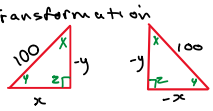
A2 tests

Wednesday, October 23, 2024 2:41 PM

My study group for A2 was Jade, Rena, Dharsan, and Noah. At the beginning we explained the logic of each question to each other so we could visualize what we have to do in 3D space and then at the end, when we were all finished we reviewed the answers for each question with sample points like (0,0,0) to make sure our answers were correct with the code that we had done.

Q1

Transformation



we know these are right angle triangles
so the angles X, Y, Z are all 45°
so find x & y with the sine rule

sine rule: $\frac{x}{\sin(X)} = \frac{y}{\sin(Y)} = \frac{z}{\sin(Z)}$

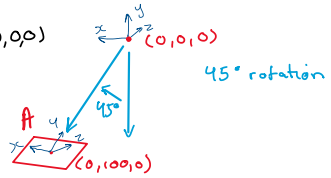
$$\frac{x}{\sin(45)} = \frac{y}{\sin(45)} = \frac{100}{\sin(90)}$$

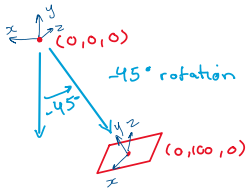
$$\frac{x}{\sin(45)} = \frac{100}{\sin(90)} \rightarrow x \cdot \sin(90) = 100 \cdot \sin(45) \rightarrow x = 100\left(\frac{\sqrt{2}}{2}\right) \rightarrow x = 70.7\text{cm}$$

$$\frac{y}{\sin(45)} = \frac{100}{\sin(90)} \rightarrow y \cdot \sin(90) = 100 \cdot \sin(45) \rightarrow y = 100\left(\frac{\sqrt{2}}{2}\right) \rightarrow y = 70.7\text{cm}$$

Translation Matrix = $\begin{bmatrix} 1 & 0 & 0 & -0_x \\ 0 & 1 & 0 & -0_y \\ 0 & 0 & 1 & -0_z \\ 0 & 0 & 0 & 1 \end{bmatrix}$

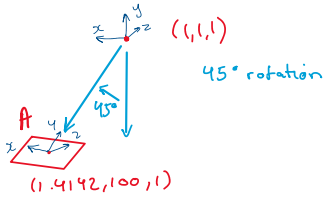
Test 1 Ck (0,0,0)

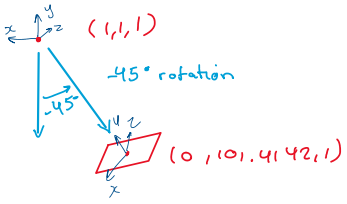




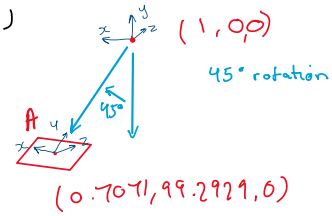
explanation: the (0,100,0) detection frame shows that 100 is the distance to the origin in the y direction

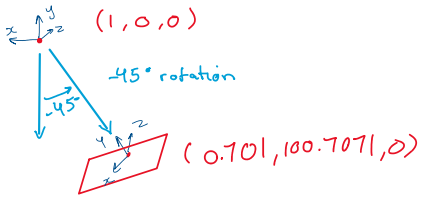
Test 2 Ck (1,1,1)





Test 3 Ck (1,0,0)





Q2

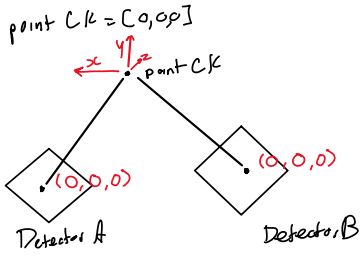
Project a point in CK space onto the two imaging detectors and report the resulting coordinates in detector image frame.

I know that the detectors are below the point CK which means it is -y. Since our y value is SAD=100 we know that -y=-100.

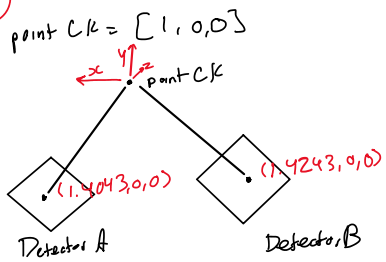
I rotate about coordinate axis (function from assignment 1) to find the sources because we know the rotation is about axis z with a +/-45 degree rotation and then multiply this homogeneous transformation matrix by the SAD. We do the same to find the point on the detector and to rotate the normal vectors of the detector plane.
I normalize the line between the point in CK and the beam source and then I could find the intersection by using this equation: t = ((A-P) ○ n) / (v ○ n)
Then to find the coordinates, I multiplied the frame transform by the intersection.

3 test cases

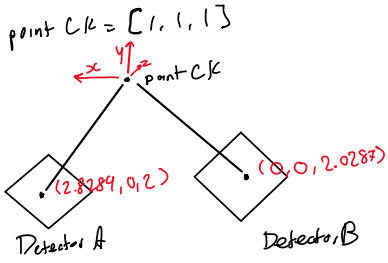
1 Base case



2



3



Q3

First the inverse of the frame transform is multiplied by the projection point with SAD=100 which finds the source points. I normalize the vector found with this equation: vec = (source - proj_A)/ |source - proj_A|
The cross product of these vectors is normal to the lines which is the direction vector for the perpendicular distance between these lines. We find the t matrix by the methodology explained in the notes and then I find the unknown values of y = mx + b and determine the symbolic intersection of the lines in 3D by finding the midpoint. REM is calculated by dividing the length by 2. This value is absolute because it is always positive.

Q4

Case 1:

```
without switching m1 and m2:
         0   12.9904   32.9760
  -21.2827         0   10.9196
  -24.7486   -5.2586         0

    1     1
    2     2
    3     3
```

In this image you can see that the REM is 0 where the detectors match up, so M1 and M1, M2 and M2, and M3 and M3. This is why the correspondence matrix is as seen in the image.

Case 2:

```
with Swap of m1 and m2 in image A:
  -21.2827         0   10.9196
         0   12.9904   32.9760
  -24.7486   -5.2586         0

    1     2
    2     1
    3     3
```

In this image you can see that the REM values where it is 0 have changed because the swap between M1 and M2 in detector 2. This causes the code to recognize a match between M1 and M2 and M2 and M1, therefore in the new correspondence matrix you can see that the code recognized the swap and plotted the correspondence matrix relative to it.

Case 3:

```
Run for a slightly different set of marker screws:
M1CK=[30, -30, 0], M2CK=[-30, 0, 0], M3CK=[0, -30, 60]:
         0         0   43.5578
         0         0   32.9760
  -24.7486  -15.4660         0

    1     2
    2     2
    3     3
```

In this image you can see that there are a few matches within the markers. Because of the ambiguity in the REM matrix the correspondence matrix cannot be correct for corresponding to 1 marker each for each marker. We can solve this by looking at the markers on the patients body.

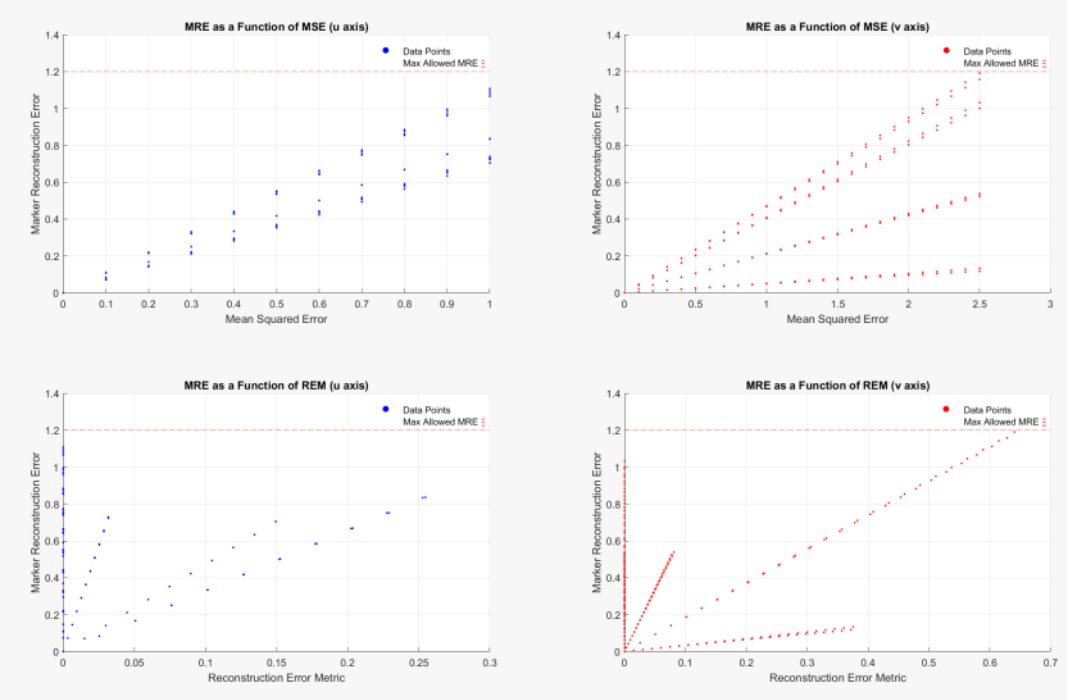
Q5

To develop a module to register a tumor target point from CT frame to CK frame, I generate the CT and CK orthogonal frames and transform the CT frame to home and same for the CK frame however inversing it so that we transform them to the same place. Then use the equation p=F * F * p.

Q6

When each marker position has an MLE vector in a random direction, it shifts slightly, introducing translational errors. As all three markers are offset randomly, this results in a shift in the computed frame (target position), effectively translating the frame. Since translation in each marker is independent, the random directions will tend to cancel out somewhat, so pure translation is less impactful than rotation for small MLE values.
The rotational error arises because non-uniform marker shifts lead to changes in the orientation of the marker frame. The rotation of the frame relative to the target can amplify displacements.
Before starting the simulation, estimate an upper bound for maxMLE when the simulation should be terminating, assuming you have sufficient statical power:
Since clinical threshold is 2mm the simulation identifies the MLE that keeps the meanTRE under 2mm. This is because it is translated and rotated which both magnify error more so it would be under 2mm.

Q7



MaxMRE is the horizontal red dashed line at the top of each plot. When any MRE exceeds the given threshold (maxMRE), the simulation stops for that axis. The results show that MRE tends to increase with higher MSE and REM values, but the relationship varies between the u and v axes, indicating that error propagation in marker reconstruction behaves differently depending on the axis along which the perturbation is applied. This difference highlights the directional sensitivity of the reconstruction process.
These graphs are all linear because the MSE is added by 0.1 each time in the code so the error is not random which shows up in the graph as a linear function.

MRE as a Function of MSE (Top Row):
The left plot (u-axis) and right plot (v-axis) both show MRE vs MSE where you can see there is a clear positive trend. maxMSE for Clinically Acceptable maxMRE, as the MSE increases, the MRE generally increases, suggesting a point where MSE becomes too high to maintain acceptable MRE levels. This trend is expected, as higher segmentation errors (MSE) lead to more significant reconstruction errors (MRE). The plots show clusters, indicating points at which MSE begins to cause an exponential increase in MRE. The different scaling on the x-axes for the u-axis and v-axis plots suggests that the v-axis MSE range allows for larger values while still maintaining clinically acceptable MRE levels. This might imply that segmentation errors in the v-axis are less sensitive to MRE increases than those in the u-axis.

MRE as a Function of REM (Bottom Row):
For both the u and v-axis plots. The REM measures reconstruction error metrics, and a perfect REM (close to zero) would yield a linear relationship with MRE. We observe a symmetric pattern, with MRE increasing as the absolute value of REM moves away from zero. The pattern is similar in both the u and v directions, indicating that REM could be a reliable predictor of MRE across both axes.