Importing Contours from DICOM-RT Structure Sets with ITK4

Release 1.00

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Abstract

This paper presents code for reading contours from DICOM RT structure set files into binary labels. This is a common requirement for transferring expert manual segmentations from radiotherapy treatment planning software into external image analysis environments (such as ITK). An implementation of RT structure set importing is provided with sample data from a prostate cancer radiotherapy planning volume. This is an update to the 2009 Insight Journal paper "Importing Contours from DICOM-RT Structure Sets" which worked with ITK 3.x and a local GDCM2 install.

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1 Introduction

In 2009 we published an insight journal paper explaining how to use ITK 3x and a local install of GDCM 2 to convert DICOM-RT structures into binary labels [1]. ITK4 now supports the extraction of structures from a DICOM RT structure file removing the need to build using a separate GDCM build. The code and sample data demonstrate how to convert structures into individual binary images for further analysis or visualization.

This conversion is particularly useful to:

i) Develop average shape atlases and shape models from pre-existing expert segmentations which are routinely made in the course of radiotherapy treatment planning;

ii) Enable quantitative comparisons between automatic and expert manual segmentations (eg. Dice similarity coefficients / Hausdorff distance);

iii) Enable visualization of manual segmentation in open source tools.

There are other applications which provide this functionality: A widely used example of these is the Computational Environment for Radiotherapy Research (CERR) (available for free download from http://radium.wustl.edu/CERR/about.php). However CERR requires Matlab and does not export contours to binary files. Osirix (http://www.osirix-viewer.com/) is an open source ITK/VTK based application which can load RT structure files, however it cannot export them to binary image files, and it only runs on Apple Macs. RT_Image from Stanford University (http://rtimage.sourceforge.net/) requires the proprietary Interactive Data Language (IDL). Recently the SlicerRT plugin [2] https://www.assembla.com/spaces/slicerrt/wiki/SlicerRt_users_guide has provided a comprehensive suite of open source DICOM-RT functionality.

2 DICOM-RT Structure Files

A good overview of the RT structure set modules and tags has been previously reported in Gorthi et al [3]. In similar code to the GDCM 2.0 [4] example program *gdcmscene.cxx*, we have used the following tags to extract data from a single structure file:

```
Tag (3006, 0020) - Identify the start of structure set ROI sequence.
Tag (3006, 0039) - To identify start of ROI contour sequence
Identify the number of structures found.
For each structure
      Tag (3006, 0026) Identify user-defined name of ROI.
      Tag (3006, 0040) Extract the contour sequence.
      For each item in the current structure:
            Tag (3006, 0050) Extract contour data.
      Loop
Loop
```

3 Software Requirements

The following software needs to be installed:

- **CMake 2.4** or higher (http://www.cmake.org)
- **Insight Toolkit 4.1** or higher (http://www.itk.org/)

4 Usage

The program is a simple command line utility which is run with three parameters:
The input DICOM directory; the location of the structure file and the structure prefix.

Example command line with sample data:

```
/home/Dev/itkDICOMRT/bin/itkReadDICOMRT ITK4SampleDCMRT/
ITK4SampleDCMRT/RS.1.2.246.352.71.4.886768594.5257.20090622110825.dcm PatientX
```

Example output:

```
The directory: ITK4SampleDCMRT/
Contains the following DICOM Series:
1.2.840.113619.2.135.3596.3078484.5103.1193178135.961
Now reading series: 1.2.840.113619.2.135.3596.3078484.5103.1193178135.961
Writing the image as PatientX.nii.gz
Parsing: ITK4SampleDCMRT/RS.1.2.246.352.71.4.886768594.5257.20090622110825.dcm
media storage: 1.2.840.10008.5.1.4.1.1.481.3
Number of structures found:7
Structure 1. Number of regions: 32
1. Structure name: MRI_RECTUM_RT
Inserting region with 26 points into slice: 10
Inserting region with 42 points into slice: 11
Inserting region with 60 points into slice: 12
Inserting region with 66 points into slice: 13
Inserting region with 66 points into slice: 14
Inserting region with 66 points into slice: 15
Inserting region with 68 points into slice: 16
Inserting region with 66 points into slice: 17
Inserting region with 60 points into slice: 18
Inserting region with 58 points into slice: 19
Inserting region with 52 points into slice: 20
Inserting region with 48 points into slice: 21
Inserting region with 56 points into slice: 22
Inserting region with 56 points into slice: 23
Inserting region with 56 points into slice: 24
Inserting region with 58 points into slice: 25
Inserting region with 62 points into slice: 26
Inserting region with 72 points into slice: 27
Inserting region with 84 points into slice: 28
Inserting region with 100 points into slice: 29
Inserting region with 96 points into slice: 30
Inserting region with 96 points into slice: 31
Inserting region with 88 points into slice: 32
```

```
Inserting region with 78 points into slice: 33
Inserting region with 62 points into slice: 34
Inserting region with 52 points into slice: 35
Inserting region with 36 points into slice: 36
Inserting region with 32 points into slice: 37
Inserting region with 32 points into slice: 38
Inserting region with 34 points into slice: 39
Inserting region with 42 points into slice: 40
Inserting region with 58 points into slice: 41
File written: PatientX_MRI_RECTUM_RT.nii.gz
```

5 Method

The image volume is initially generated from the DICOM files to identify image spacing, size, etc. The DICOM-RT file is then processed: As each structure is represented as a set of points for a single slice, these points are extracted in sequence from the RT structure file; transformed from physical to image space and stored in pointlists which are then used to generate itk::PolygonSpatialObjects. These polygons are inserted into a temporary 2D slice using the itk::SpatialObjectToImageFilterType. Each slice is then inserted into a 3D volume and the next set of points considered. The 3D volume for each structure is saved.

Inputs:

1. Directory containing the image data (eg. `ITK4SampleDCMRT/`).
2. DICOM RT structure file (this usually is called RS*.dcm)

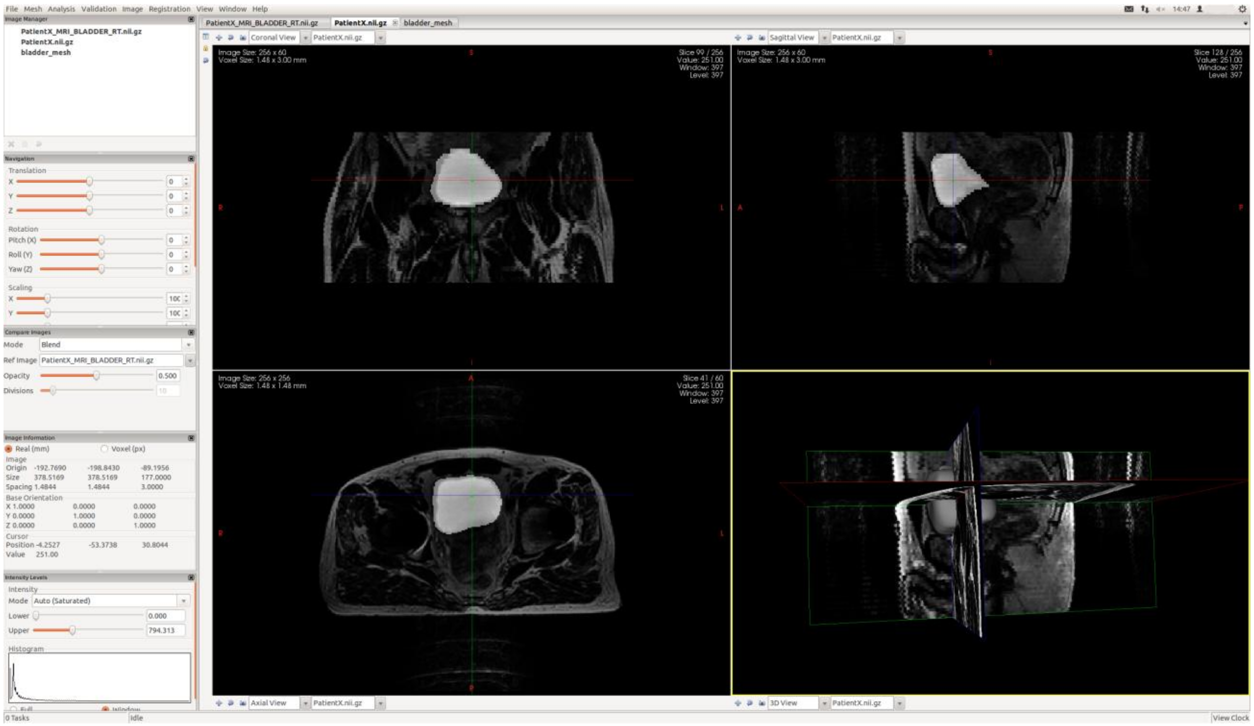
   (eg. `ITK4SampleDCMRT/RS.1.2.246.352.71.4.886768594.5257.20090622110825.dcm`).
3. Output prefix which is added to the start of the filename for each structure. (eg. `PatientX)` .

Outputs:

1. An image volume (eg. `PatientX.nii.gz`).
2. A single binary volume (Label=1, Background=0) for each structure in the input DICOM RT structure file (eg. `PatientX_MRI_RECTUM_RT.nii.gz`).

6 Results

The code has been tested on hundreds of MRI, CT Cone Beam CT volumes (for example [5-8]). As yet we haven't attempted to optimize performance (future work). The length of time required to parse a structure depends on the number of points and image size (large structures such as CT pelvic bones, body outline or planning couch contours can take a minute or so to convert).



Translation X 0 Y 0 Z 0
Rotation Pitch (X) 0 Roll (Y) 0 Yaw (Z) 0
Scaling X 100 Y 100
Mode Blend
Ref Image PatientX_MRI_BLADDER_RT.nii.gz
Opacity 0.500
Divisions 10
● Real (mm) ○ Voxel (px)
Origin -192.7690 -198.8430 -89.1956
Size 378.5169 378.5169 177.0000
Spacing 1.4844 1.4844 3.0000
Base Orientation X 1.0000 0.0000 0.0000 Y 0.0000 1.0000 0.0000 Z 0.0000 0.0000 1.0000
Cursor Position -4.2527 -53.3738 30.8044 Value 251.00
Intensity Mode Auto (Saturated)
Lower 0.000
Upper 794.313
Image Size: 256 x 60
Voxel Size: 1.48 x 3.00 mm
Slice 99 / 256
Value: 251.00
Window: 397
Level: 397
Slice 128 / 256
Image Size: 256 x 256
Voxel Size: 1.48 x 1.48 mm
Slice 41 / 60

Fig 1. The bladder contour from the sample DICOM-RT files has been extracted and is overlaid on the patients T2w MR scan. This output is shown in the open source MILXView viewer (http://research.ict.csiro.au/software/milxview).

7 Test Data

A sample DICOM_RT directory is provided containing a pelvic MRI voume (Fig. 1) and the RS file.

The RS file contains the following four structures:

1. MRI_PROSTATE_RO
2. MRI_BLADDER_RT
3. MRI_BONEOUTER_RT
4. MRI_RECTUM_RT

8 Acknowledgements

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