



Developing Tools for Improving Prostate Cancer Diagnosis using MRI

Teodora Szasz², Aritrick Chatterjee¹, Michael Hochman², Gregory Karczmar¹, Aytekin Oto¹

¹ Department of Radiology, ² Research Computing Center, The University of Chicago

Prostate Cancer (PCa) is the most common non-cutaneous cancer in men [Siegel et al., 2016]. Magnetic Resonance Imaging (MRI) is increasingly being used in PCa diagnosis. To maximize positive outcomes and to avoid unneeded, often life-altering surgery, there is an urgent need to distinguish low-risk tumors from those that may become life-threatening. The ability to accurately assess the risk of a specific patient's tumor would allow clinicians to minimize unnecessary procedures while ensuring the best patient outcome.

MRI Research Center and Research Computing Center are developing software tools that perform MRI analysis. During Mind Bytes 2017 we demonstrated our tool for Prostate Cancer Multi-Parametric MRI Review (PCampReview), a module of 3D Slicer software package that facilitates review and segmentation of multiparametric (mp-MRI) datasets.

During last year, we developed the Quantitative MRI for Detection of Cancer (QMDC) database system containing mpMRI, histology, and other datasets available at the UChicago Department of Radiology. Moreover, we are also developing a web-application accessible to the Department of Radiology to upload datasets and metadata associated to it, display the datasets and perform registration between mpMRI images and co-registration between whole mount histopathology and MRI (Fig. 1).

Currently, our focus is on improving QMDC platform by developing query different options in the database, 3D reconstruction of MRI and histopathology datasets, performing 3D non-rigid registration between MRI and histopathology, developing prostate-cancer risk maps using deep learning methods, and integrating all the developed tools in a single platform that will support multiple simultaneous users, software interoperability, and operating system independence.

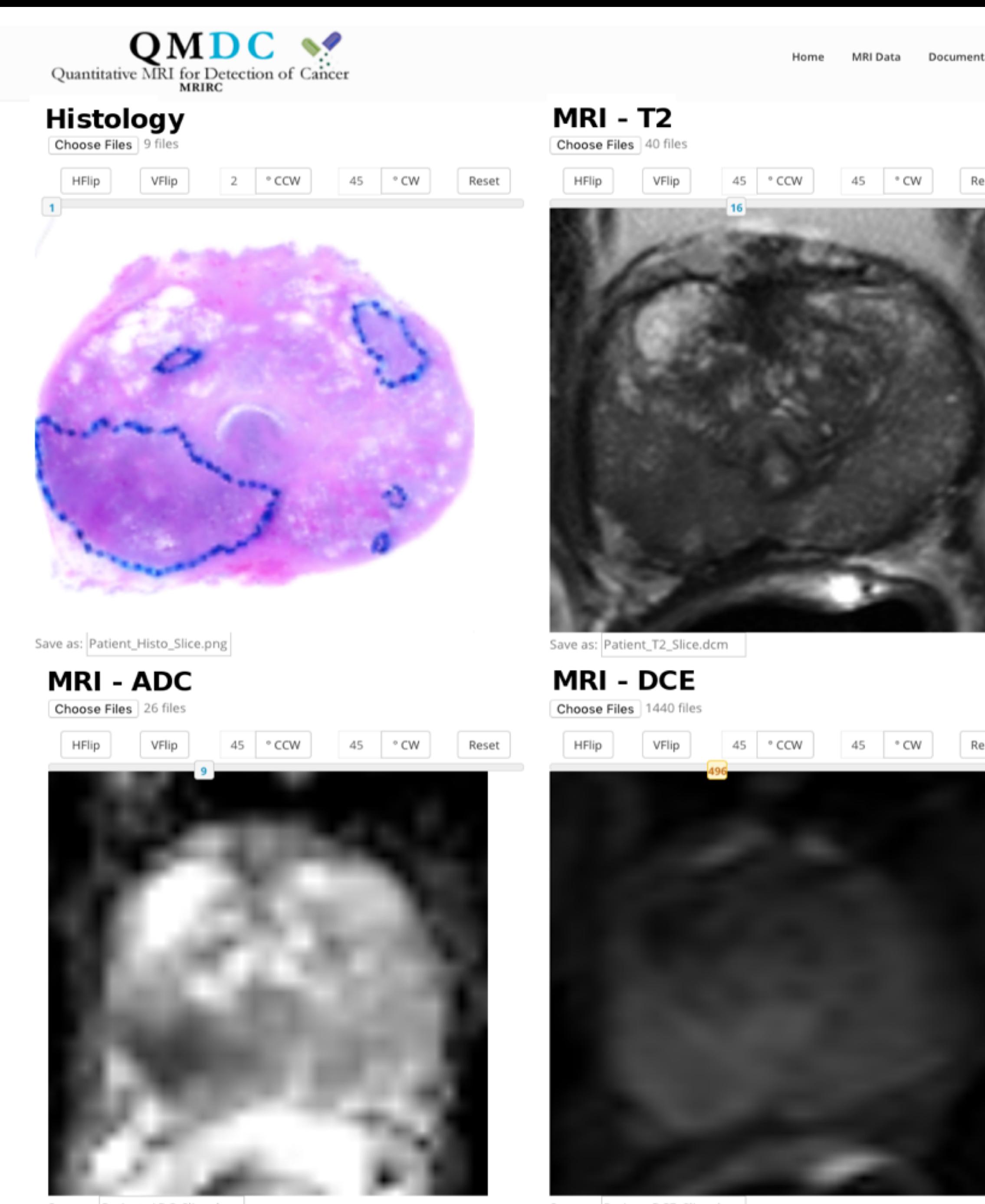


Fig. 1: QMDC tool for displaying and registering mpMRI data sets with histopathology images.

3D Non-Rigid Registration between MRI and Histopathology - pipeline -

Aligning 3D volumes of histopathology and MRI is a real challenge due to the differences in number of slices, acquisition, and non-linear distortions present in the images. We developed a pipeline that performs non-rigid registration based on landmark points defined by the user.

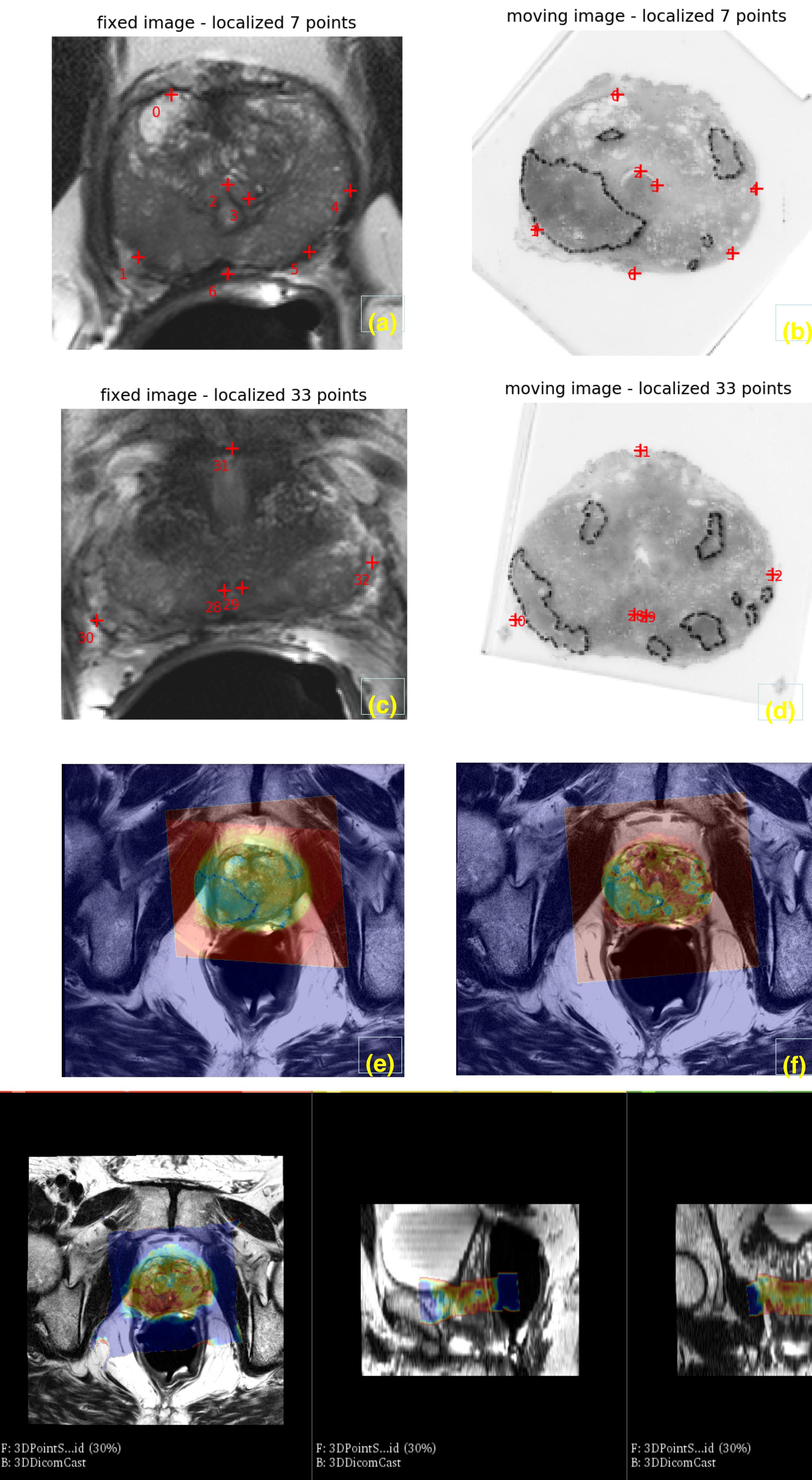


Fig. 2: 3D non-rigid registration pipeline between MRI and histopathology dataset: (a) The user selects landmarks (corresponding points) in both MRI (slice 14/40) and histopathology image (slice 1/9). (b) Selecting landmark points is done in every slices of the 3D volume where there is correspondence between one point in MRI and another point in histopathology: (c) MRI (slice 19/40) and (d) histopathology (slice 5/9). In the initial step, a PointSet-toPointSet rigid registration method is applied: rigid registered images (e) slice 14, (f) slice 19. In the final step, a non-rigid transform is applied. The axial, sagittal and coronal views are displayed in (g).

3D Reconstruction from MRI series

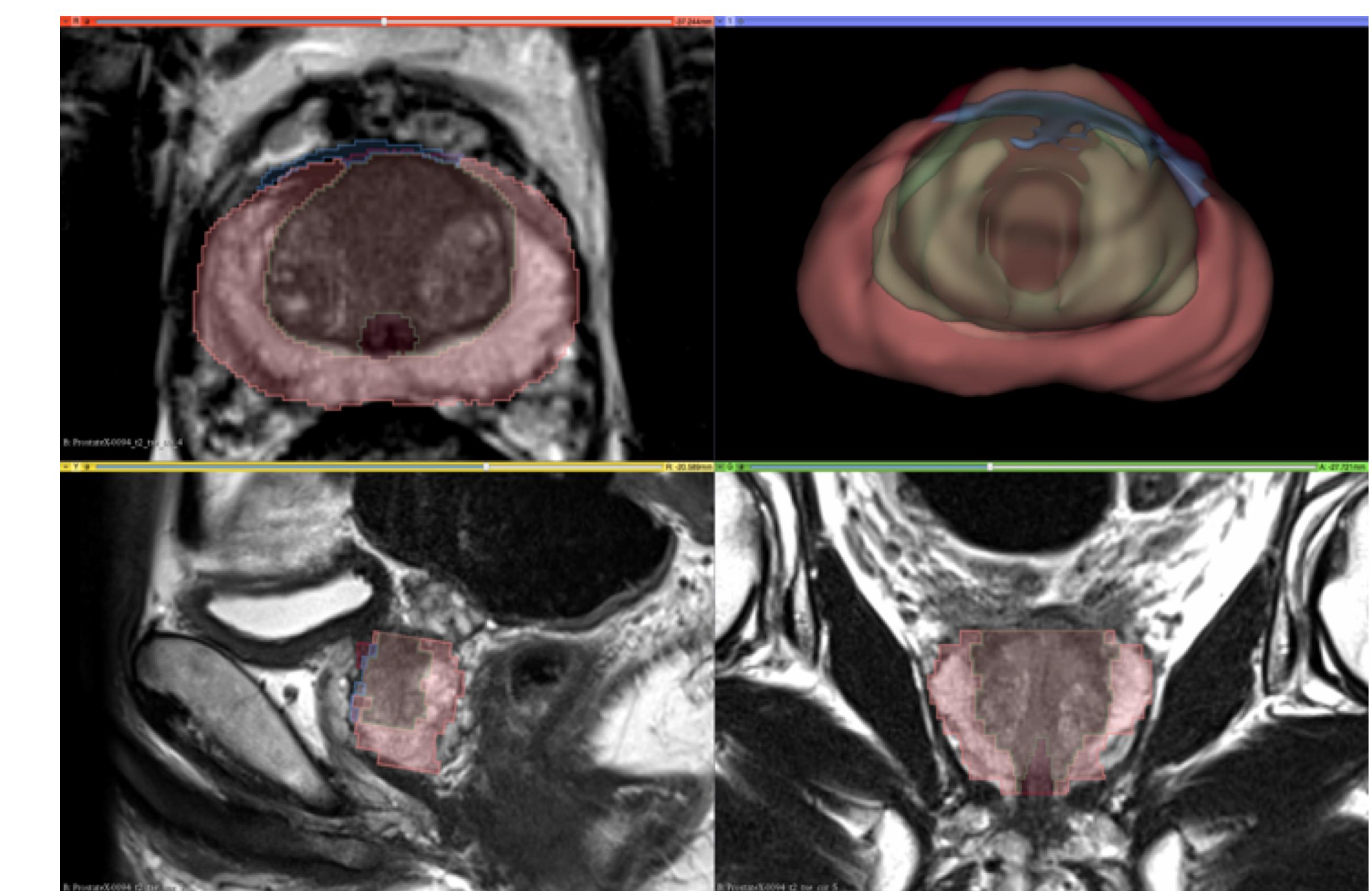


Fig. 3: 3D volume model of the prostate gland, generated using MRI dataset

A pipeline to reconstruct 3D volume model from MRI series was generated. The 3D model was created based on the whole prostate segmentation and segmentation of sectors of the prostate gland. [Slicer](#) software tool was used to segment the sectors of the prostate gland and to generate the 3D model.

QMDC tool: User interface with the database

The figure shows two forms from the QMDC tool:

- FILL OUT THE FORM** (Clinical Information):
 - Add Total PSA:
 - Total PSA from 2018-05-03:
 - Biopsy Date: 2018-05-03
 - Total Number of Cores: 3
 - Positive Cores: 1
 - Location: Primary Gleason: 3, Secondary Gleason: 3
 - Add Biopsy:
 - Biopsy from 2018-05-03:
 - Biopsy Date: 2018-05-03
 - Total Number of Cores: 3
 - Positive Cores: 1
 - Location: Primary Gleason: 3, Secondary Gleason: 3
- FILL OUT THE FORM** (Research Analysis Information):
 - Number of Voxels: um³/ms
 - Mean ADC: um³/ms
 - Standard Deviation: um³/ms
 - ADC 10th percentile: um³/ms
 - Add Other Measure:
 - T2: Standard Clinical Dose (SD)
 - Low Clinical Dose (LD)
 - Quadrant Mapping of HM-MRI Data
 - Research Analysis Information Notes:
 - Hybrid MRI Results:
 - HM-MRI fractional volumes of stroma: %
 - HM-MRI fractional volumes of epithelium: %
 - HM-MRI fractional volumes of lumen: %
 - Was PCa lesion detected?
 - Histology fractional volumes of stroma: %
 - Histology fractional volumes of epithelium: %
 - Histology fractional volumes of lumen: %

Fig. 4: After uploading the MRI dataset, the user inserts the metainformation corresponding to a study and a subject. This figure presents two of the multiple forms that the user will fill out: (a) clinical information and (b) research analysis information.

QMDC database was developed to incorporate both clinical and research information of a study and subject. The data is inserted by the user using predefined forms. The datasets inserted into the database can be visualized with the tool integrated within QMDC (Fig. 1). Moreover, the datasets can also be segmented and labeled using PCampReview software tool on Midway. The medical datasets, the database and the tools for manipulating the datasets are available to the user via Midway cluster.