**Question 6 Explanation and Discussion: Target Registration Error Simulation**

To see how sensitive the X-ray set up is to errors caused by slight movements in the markers we can run a simulation that displaces the markers in the A and B x-ray detector frames.

The magnitude of this displacement starts at zero and increases by 0.1mm until the generated target is more than a mm away from the ground truth target.

We can think of this simulation as a random walk-through potential target points within the envelope sphere. The maximum displacement (Emax) that gets applied to each marker point in A and B tells us how sensitive the x-ray detectors need to be in order to have certainty that the target is within 1mm of the real tumor target.
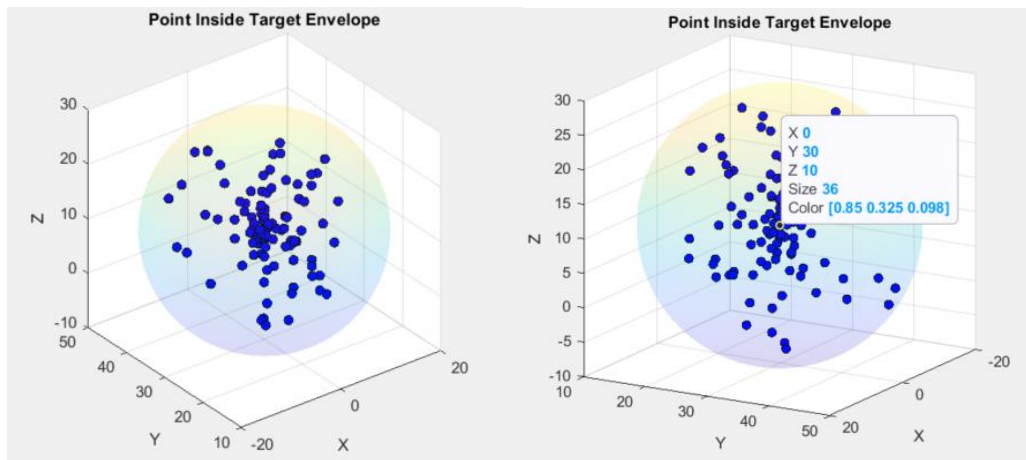

We can see the 100 (N) points generated within the Tumor sphere. The use of random points gets paired with the displaced marker points (spoiled marker points) to simulate a scenario in which both the target and markers drifted a certain distance from the original locations. For each randomly generated point we can take the spoiled markers and generate a new target in that frame with an increasingly large displacement and therefore inaccuracy of where the original marker was.

This relationship can be seen from the plots of the displacement applied to the markers E-Max and the associated average and maximum TRE values generated across the random points:
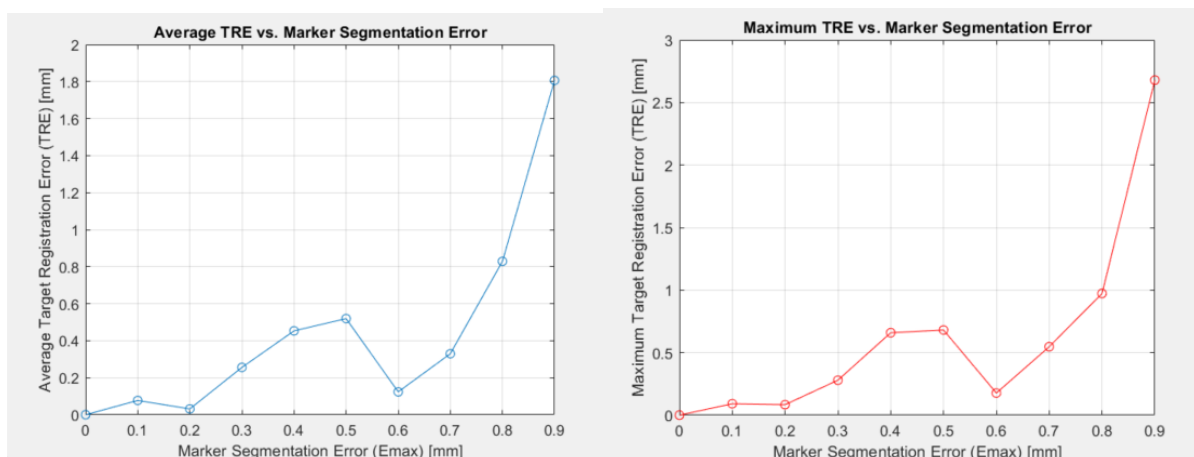
Although this relationship of TRE to Marker Segmentation error will change due to the random generations, the general trend of linear growth in TRE as Emax increases is kept across all trials:
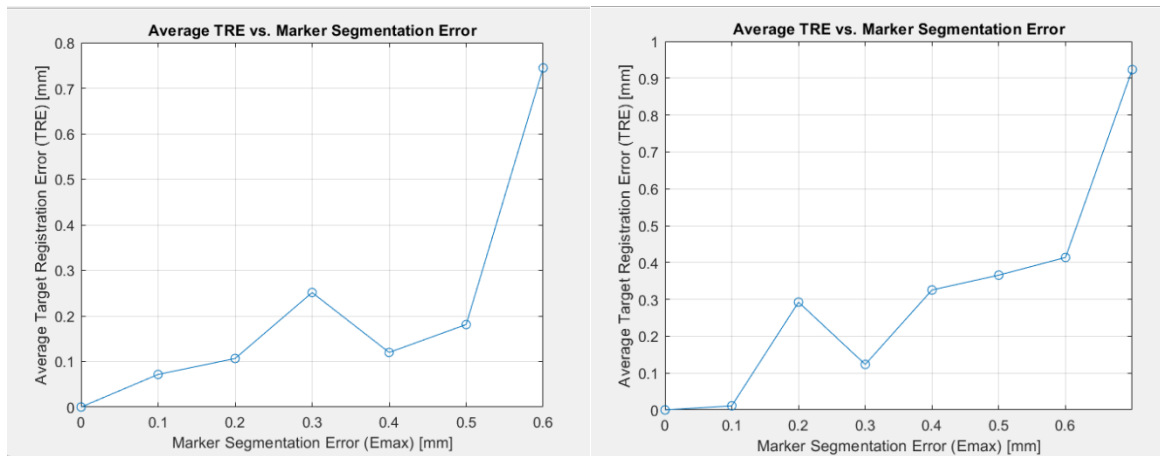
It is clear from these plots that any Marker segmentation over 0.5 will most likely cause a Target registration error of over 1mm. We can see with an increased Max TRE to 10mm the increasing marker segmentation increases the TRE but it also becomes more susceptible to the variance of the random points.
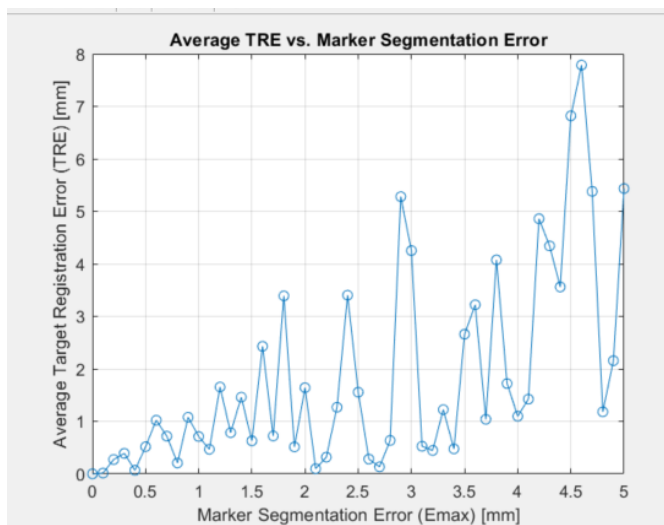
It appears that the target reconstruction is sensitive to marker segmentation errors. The relationship between marker segmentation error (E-Max) and Target Registration Error (TRE) shows a linear growth, indicating that errors in marker segmentation can lead to significant errors in target reconstruction.

The fact that a segmentation error of around 0.5 mm corresponds to a TRE of about 1mm highlights this sensitivity. In the context of medical imaging and treatment, especially in cases like tumor targeting, a 1mm error can be significant and could potentially lead to less effective treatment or harm to surrounding healthy tissues.

Considering the dimensions of the screw, the object magnification in the X-ray imaging system, and the resolution of the detectors, it is crucial to have highly accurate and precise marker segmentation to ensure the reliability of the target reconstruction. If the system has a high magnification, even small

errors in the physical space could be magnified in the image space, leading to larger errors in target reconstruction. Similarly, if the resolution of the detectors is not high enough to accurately capture the position of the markers, this could also contribute to segmentation errors.

In summary, the target reconstruction appears to be fragile and susceptible to marker segmentation errors, necessitating high precision in marker segmentation to ensure accurate and reliable target reconstruction.