"** button (gold, first row, fifth button).
- This action resets the current slice to its original, un-annotated state, effectively removing all temporary annotations, segmentations, and any applied masks.
- It also clears any stored mask data and resets the internal color index.

13. Additional Features and Information

13.1. About the Tool

Accessed via the "≡" menu, the "About" dialog provides:

- A comprehensive description of DicomDoodle's capabilities and its underlying technology.
- The author's name (Pushp Lochan Kumar) and contact email (pushpl@iisc.ac.in) for feedback and support.

13.2. Citations

Also accessed via the "≡" menu, the "Citations" dialog lists the academic references and URLs for all major open-source libraries and modules used in DicomDoodle's development, including PyQt5, NumPy, OpenCV, PyDICOM, Ultralytics, HighDICOM, and Pillow. Users are encouraged to cite these works if the tool is used in research or projects.

13.3. Progress Feedback

- During time-consuming batch operations (e.g., Save Blank Masks, Save Auto Detected Masks), a dedicated splash screen with a progress bar will appear.
- This splash screen provides real-time feedback on the number of slices being processed (e.g., "Processing X/Y slices").
- Upon completion, a "Finished" dialog will pop up, displaying the total time taken for the operation.

13.4. Multi-Frame DICOM to Single DICOM Conversion

Modern DICOM acquisitions can sometimes be stored as multi-frame files, containing multiple 2D slices within a single .dcm file. DicomDoodle provides a utility to convert these into a series of single-frame DICOM files, which are often easier for legacy systems or other tools to process.

1. From the main menu bar, select **"Convert Multi Frame Dicom to Single Dicom"**.
2. A new window titled "3D DICOM Viewer" will open (this viewer doubles as the multi-frame converter).
3. Click **"Open DICOM File"** and select a multi-frame DICOM file.
4. Once loaded, click **"Save Slices"**. The tool will prompt you to choose an output directory and then save each frame as an individual DICOM file, meticulously copying relevant metadata (e.g., ImagePositionPatient, SliceThickness, WindowCenter/Width) to ensure each new single-frame file is a valid and accurate representation of its original frame.
5. A progress bar will show the conversion status, and a success message will appear upon completion.

14. Usage Tips and Troubleshooting

- **File Organization:** Always keep your original DICOM files in a clean, dedicated folder. DicomDoodle will save all generated segmentation files (_seg.dcm) directly into the same folder.
- **Color Coding:** Utilize the different color options to distinguish between various types of boundaries or pathological regions (e.g., red for tumor core, green for edema, blue for necrosis). These colors map to specific SegmentLabels for better organization and interpretation.
- **Zoom and Precision (Manual Drawing):** In the "Manual Drawing Tool" window, use the mouse wheel to zoom in for highly precise annotations and fine-tuning.
- **Error Handling (DICOM Metadata):** DicomDoodle relies on standard DICOM tags (e.g., InstanceNumber, PixelSpacing, ImagePositionPatient, FrameOfReferenceUID). If a DICOM file is incomplete or lacks critical attributes, the tool may raise warnings or errors. Ensure your source DICOM files are standard-compliant for best results.
- **Performance:** Batch processing (especially auto-detection over many slices) can be computationally intensive and time-consuming. It is recommended to start with smaller ranges to test performance on your system. Using a machine with a powerful GPU will significantly reduce processing times.
- **3D Visualization:** For the 3D tumor visualization feature to work correctly, the corresponding _seg.dcm files must be present in the loaded DICOM folder. Without them, only the raw anatomical volume will be displayed.
- **Canceling Operations:** During long processing tasks, you can click "Cancel" on the progress dialog to stop the operation.
- **VTK Issues:** If you encounter VTK library not found errors, ensure VTK is correctly installed and configured for your Python environment. Refer to VTK's official installation guides.

15. Example Workflow

1. **Load DICOMs:** Click **"Load DICOM Folder"** and select a folder containing 50 MRI slices.
- **Single Slice Auto-Segmentation:**Navigate to **slice 10** using the scrollbar or mouse wheel.
- Click **"Auto Detect"**. A green bounding box appears, followed by a red segmented edge around the tumor.
- **Change Color & Segment Another Slice:**Click the **"Green (0, 255, 0)"** color button in the third row.
- Navigate to **slice 11**.
- Click **"Auto Detect"** again. A green segmented edge (now representing "Tumor | Dura Boundary") will appear.
- **Save Blank Masks:**Navigate to **slice 1**. Click **"Set Blank Mask Range 1 Start"**.
- Navigate to **slice 5**. Click **"Set Blank Mask Range 1 End"**.
- Click **"Save Blank Masks"**. This creates _seg.dcm files for slices 1-5, indicating no tumor.
- **Batch Auto-Detection:**Navigate to **slice 20**. Click **"Set Auto Detect Range Start"**.
- Navigate to **slice 30**. Click **"Set Auto Detect Range End"**.
- Click **"Save Auto Detected Masks"**. The tool will now automatically detect and save segmentations for slices 20-30.
- **Manual Annotation:**Navigate to **slice 15**.
- Click the **"Manual Draw"** button. The Manual Drawing Tool opens.
- Click the **"Yellow (255, 255, 0)"** color button.
- Draw a freehand annotation (e.g., around an edema region).
- Click **"Save Mask"**. The manual annotation is saved, and the window closes.
- **Plot Results:**Navigate back to **slice 10**.
- Click **"Plot Results"**. A new window shows the original image with the blended tumor overlay and the tumor boundary highlighted.
- **View 3D Model:**From the main menu bar, select **"View 3D Model"**.
- In the new 3D viewer window, click **"Load"** and select your DICOM folder.
- Observe the 3D rendering of the anatomy and the segmented tumors (red objects). Interact by rotating, zooming, and panning.
- Experiment with the "Anatomy Visualization" and "Volume Visualization" menu options in the 3D viewer to adjust lighting, colormaps, and add clipping planes for deeper inspection.
- **Review All Segmentations:**From the main menu bar, select **"Annotated Dicom Viewer"**.
- Load your DICOM folder.
- Scroll through the slices. You will see the annotations (red for slice 10, green for slice 11, yellow for slice 15) overlaid on their respective slices.
- **Calculate Lesion Volume:**From the main menu bar, select **"Lesion Volume Calculator"**.
- Browse and select the folder(s) for the axial, coronal, and/or sagittal series.
- Click **"Calculate Tumor Volumes"** to get a quantitative report.
- **Use Ontology Integration:**In the "Annotated Dicom Viewer", click "Add Ontology".
- Search for "glioma", select a relevant result, and assign it as "Add Segment Type".
- Observe how the metadata in your _seg.dcm files is updated with the standardized ontology codes.

16. Glossary of Key Terms

- **Annotation:** The process of marking or highlighting specific regions or features within an image.
- **Axial Plane:** An anatomical plane that divides the body into superior (upper) and inferior (lower) parts, often seen as "slices" from head to foot in medical imaging.
- **BioPortal:** A repository of biomedical ontologies developed by Stanford University, used by DicomDoodle for semantic labeling.
- **Bounding Box:** A rectangular box drawn around an object of interest, typically used in object detection to indicate the location of an object.
- **Coronal Plane:** An anatomical plane that divides the body into anterior (front) and posterior (back) parts.
- **DICOM (Digital Imaging and Communications in Medicine):** The international standard for medical images and related information. It defines the formats for medical images and their associated metadata.
- **DICOM Segmentation File (_seg.dcm):** A specialized DICOM file that stores binary or multi-label masks, indicating segmented regions of interest in corresponding original DICOM images. These files often adhere to the HighDICOM standard.
- **Edema:** Swelling caused by excess fluid trapped in your body's tissues. Often appears as bright regions in FLAIR MRI sequences.
- **FLAIR (Fluid-Attenuated Inversion Recovery):** A specific MRI pulse sequence that suppresses the signal from cerebrospinal fluid, making lesions (like tumors or edema) more visible.
- **Freehand Drawing:** A manual annotation method where users draw irregular shapes directly on the image, typically with a mouse.
- **GPU (Graphics Processing Unit):** A specialized electronic circuit designed to rapidly manipulate and alter memory to accelerate the creation of images in a frame buffer for output to a display device. Essential for deep learning model performance.
- **HighDICOM:** A Python library that provides high-level abstractions for creating and manipulating DICOM objects, especially those related to structured reporting and segmentation.
- **InstanceNumber:** A DICOM tag that typically represents the sequential order of slices within a series.
- **MRI (Magnetic Resonance Imaging):** A medical imaging technique that uses a magnetic field and computer-generated radio waves to create detailed images of organs and soft tissues within the body.
- **Multi-frame DICOM:** A single DICOM file containing multiple frames (slices or time points) of an image series.
- **Numpy:** A fundamental Python library for numerical computing, especially with arrays and matrices.
- **Ontology:** In informatics, a formal representation of a set of concepts within a domain and the relationships between those concepts. Used here for standardized medical terminology.
- **OpenCV (Open Source Computer Vision Library):** A library of programming functions mainly aimed at real-time computer vision.
- **Pixel Array:** The raw image data (pixel values) contained within a DICOM file.

- **PixelSpacing:** A DICOM tag that defines the physical distance between the centers of adjacent pixels in the image plane (e.g., in mm).
- **PyDICOM:** A Python package for reading, modifying, and writing DICOM files.
- **PyQt5:** A set of Python bindings for the Qt application framework, used for developing the graphical user interface.
- **Sagittal Plane:** An anatomical plane that divides the body into left and right parts.
- **SAM (Segment Anything Model):** A powerful, promptable segmentation model developed by Meta AI, capable of segmenting any object in an image with high accuracy, given a prompt (like a bounding box).
- **Segmentation:** The process of partitioning a digital image into multiple image segments (sets of pixels, also known as superpixels). It's used to locate objects and boundaries (lines, curves, etc.) in images.
- **SegmentLabel:** A DICOM tag within a SegmentSequence that provides a human-readable label for a specific segmented region.
- **SegmentedPropertyCategoryCodeSequence:** A DICOM attribute that describes the broad category of the anatomical structure or property that has been segmented (e.g., "Organ", "Tissue").
- **SegmentedPropertyTypeCodeSequence:** A DICOM attribute that describes the specific type of the anatomical structure or property within its category (e.g., "Brain", "Tumor", "Edema").
- **SliceThickness:** A DICOM tag that indicates the nominal slice thickness of the tomographic plane, usually in mm.
- **Sphericity:** A measure of how spherical an object is, calculated from its volume and surface area. A perfect sphere has a sphericity of 1.0.
- **Texture Analysis (GLCM - Gray-Level Co-occurrence Matrix):** A method for extracting statistical features from images based on the spatial relationship of pixel intensities, used to quantify properties like contrast and homogeneity.
- **Tumor:** An abnormal mass of tissue.
- **UID (Unique Identifier):** A globally unique string of numbers used in DICOM to identify objects like studies, series, and instances.
- **Ultralytics:** The company and framework behind the YOLO (You Only Look Once) and SAM models, providing high-performance deep learning solutions.
- **Voxel:** A three-dimensional pixel; the smallest distinguishable box-shaped part of a 3D image.
- **VTK (Visualization Toolkit):** An open-source, freely available software system for 3D computer graphics, image processing, and visualization.
- **YOLO (You Only Look Once):** A popular real-time object detection system capable of identifying and localizing objects within an image.

FAQ

1. What is the primary purpose of the DicomDoodle tool, and what two main deep learning models does it integrate for its core functionality?
2. Describe two different ways a user can navigate through DICOM slices in the main DicomDoodle viewer.
3. Explain the difference between "Single Slice Auto-Detection" and "Batch Auto-Detection" using YOLO and SAM.
4. How does DicomDoodle support manual segmentation? Briefly describe two methods available to the user.
5. What happens when a user clicks the "Save Results" button after performing a segmentation on a single slice?
6. Explain the significance of changing segmentation colors in DicomDoodle beyond just visual differentiation.
7. What two specific views are presented in the "Segmentation Results" window when a user clicks "Plot Results"?
8. Describe the key functionality of the "Annotated Dicom Viewer" and what types of files it is designed to load.
9. What advanced visualization capabilities are available in the "DICOM 3D Volume Viewer" that go beyond basic 3D rotation and zoom?
10. How does the "Add Ontology" feature in the "Annotated Dicom Viewer" enhance the semantic value of saved segmentation files?

FAQ Answer Key

1. The primary purpose of the DicomDoodle tool is to streamline the annotation, segmentation, and visualization of DICOM medical images, particularly MRI data. It integrates the YOLO model for object detection and the SAM model for precise segmentation of regions of interest like tumors.
2. Users can navigate through DICOM slices either by scrolling the mouse wheel (up for the previous slice, down for the next) or by dragging the slider on the horizontal scrollbar located at the top of the main window. Both methods dynamically update the displayed slice and the window title.
3. "Single Slice Auto-Detection" applies YOLO and SAM to only the currently viewed DICOM slice, detecting a bounding box and then segmenting within it. "Batch Auto-Detection" allows the user to define a range of slices, and the tool automatically processes each slice in that range, performing detection and segmentation, and saving the results as separate segmentation files.
4. DicomDoodle supports manual segmentation through two methods: users can draw a manual bounding box and then right-click "Detect" to trigger SAM segmentation within that specific region, or they can use the dedicated "Manual Draw Tool" for freehand annotations with various colors and an eraser.
5. When a user clicks "Save Results" after a segmentation, the current segmentation mask is saved as a DICOM segmentation file (<original_filename>_seg.dcm) in the same directory as the

original DICOM file. A "Mask already saved for this slice" message then appears in the graphics view.

6. Changing segmentation colors in DicomDoodle is significant because each color is mapped to a specific SegmentLabel and SegmentedPropertyTypeCodeSequence within the output DICOM segmentation file. This provides semantic meaning to the annotations, differentiating between types of boundaries (e.g., "Tumor & Brain Boundary" for red, "Tumor & Dura Boundary" for green).

7. When a user clicks "Plot Results," the "Segmentation Results" window displays two synchronized views: the left view shows the original image with the segmented tumor overlaid and blended, while the right view shows the original image with only the boundary (edge) of the segmented tumor highlighted.

8. The "Annotated Dicom Viewer" is designed for reviewing entire DICOM series that have existing segmentation overlays. It loads folders containing both original DICOM files and their corresponding _seg.dcm files, displaying the annotations overlaid in their assigned colors and showing segment category and type labels.

9. Beyond basic 3D rotation and zoom, the "DICOM 3D Volume Viewer" offers advanced visualization capabilities such as adjustable lighting (azimuth, elevation, intensity), various colormaps, advanced shading, edge enhancement, tissue density control, and interactive clipping planes along X, Y, and Z axes to virtually slice through the volume. It also displays calculated tumor metrics.

10. The "Add Ontology" feature in the "Annotated Dicom Viewer" allows users to search BioPortal for standardized medical concepts and assign them as "Segment Category" and "Segment Type" to their segmentation files. This updates the DICOM metadata with machine-readable, semantically rich information, improving data interoperability and standardization.