MAXIMUM INTENSITY PROJECTION & CO-REGISTRATION
Diagnostic Imaging Lab 1

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1 Task 1. Maximum Intensity Projection

1.1 Compulsory Task

1.1.1 Code List

- **CT_MIP.m** : Main script to call other functions. Firstly, load the volume from DICOM files and compute maximum intensity projections (MIP) from three views respectively. For optional task, two solutions are provided in rotate_volume.m and rotate_views.m. A movie is created of 360 projections by write_video.m.

- **load_DICOM_volume.m** : A given function to load DICOM images.

- **MIP.m** : A function applies MIP on a volume to generate views of axial plane, coronal plane or sagittal plane. The explanation is shown in Section 1.1.2.

- **show_view.m** : Plot an input image that created by the function in MIP.m.

- **rotate_volume.m** : Rotate whole volume along axial plane. In each rotation, apply MIP method to project the volume from coronal view. All views in 360 angles are reserved. The explanation is described in Section 1.2.

- **rotate_views.m** : In this solution, the volume is fixed, rotating the viewing angle to project maximum values of the volume. The explanation is described in Section 1.2.

- **write_video.m** : Create a .avi video file, which consists of all projections generated from function rotate_volume or rotate_views.

- **paralleltomo.m** : A built-in function of ART-tools, which compute the rays that cross the volume in different viewing angles.

1.1.2 Explanation of Method

To illustrate the MIP method, we display a simple case as shown in Figure 1. In the example, a 5x5x5 volume is taken into consideration. In Figure 1a, gray part is the top slice of the volume, which is observed from two viewpoints to form projections, i.e. coronal view and sagittal view. In each observation, only the voxel with maximum intensity is reserved in every parallel ray. Applying MIP method on each slice

gives projections of whole volume in different views. Figure 1b uses the same way to observe slices from top view to generate axial view projection of the volume.
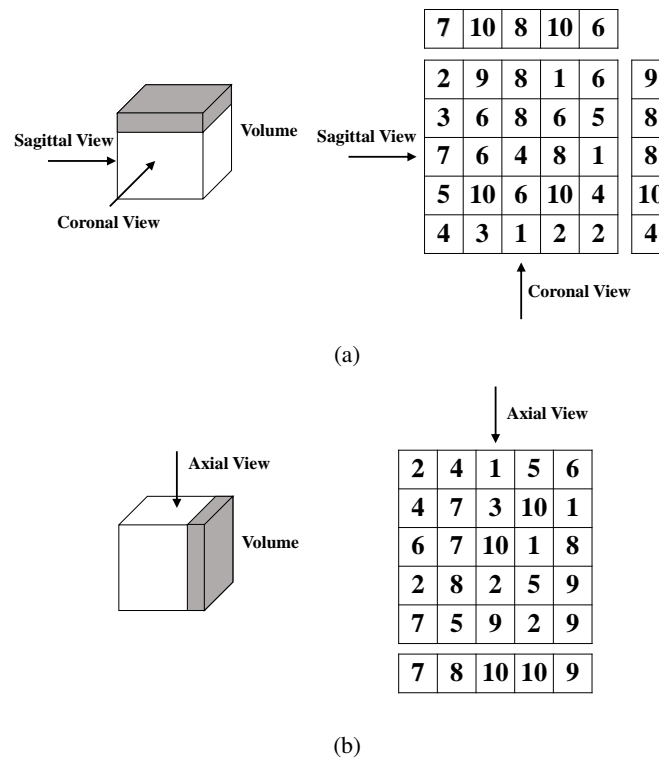

(a)

(b)

Figure 1: Explanation of MIP on (a) coronal view and sagittal view, (b) axial view.

1.1.3   Results Images

Three projections of sample volume, axial view, coronal view and sagittal view, are shown in Figure 2, from which it can be seen that the information of tissues' surface can be displayed in projections. However, 2D MIP is not able to provide relative 3D positions of inner structure of body, leading to the need for 3D volume rendering.
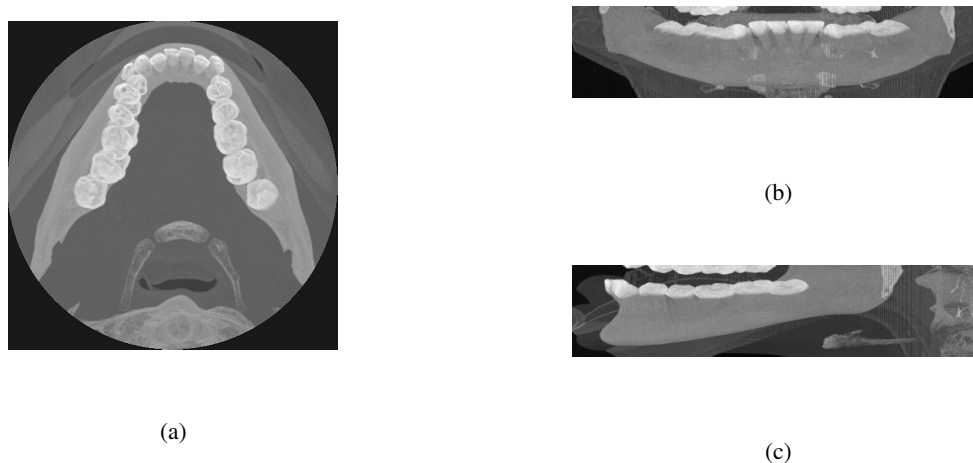

(a)

(b)

(c)

Figure 2: MIP of (a) axial view, (b) coronal view, (c) sagittal view.

1.2 Optional Task

A 3D volume rendering is created in this section by applying MIP around the volume. Coronal views projected from 360 viewing angle are formed to an animation. Two solutions are provided to carry out projection as shown in Figure 3. The one method is that the whole volume is rotated at different angles, and coronal view of the volume is projected at a settled viewpoint. In another method, viewpoints are moved around the volume to observe it from various angles, which generates projection at each angle. The function in paralleltomo.m of ART-tools demonstrates the parallel rays that through the volume at each viewing angle, which is used to obtain the MIP result in second solution. The animation, named as MIP_360.avi, can be found in the folder.

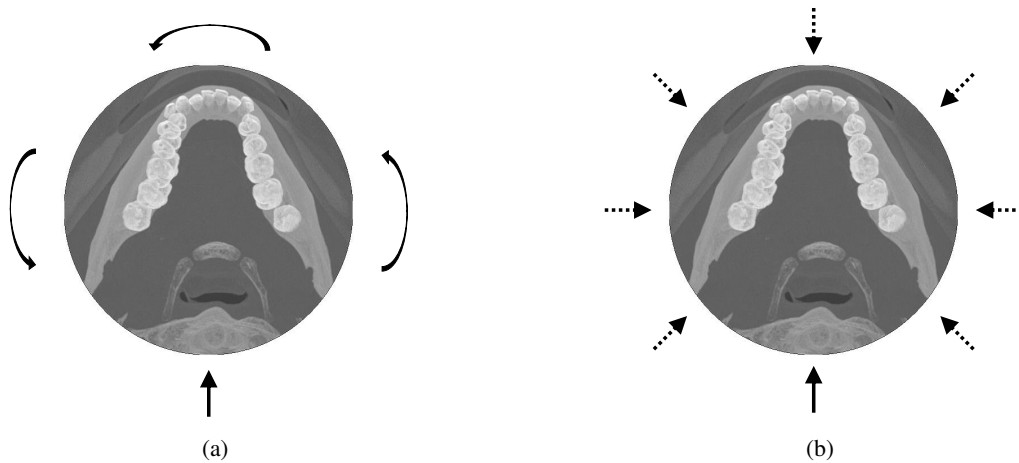(a)   (b)

Figure 3: Illustration of the process to project volume on many viewing angles. (a) Solution 1: fix the viewing angle, rotate the volume. (b) Solution 2: fix the volume, rotate the viewing angles.

2 Task 2. Co-registration of CT & MR Data

2.1 Compulsory Task

2.1.1 Transformation matrix

The transformation matrix can be found in the **Volume** in *Slicer*, the matrix T_t is:

$$T_t = \begin{bmatrix} 1.00 & -0.01 & -0.08 & -4.34 \\ 0.01 & 1.00 & 0.03 & -2.71 \\ 0.08 & -0.03 & 1.00 & -75.49 \\ 0.00 & 0.00 & 0.00 & 1.00 \end{bmatrix}$$

2.1.2 Screen captures of the alignment

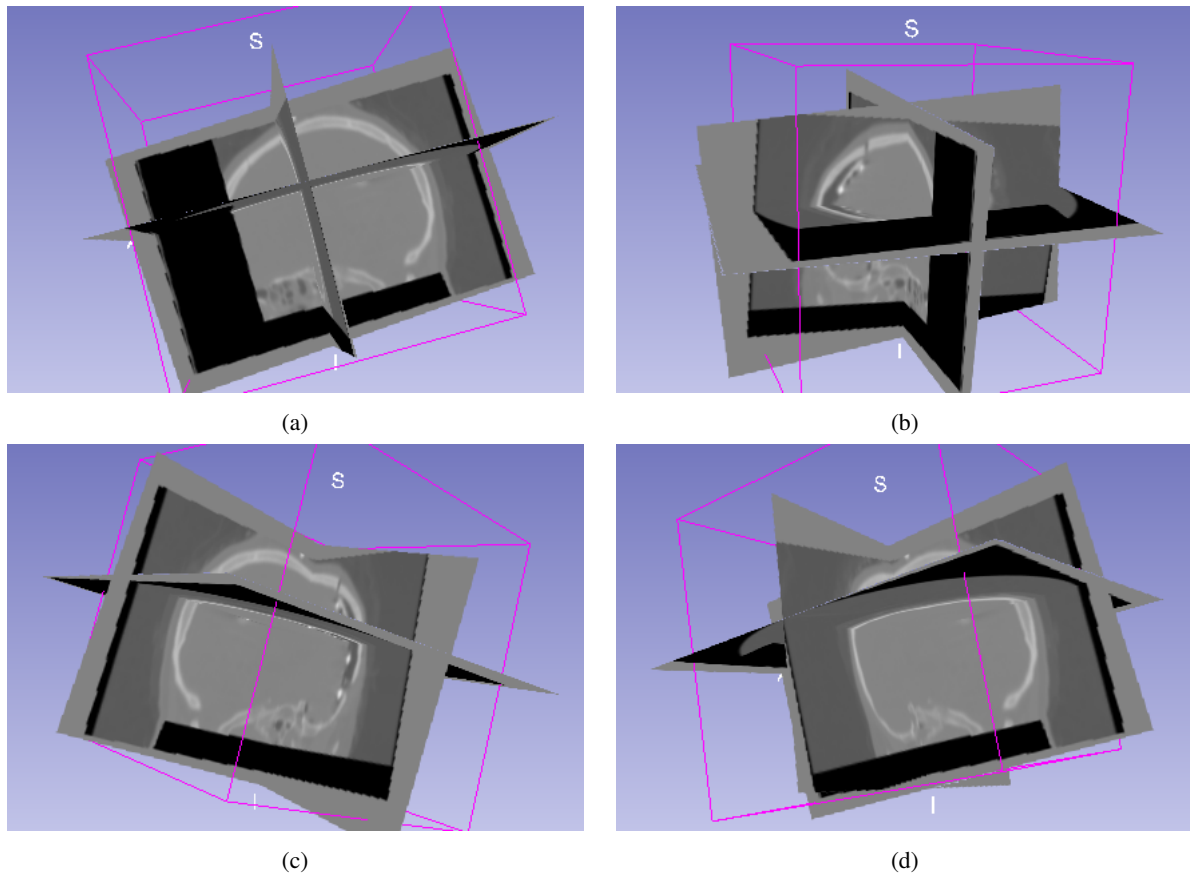We got 10 screen captures of the alignment, 4 of them are shown as Figure 4:

(a)

(b)

(c)

(d)

Figure 4: 4 screen captures of the alignment

2.1.3 Questions

Question1:

In this task, we use the rigid body transformation which is belong to the geometrical transformation category. According to the paper 1, feature-based category is what we use. CT image and MR image don't have similar intensity values, but have similar feature, so it's feature-based rather than area-based.

Question2:

The mutual information(MI) "is a measure of statistical dependency between two datasets", it provides better performance in multimodal images. In the case of two variables, MI can be measured by: $MI(X,Y) = H(X) + H(Y) - H(X,Y)$, $H(X)$ means the entropy of X. In the case of multimodal images, if we want to match one point in the fixed image, we may have multi alternatives, it's hard to distinguish which one is better. However, MI could use useful maximum measurement to tell us which one is the best.

Question3:

Normally, we have the rigid transformation equation in 3D like: $\mathbf{x}' = R\mathbf{x} + \mathbf{t}$, R is a 3×3 matrix for rotation, and $\mathbf{t}$ is the translation matrix. Sometimes, the affine transformation can be represented by homogeneous

coordinates, which means the R and $\mathbf{t}$ matrix are integrated into one 4×4 matrix $\mathbf{M} = \begin{bmatrix} R & \mathbf{t} \\ 0 & 1 \end{bmatrix}$, a new matrix M combine the rotation and translation information, and new linear equation is $\mathbf{u}' = M\mathbf{u}$, now $\mathbf{u}' = \begin{bmatrix} \mathbf{x}' \\ 1 \end{bmatrix}$, $\mathbf{u} = \begin{bmatrix} \mathbf{x} \\ 1 \end{bmatrix}$.

Question4:

To be honest, we are not sure about this question. According to the wiki of slicer, negative intensity values mean background pixel, so we think these negative values around edge maybe sampled from background pixel. The solution is resampling. Can't see any water/tissues in this head.

2.2 Optional Task

In this optional question, we use the affine transformation method which including rotation, translation, scaling and shearing. So, we can see affine transformation has more transforms – scaling and shearing-than only rigid body transformation. The mathematics expression of affine transformation is:

$$\mathbf{u}' = A\mathbf{u} + \mathbf{b} \tag{1}$$

A and b have many transform information, matrix expression as following:

$$\begin{bmatrix} \mathbf{u}' \\ 1 \end{bmatrix} = \begin{bmatrix} \mathbf{s}, \mathbf{h}, R & \mathbf{s}, \mathbf{t} \\ 0 & 1 \end{bmatrix} \begin{bmatrix} \mathbf{u} \\ 1 \end{bmatrix} \tag{2}$$

(**s,h**,R means it combines scaling, shearing and rotation information, **s,t** means it combines scaling and translation information.)

The transform matrix of affine transformation T_a in this task is:

$$T_a = \begin{bmatrix} 0,898 & -0.432 & -0.001 & 41.0435 \\ 0.0743 & 0.8858 & -0.0023 & 20.4892 \\ -0.1354 & -0.1332 & 0.9240 & 231.1834 \\ 0.00 & 0.00 & 0.00 & 1.00 \end{bmatrix}$$

compared to the transformation matrix T_t in *Slicer* task:

$$T_t = \begin{bmatrix} 1.00 & -0.01 & -0.08 & -4.34 \\ 0.01 & 1.00 & 0.03 & -2.71 \\ 0.08 & -0.03 & 1.00 & -75.49 \\ 0.00 & 0.00 & 0.00 & 1.00 \end{bmatrix}$$

We can see that in rigid transformation, the upper left 3×3 matrix in transform matrix, its absolute value is symmetric, which means it only has rotation information, but the matrix in affine transformation is not because it combines more transform information. In addition, the values of **s,t** part in affine transform matrix are much larger.