Lauren Yates 10195969
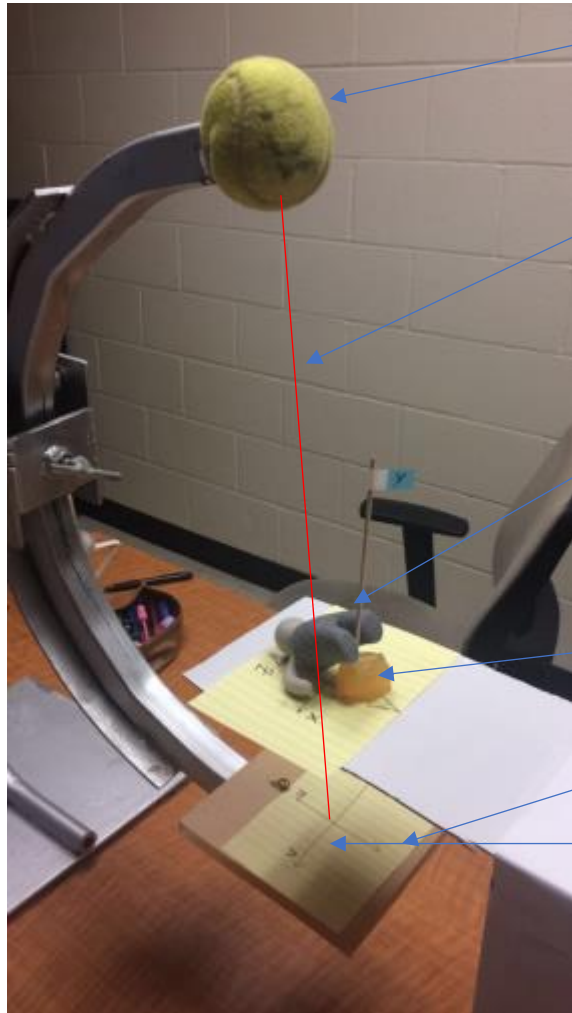
Tumor Reconstruction in C-Arm Fluoroscopy

Part 1: Questions

Rotation angle = AP pose (0˚ rotation)

Source

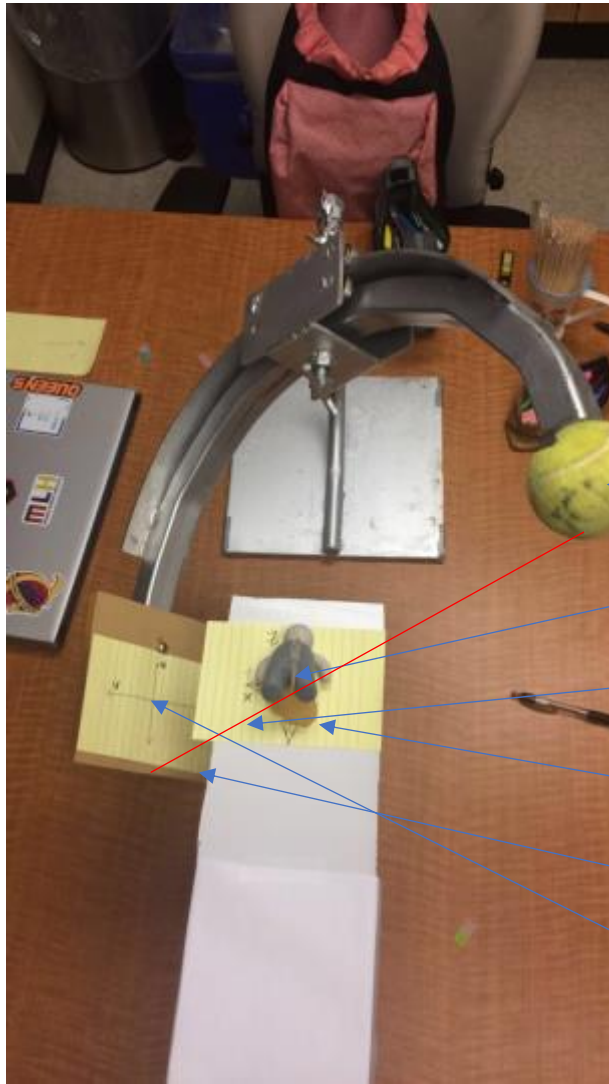Example projection line from source to detector

C-Arm Coordinate System (z is towards C-Arm, x is off to the side, y is perpendicular to the ground)

Tumor

Detector Plane

Detector Coordinate system (u is aligned with z, v is aligned with x, w is aligned with y but w=0)

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Rotation Angle = 45˚

Source

C-arm coordinate system

Example projection line from source to detector

Tumor

Detector Plane

Detector Coordinate System (no longer aligned with the c-arm coordinate system)
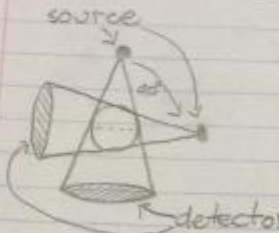
2.

MacBook Pro

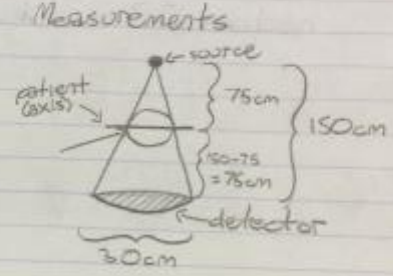Lauren Yates 10195969

CISC 330 - Assignment 2

QUESTIONS

1. question answered in word document.

2. workspace of C-arm center = sphere formed in the intersect of all possible cones projected from source to detector

source

Measurements
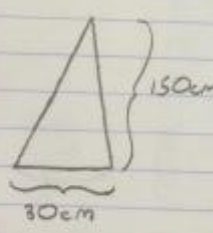
detector

source

patient (axis)
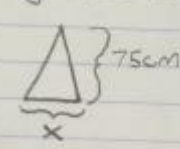
75cm

150cm

150-75 = 75cm

detector

30cm

→ workspace of C-arm center is centered at the axis (+75cm from detector and -75cm from source)

Use similar triangles to find diameter of the sphere

150cm

30cm

75cm

x

$$\frac{30cm}{150cm} = \frac{x}{75cm}$$

$$x = (30 \times 75)/150 \, cm$$

$$\therefore x = 15 \, cm$$

The diameter of the sphere is 15 cm, use the radius (15/2 = 7.5) and volume of a sphere equation ($v = \frac{3}{4} \pi r^3$) to find volume of work space

$$v = \frac{3}{4} \pi (7.5)^3 \cong 1767.15 \, cm^3$$

∴ the workspace of the C-arm is a sphere centered at the origin (0,0,0) with the volume of approx. 1767.15 cm³

3. Using a mobile C-arm unit introduces mechanical imperfections at worsen the target localization error in the detector. Having a C-arm unit on wheels may cause accidental motion and move the c-arm and target off center when rotating the C-arm for another image. The axis also may wobble when rotating the C-arm resulting in an off-centre image making it harder to calculate the intersect of the back-projection lines and therefore the center of the sphere. There may also be a mechanical deformation in the machine itself or the patient may move between imaging. The rotation angles, SSD, SAD, and Detector center may not be known accurately either due to machine error which throws off the calculation too.

Part 2: Point Projector

Description: This function takes a rotation angle alpha and a given point in C-arm coordinates and calculates the location of the point on the detector plane in detector coordinates (where the w axis = 0). Instead of rotating the plane and source, the function rotates the given point in the opposite direction and calculates the intersection of that new rotated point. Mathematically these results are the same, and this method avoids the need for calculating and transforming coordinate systems.

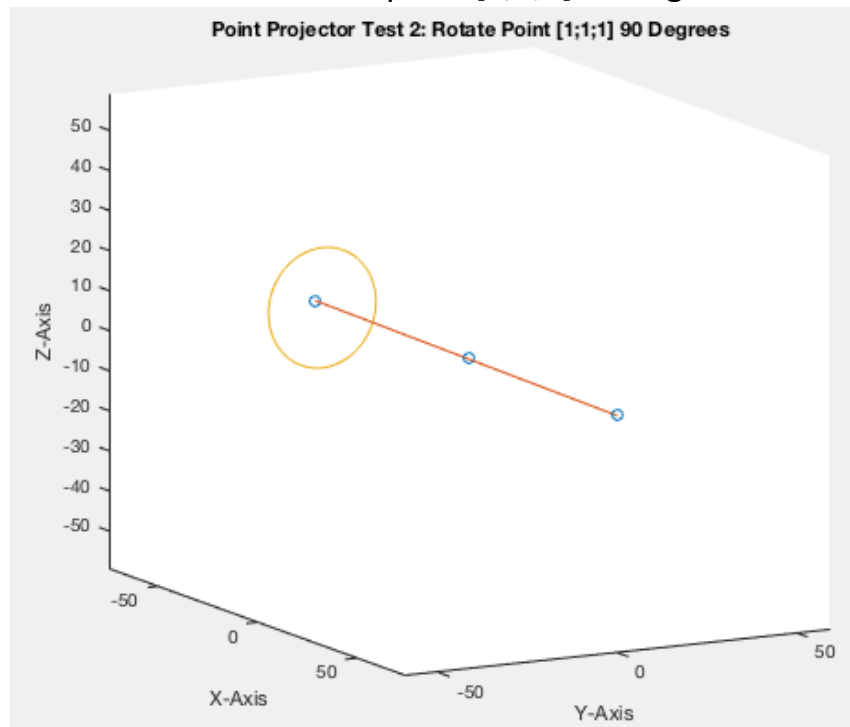Ground Truth 1: Rotate Point [0;0;0] 0 degrees
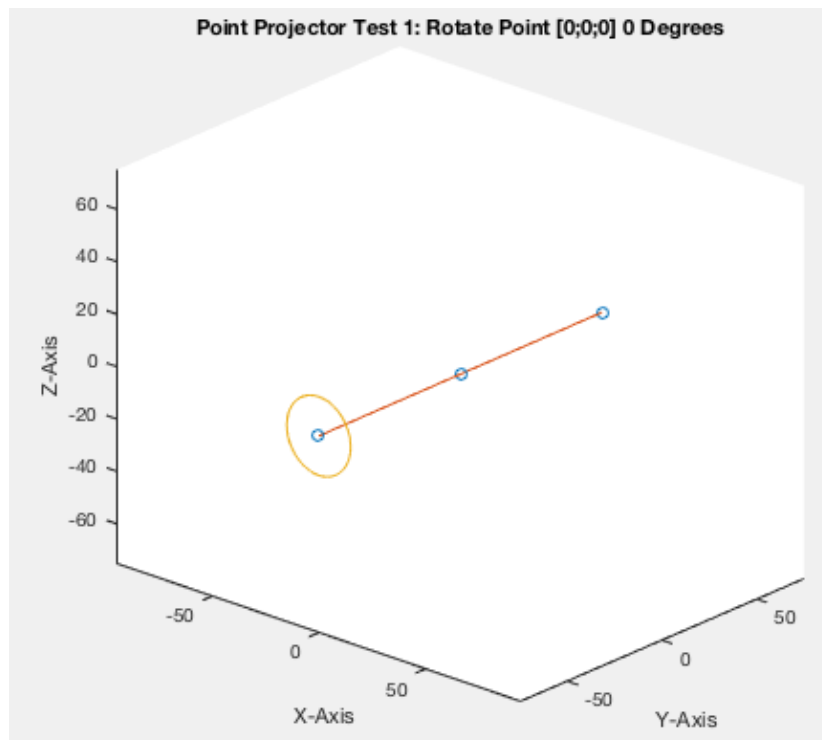

```
proj =

    0
    0
    0
```

Observing the graph and output above, we can see that the projected point is in the center of the detector plane. This projected point matches the pre-calculated answer and logically makes sense because the point in detector coordinates is in the middle of the detector. Projecting the center of the tumor with or without rotation will result in a projection on the center of the detector.
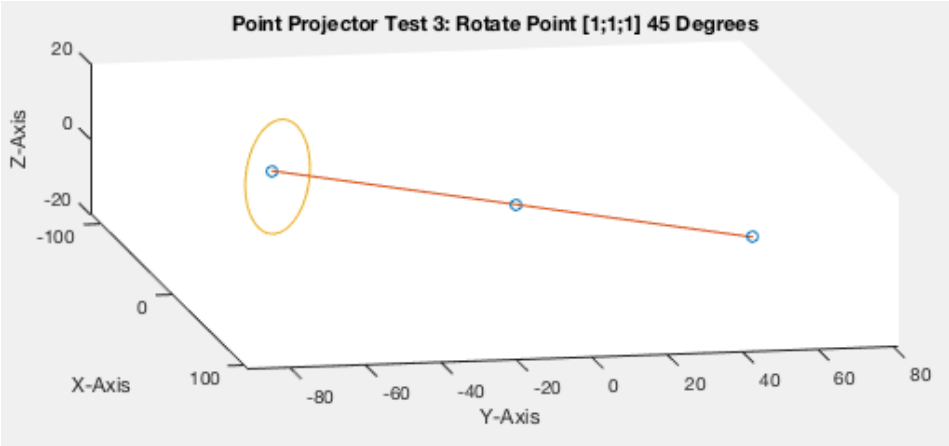
Ground Truth 2: Rotate point [1;1;1] 90 degrees

proj =

    1.9737
    1.9737
         0

Observing the graph and output above, we can see that the projected point is on the detector plane and is not in the center of the detector. This output result matches the pre-calculated answer and makes sense because the given point is not the center of the tumor and therefore the projection of the point onto the detector will not be directly beneath the provided point.

Ground Truth 3: Rotate Point [1;1;1] 45 degrees

Point Projector Test 3: Rotate Point [1;1;1] 45 Degrees

proj =

    2.8284
    2.0000
         0

Observing the graph and output above, we can see that the projected point is on the detector plane and is not in the center of the detector. This output result matches the pre-calculated answer and makes sense because the given point is not the center of the tumor and therefore the projection of the point onto the detector will not be directly beneath the provided point.
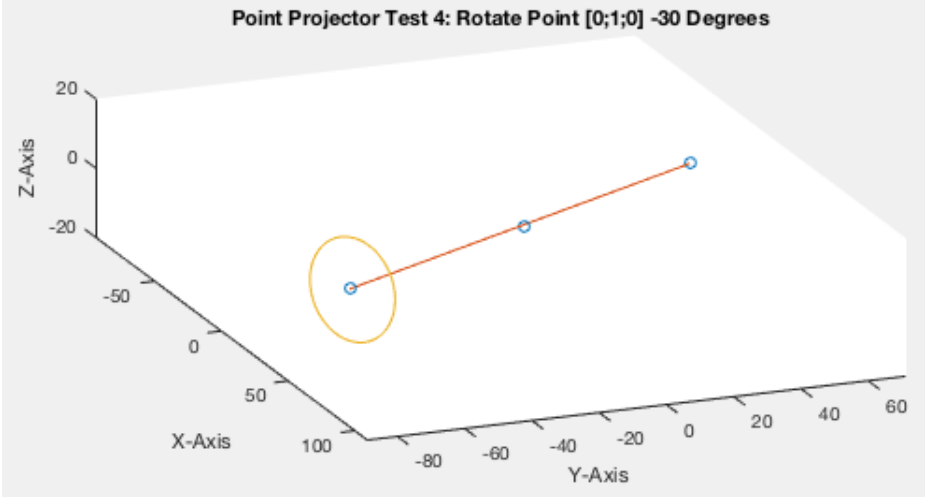
Ground Truth 4: Rotate point [0;1;0] -30 degrees

Point Projector Test 4: Rotate Point [0;1;0] -30 Degrees

proj =

    -1.0117
         0
         0

Observing the graph and output above, we can see that the projected point is on the detector plane and is not in the center of the detector. This output result matches the pre-calculated answer and makes sense because the given point is not the center of the tumor and therefore the projection of the point onto the dete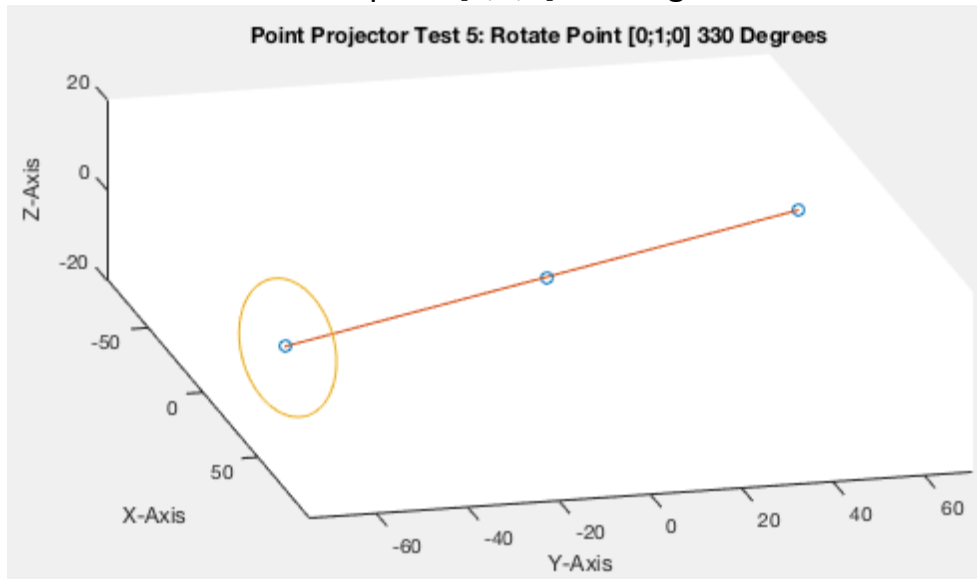ctor will not be directly beneath the provided point. This ground truth test verifies that the function works for negative angles as well.

Ground Truth 5: Rotate point [0;1;0] 330 degrees

Point Projector Test 5: Rotate Point [0;1;0] 330 Degrees
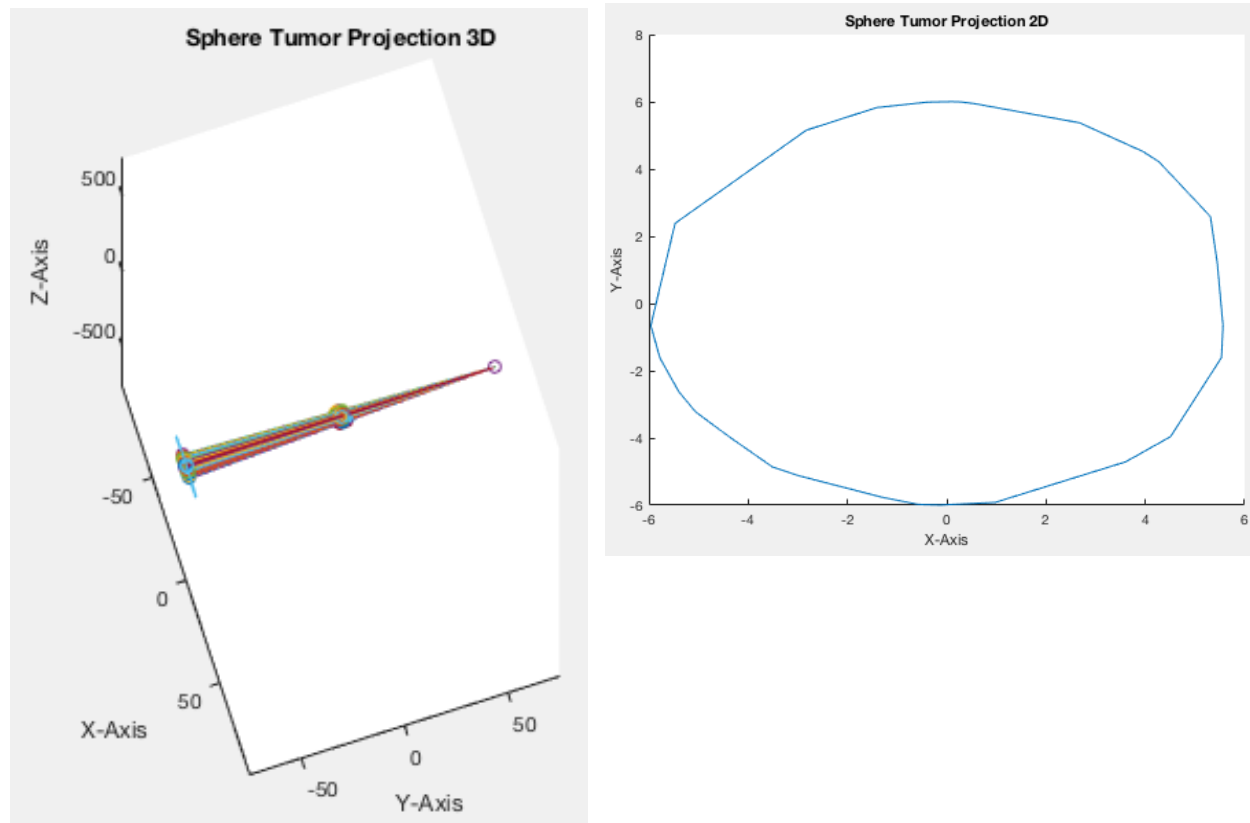
proj =

    -1.0117
         0
         0

Observing the graph and output above, we can see that the projected point is on the detector plane and is not in the center of the detector. This output result matches the pre-calculated answer and makes sense because the given point is not the center of the tumor and therefore the projection of the point onto the detector will not be directly beneath the provided point. This ground truth also further verifies the validity of the function because it has the same output as the previous ground truth, which was rotated -30 instead. Since these two rotations are equal, it makes sense that their projected points on the detector plane will also be equal.

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Part 3: Tumor Projector

Description: This function takes an array of tumor points given in C-arm coordinates and creates an array of the projected points in detector coordinates using the PointProjector function. It then takes the projected points and finds the edges of the projected contour/shadow and removes any points that are in the shadow.

Ground Truth 1: Sphere Projection

The graph on the left illustrates the 3D projection of every point projected from the source to the detector plane. The graph on the left illustrates the 2D shadow created when the randomly generated sphere points are projected onto the plane. The circle in the graph on the right is not perfectly circular, but this is understandable because the randomly generated points do not ensure hitting every part and contour of the sphere, thus making it challenging to get a perfectly circular shadow. Therefore this tumor contour is visually correct. It is centered at (0,0,0) and has a radius of approximately 3cm.

Ground Truth 2: Ellipsoid Projection
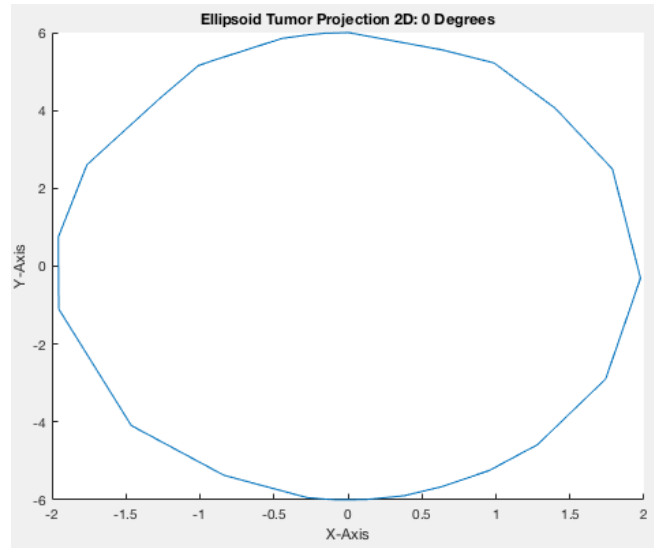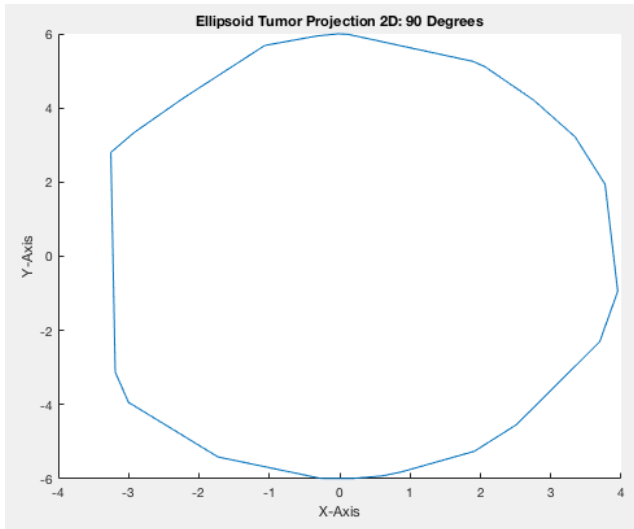
The Graph on the left illustrates the shadow/contour of the ellipsoid taken from a rotation of 90 degrees. The Graph on the right illustrates the shadow/contour of the ellipsoid taken from a rotation of 0 degrees. These contours are not perfectly circular, which makes sense because the shape is an ellipsoid and not a sphere. The sizes of the projections are accurate as well because the size of the ovals are slightly bigger than the dimensions of the given ellipsoid. The flat side of the oval in the graph on the left can be explained by lack of point coverage for that angle.

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Part 4: Super-Sphere

Description: This function takes an array of angles and an unknown (varying) number of tumor silhouette arguments and calculates the radius of the super sphere covering these points around the center in C-arm coordinates. The function does this by calculating the distances of every point from their contour center and finds the largest distance of them all. This distance is then set as the radius of the sphere but is divided by 2 because of similar triangles (calculated in part 1). The test function then uses this information and plots the super-sphere and the randomly generated points as a visualization.

Ground Truth: Ellipsoid


Ellipsoid Points and Super Sphere
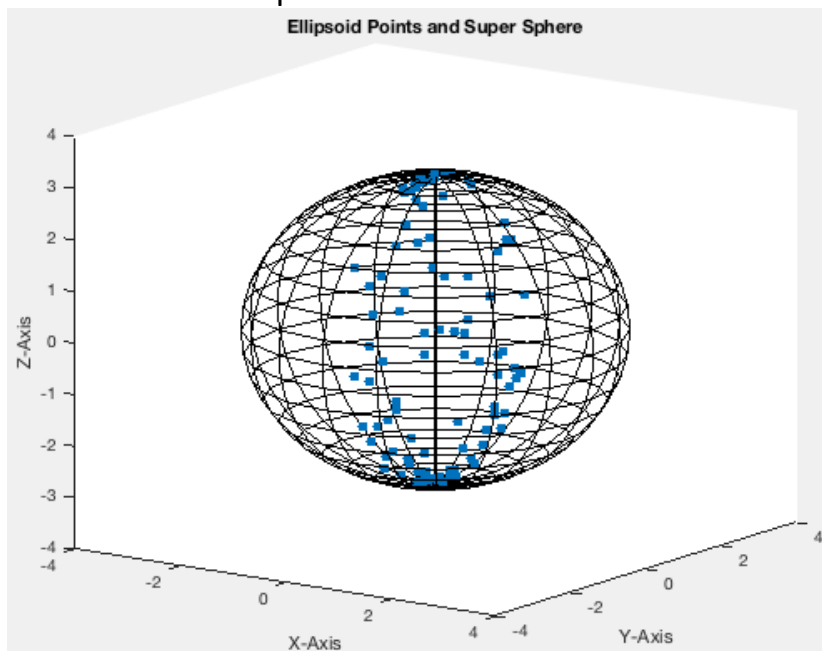
The Graph above illustrates the randomly generated ellipsoid points (blue), and the super-sphere surrounding them (transparent grid). As seen in the graph, the super sphere fits exactly around the given ellipsoid, fitting around the longest ends of the ellipsoid perfectly. This result is conclusive with the function written as it uses the furthest point distance from the projections to find the radius of the sphere.
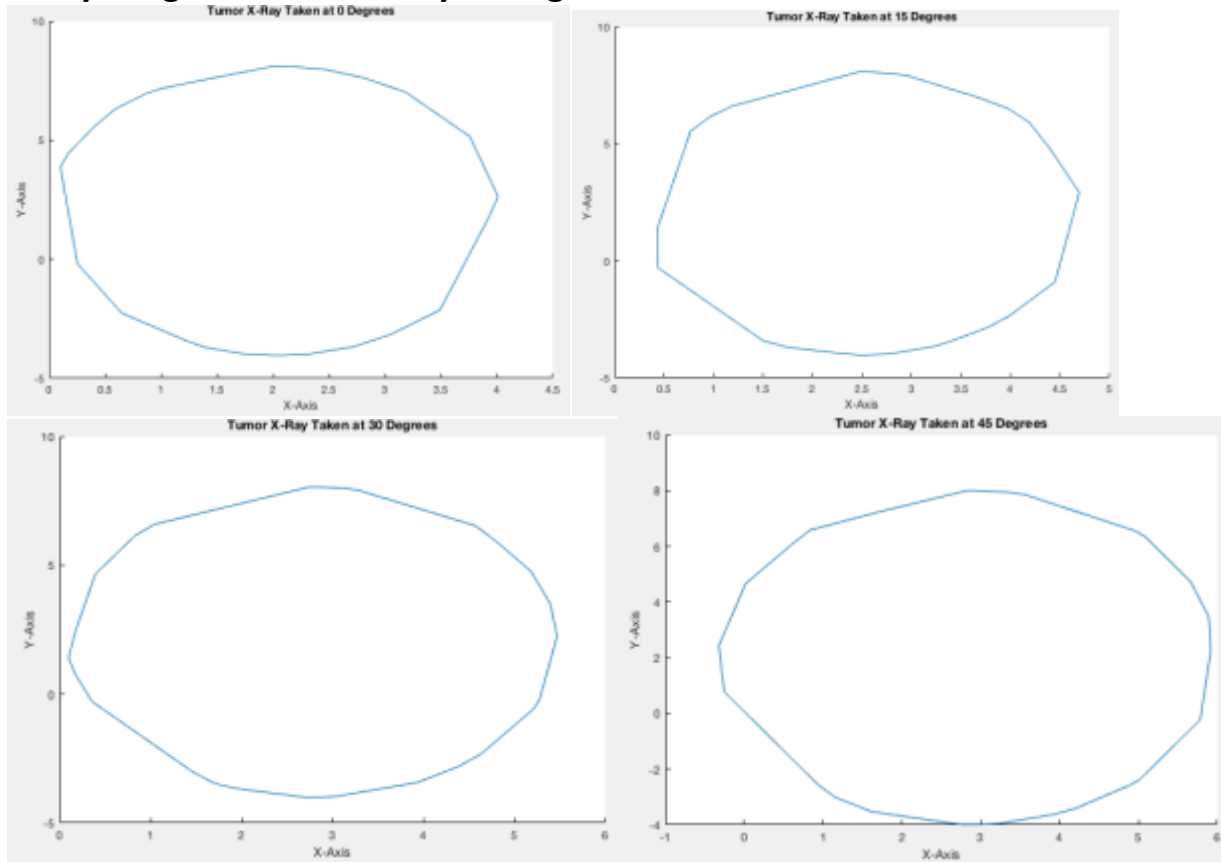
Part 5: Tumor Reconstructor
Description: This function takes a vector of imaging angles and an array of tumor silhouettes and returns an array of triangles defining the tumor surface
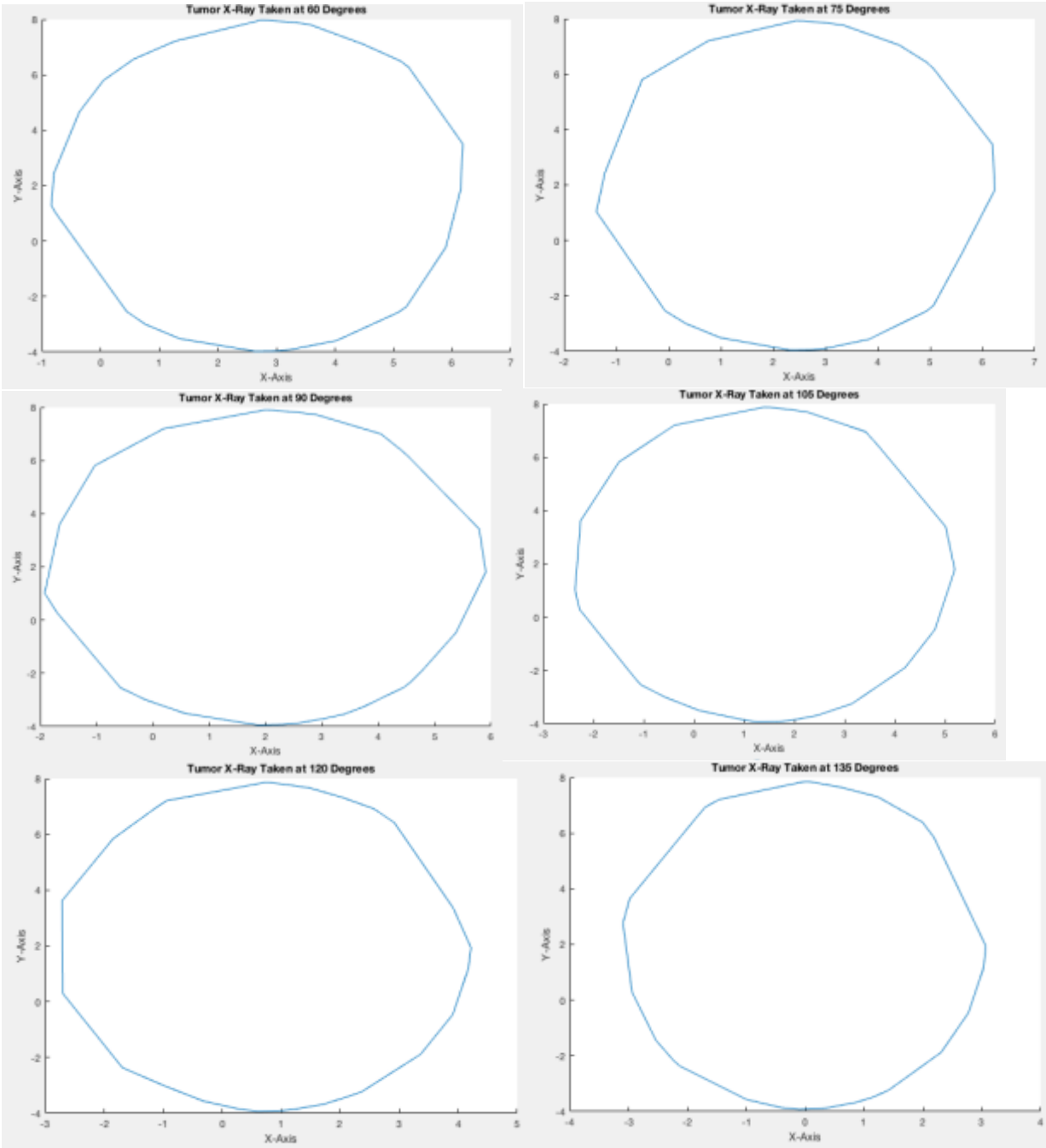
and the volume of the tumor using the convex hull MATLAB function convhull. This function works by calculating the centers of all the tumor silhouettes and back projecting to the source. The intersection of all those lines is then calculated and used as the approximate center of the reconstructed tumor. The method of using voxels and a super-cube and super-sphere is then used to find which points are in the tumor and which ones aren't. See sketches below for further explanation.
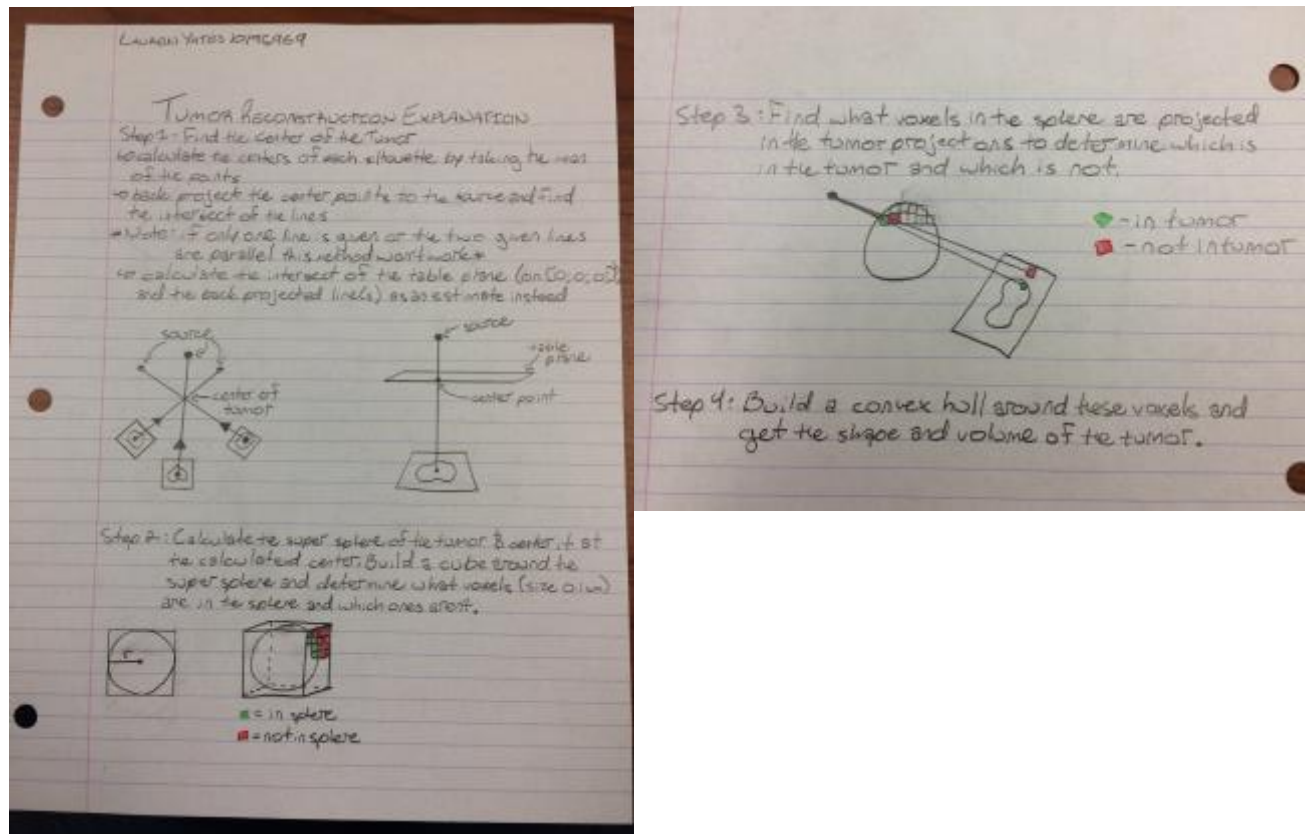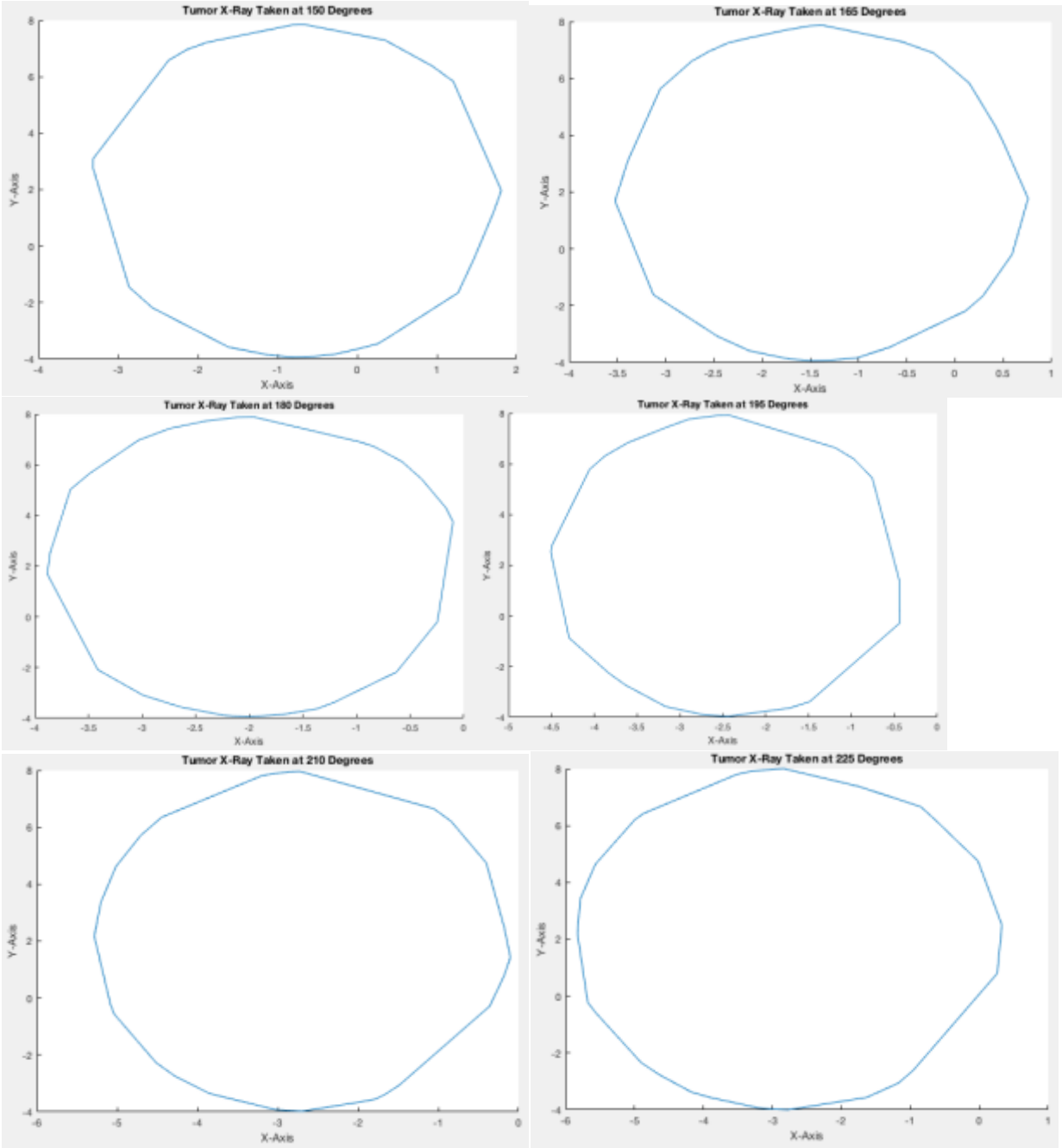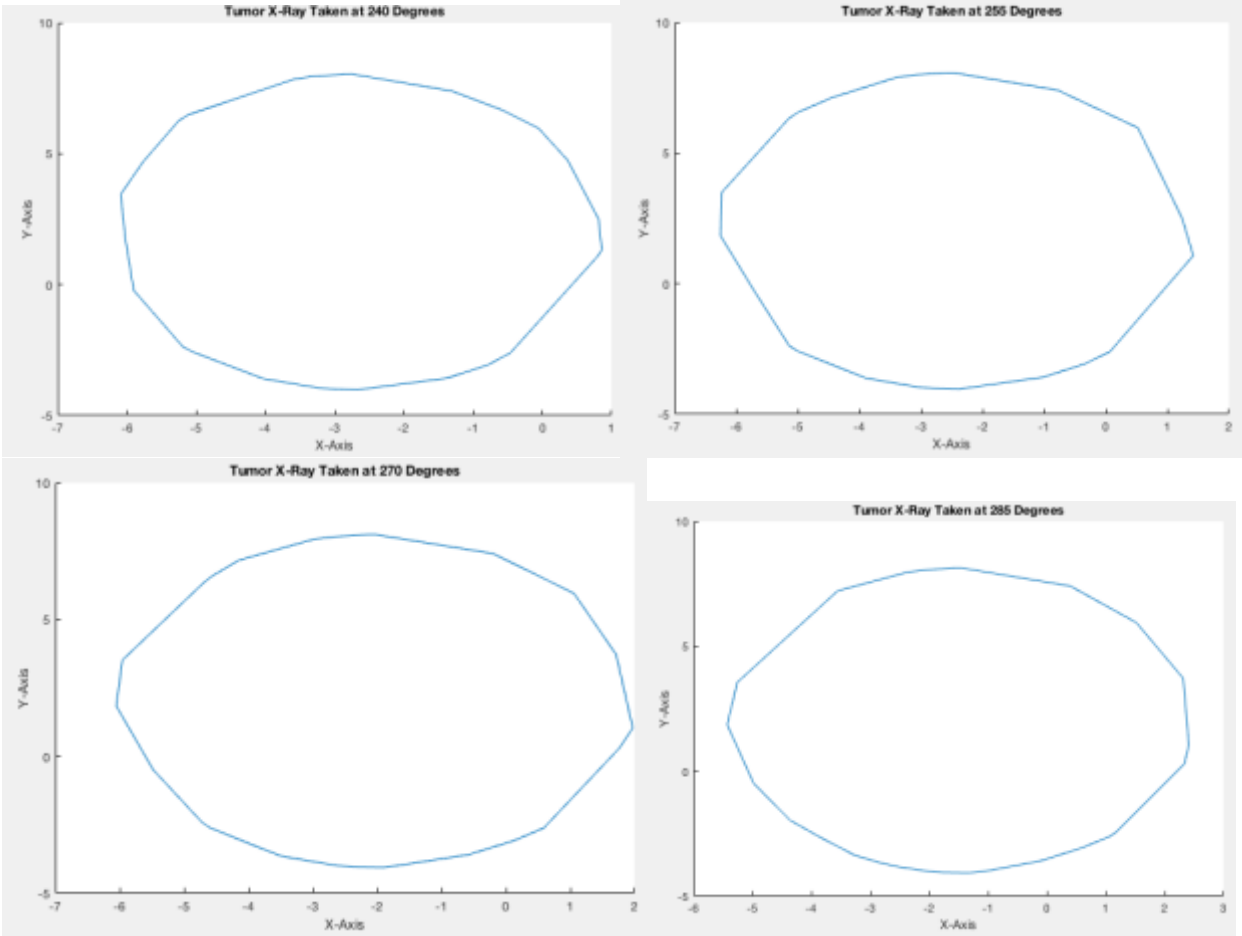

This method doesn't work very well if only one X-Ray image is given or 2 X-Ray images that are 180 degrees apart (parallel) are given. This is because the center of the tumor can no longer be calculated and a new estimate center is found that is less accurate. This method also doesn't work if there's an error with calculating the super-cube and super-sphere because otherwise points will be missed for the tumor and the shape will be wrong.
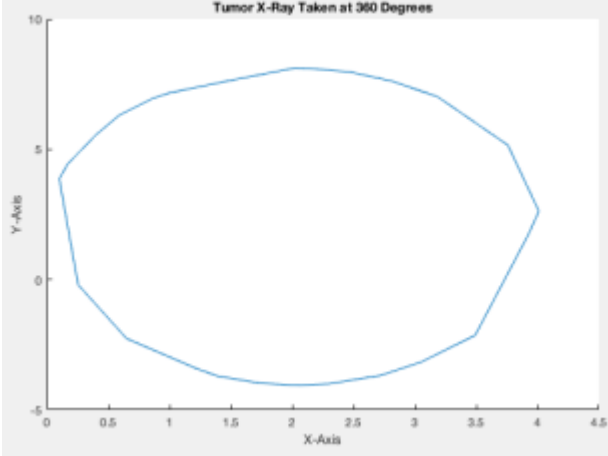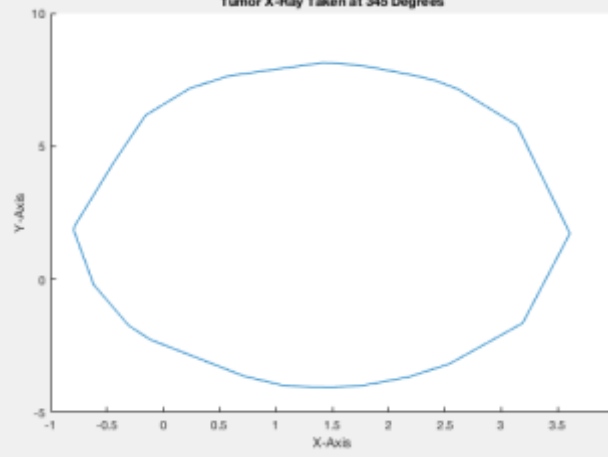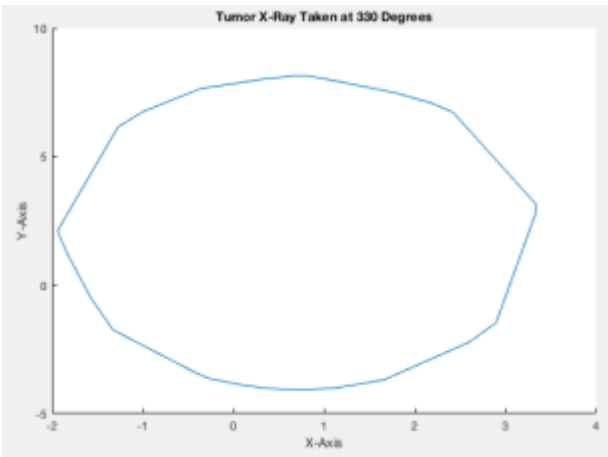
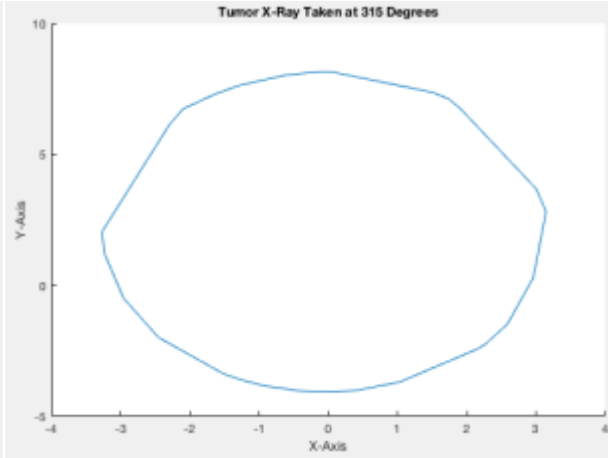## X-Ray images of tumor every 15 degrees

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Tumor X-Ray Taken at 150 Degrees

Tumor X-Ray Taken at 165 Degrees

Tumor X-Ray Taken at 180 Degrees

Tumor X-Ray Taken at 195 Degrees

Tumor X-Ray Taken at 210 Degrees

Tumor X-Ray Taken at 225 Degrees

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Tumor X-Ray Taken at 300 Degrees

Tumor X-Ray Taken at 315 Degrees

Tumor X-Ray Taken at 330 Degrees

Tumor X-Ray Taken at 345 Degrees

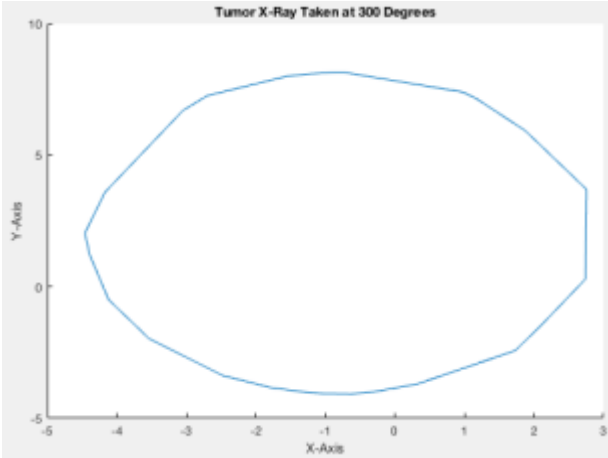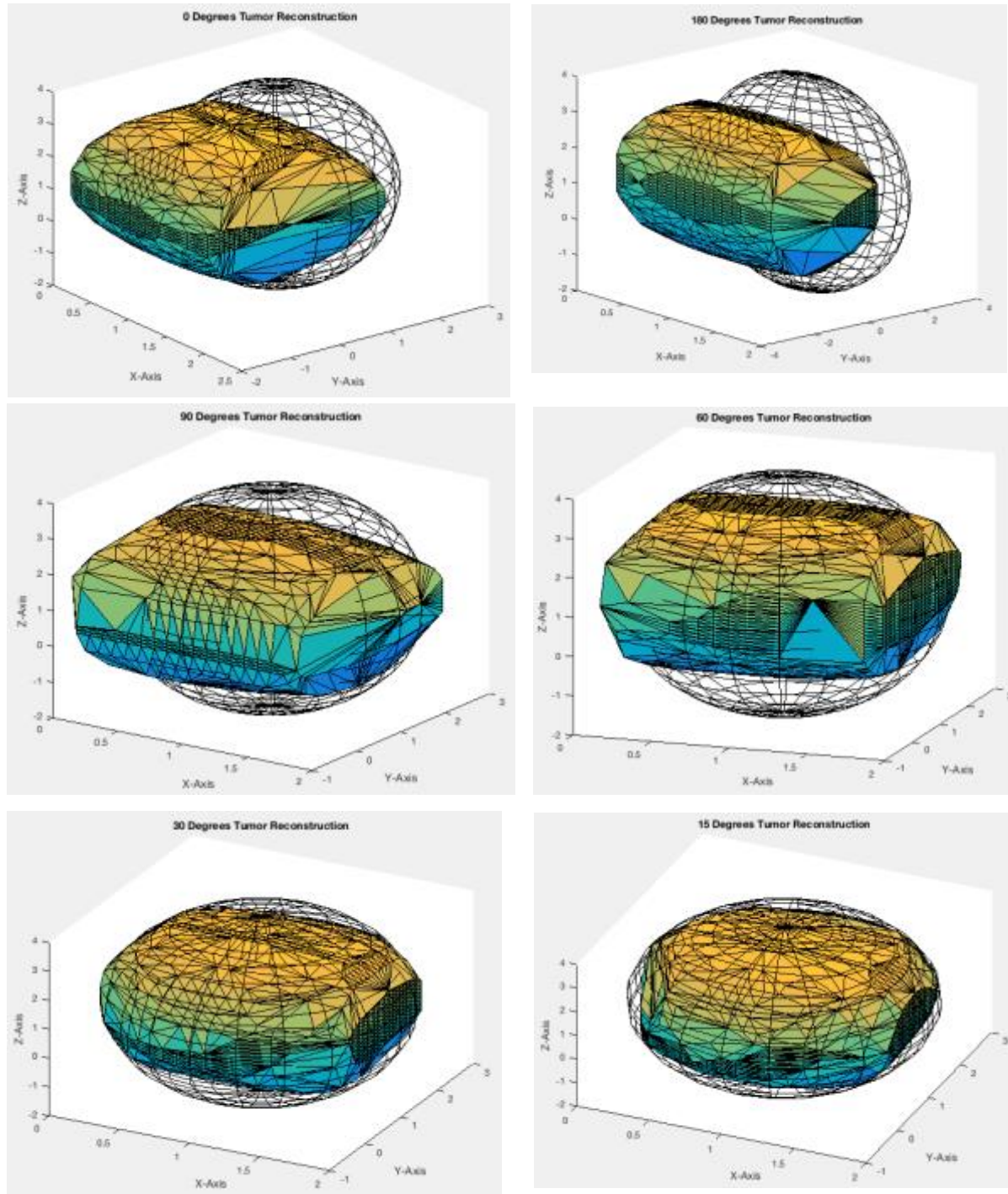Tumor X-Ray Taken at 360 Degrees

Tumor Reconstruction and Original Tumor Plots

Observing the 6 graphs above, a clear trend can be observed. As the angle of rotation gets smaller and the number of rotations increases, the reconstructed tumor begins to fit the original ellipsoidal tumor better and better. This is because

the more images taken at smaller increments/angles, the more projections you will have on the plane. By having more projections you're able to more accurately estimate where the center of the ellipsoid is and determine what voxels in the super sphere are also in the tumor. The first two graphs are not centered in the original ellipsoidal tumor because an accurate center could not be calculated. Because there was either only one line or two parallel lines, an intersection of the lines couldn't be calculated. Instead, the intersection of the patient/table plane located at [0;0;0] and the back projected line(s) was used instead.

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Volume vs. Number of X-Ray Images Graph
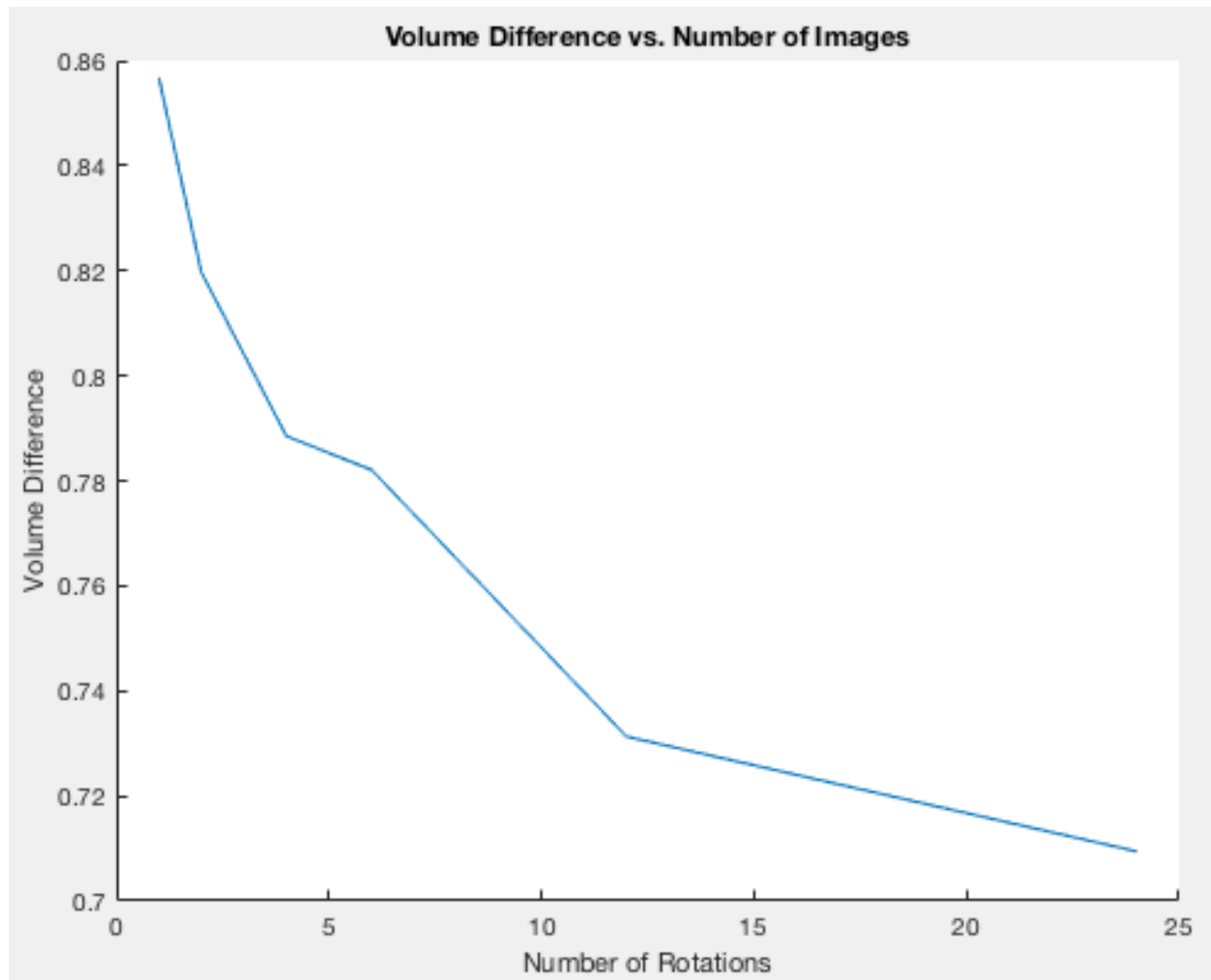
The chart above illustrates the change in volume ratio to number of rotations. As seen in the graph, there is a clear decrease in difference in volume as the number of rotations increases. This makes sense because as the number of rotations increases, the more accurate representation of the ellipsoid/tumor. Because it becomes more accurate, the volume of the reconstructed ellipsoid becomes closer to the actual volume making the ratio smaller.