

Tumor Reconstruction in C-arm Fluoroscopy

We will treat a tumor of convex shape that we managed visualize by C-arm fluoroscopy with using intravenous contrast. For planning the treatment, we need to reconstruct the tumor in the coordinate system of the C-arm. We positioned the C-arm relative to the patient so that the tumor is roughly in the center of the C-arm and tumor shows up roughly in the center of the detector in all images.

We will use rotational C-arm to take images from in multiple different angles (Fig 1). In each image made in the detector, the radiologist draws a contour of the tumor, represented by a polygon as an ordered set of points in image coordinates (a.k.a. detector coordinates) as shown in Fig 2.

For treatment planning purposes, you need to reconstruct and visualize the tumor's outer shell from C-arm images compute its volume. You need to design how many images you will take and from what angles in order to meet the required clinical accuracy.

In the given C-arm, the source-detector distance is $SDD=150$ cm, the source-axis distance is $SAD=75$ cm. The detector is circular with a diameter of 30 cm.



Fig 1.

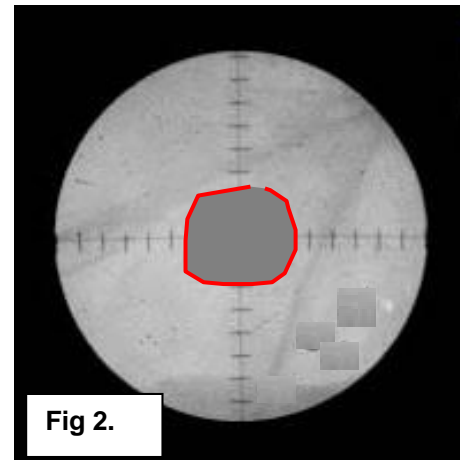
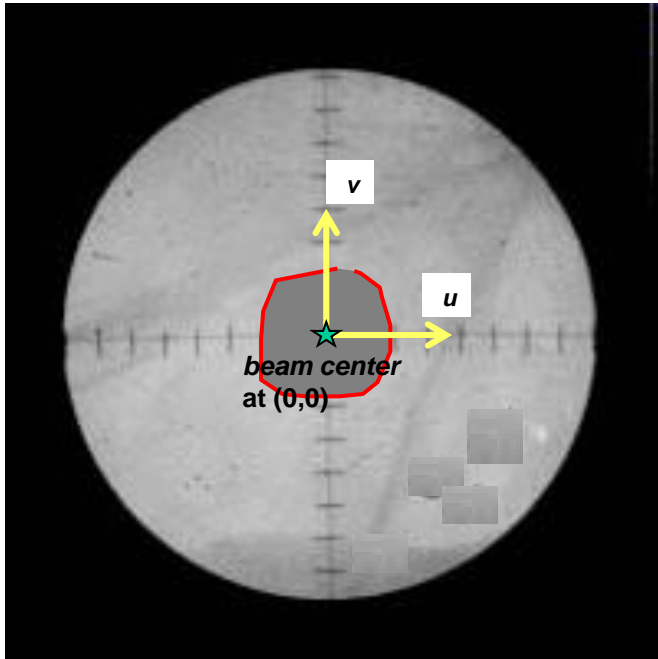


Fig 2.

Coordinate systems



In each image, the radiologist draws the contour of the tumor, it is available to you as a polygon. u and v are measured from center of the X-ray beam

Assumptions

- The patient stationary during imaging
- In each image, the target has been segmented as a polygon, i.e. an ordered set of points $S(u,v,0)$, where u and v are measured from center of the X-ray beam, and the image plane is $w=0$
- Each polygon in the image has M vertices
- The beam center is at $(u=0, v=0, w=0)$
- The $(u,v,0)$ image coordinates have been converted to metric coordinates by knowing the pixel size.
- There is no distortion in the images

Coordinate Systems

- The patient is in supine position on the table
- $+z$ axis points from toe to the head, the long axis of the table
- $+x$ axis points toward the right hand
- $+y$ axis points to the ceiling
- The gantry (detector/source unit) rotates only about the z axis
- In home position at zero rotation, the detector u and the C-arm z vector are identical AND detector v and C-arm x are identical; the X-ray shoots straight down from ceiling to floor (called anterior-posterior view, "down view" a.k.a. AP view.)

Questions and Problems [100 pts]

QUESTIONS [15 pts]

1. C-arm model. Construct a 3D geometry model of the X-ray projection and reconstruction problem. Make a 3D drawing, label the source, detector, relevant coordinate systems, tumor, projection lines, X-ray angle and the associated vectors, lines, planes, etc. Make sketches, one in AP pose (zero rotation) and one +45 degree rotation. *You may like to build a mock setup on your desk, cut out a cardboard couch top and X-ray detector, mark coordinate axes with stickers. Without this helper, it may be difficult to comprehend the setup and coordinate directions in 3D space. Snap pictures at 0 and +45 angles, annotate the images as necessary. There is a C-arm model in the Perk Lab, feel free to use it* [5 pts]
2. Compute the workspace around the C-arm center – the space that can be fully imaged with this device without truncation, assuming that you can do a full 360 degree rotation about both axis. Make a drawing, annotate, derive the math, explain. *You can do manual computation, no need for MATLAB* [5 pts].
3. Explain the error sources in target reconstruction with a real-life mobile C-arm unit [5 pts]

POINT PROJECTOR [15 pts]

Develop a module to project a point given in C-arm coordinates $P(x,y,z)$ to the detector at some α imaging angle, resulting in a point in detector coordinates $Q(u, v, w=0)$. Explain your approach (verbally in comment), implement, test.

Input: α imaging angle, $P(x,y,z)$

Output: $Q(u, v, w=0)$

Test: Test the point projector with 5 suitable ground truth test cases, in which you a priori know the answer. Make a 3D plot, and observe the results, determine they are visually accurate.

TUMOR PROJECTOR [15 pts]

Develop a module to generate silhouette of a closed convex tumor object on the detector at some C-arm imaging angle. The tumor is defined by an array of its surface points. The result is a polygon on the detector plane. Explain your approach (verbally in comment), implement, test.

Input: imaging angle, array of tumor points in C-arm coordinate system (x,y,z)

Output: tumor contour as array of points in detector coordinate system $(u, v, w=0)$

Testing: (1) Run the Tumor-Projector to project a sphere placed in the center of the C-arm coordinate system, radius of 3cm. (2) Run the Tumor-Projector to project forward an ellipsoid placed in the center of the C-arm coordinate system, with principal axes $a=1, b=2, c=3$ (cm) at 0, at 0 and 90 degree projection angles. Make 2D plots and observe the results, determine they are visually correct.

Questions and Problems (continued)

SUPER-SPHERE [15 pts]

Develop a module that computes super-sphere which is the smallest sphere that centered in the in the center of the C-arm coordinate system and completely encompasses tumor object to be reconstructed. Explain your approach (verbally in comment), implement, test.

Input: vector of imaging angles, array of tumor silhouettes in detector coordinate system ($u, v, w=0$)

Output: radius of the super-sphere (R_s)

Testing: Use the Tumor-Projector to project forward an ellipsoid placed in the center of the C-arm coordinate system, with principal axes $a=1$, $b=2$, $c=3$, imaged at 0° and 90° projection angles, compute its super sphere. Make a 3D plot of the ellipsoidal tumor and the super sphere, and observe the results, determine they are visually correct.

TUMOR RECONSTRUCTOR [20 pts]

Develop a function to reconstruct the tumor's outer shell as a closed convex surface tumor from its silhouettes and compute the tumor volume.

Provide a block diagram, pseudo code, text, etc. to fully explain all relevant details of your method. Explain the limitations and computational bottlenecks of your method. [5 pts]

Implement your reconstruction method [15 pts]

Input: vector of imaging angles, array of tumor silhouettes.

Output: array of triangles defining the tumor surface; tumor volume.

Questions and Problems (continued)

TEST AND ANALYSIS [20 pts]

Place a ground truth ellipsoidal tumor in (1,1,1) point of the C-arm coordinate system, with principal axes $a=1$, $b=2$, $c=3$. In a full-panoramic (360 degree) span, create synthetic X-ray images using the Tumor Projector module, at every 15 degrees.

Reconstruct the tumor gradually, using images at every 0, then every 180, then every 90, then at every 60, then every 30, and finally at every 15 degrees; thus gradually using 1,2,4,6,12, 24 images).

In each case, make a 3D plot of the reconstructed tumor over the original tumor – observe how the shape reconstructed tumor changes and explain your findings.

In each case, also compute the volume reconstruction accuracy (volume ratio of the reconstructed and ground truth tumor), make a plot of it as the function of the number of X-ray images used. Observe how the volume reconstruction accuracy changes and explain your findings.

NOTE: You will need to select an appropriate voxel size to discretize the reconstruction space inside the super sphere. If the voxel size is too large, the reconstruction will be too coarse. If the voxel size is too small, the reconstruction runs impractically long times. About 1 mm seems appropriate, but you may like to start with a coarser resolution to speed up development and testing and run again with a final resolution.

NOTE: in creating the test spheres and ellipsoids, 20x20 surface facets seem sufficient.

General Instructions

- Always explain how you solve a problem. Use drawings, math formulas, text, block diagram, pseudo code - anything that you find them appropriate to convey your ideas. I must know that you understand what you are doing and I must be able to follow your reasoning. Depending on the quality and depth of your reasoning and discussion or results you may pick (or lose) lots of points.
- Write proper header and richly comment your code. There is no such thing as too much comment. Good style and neatness will earn you valuable points. The lack of these will cause reduction.
- Always consider the validity (or deformity) of the input data; incomplete testing will lead to deduction of marks.
- Test each module fully, construct several test cases with known ground-truth answer.
- Write a testing m file(s) for each module or problem if appropriate
- Capture the output, to show that your program does what it is supposed to do. Make plots and tables when requested or when they makes sense. Add explanation text as you see it useful.
- Use decimal digits sensibly and consider what is precision is practical for the given problem. Generally, resolution finer than 0.1 millimeter is not practically achievable in such a surgical navigation system, so this should be your limit. Use decimal floating point format in your outputs. Do not use exponential number format.
- Create MATLAB functions for recurring tasks
- Submit the m files and the captured output file, as well as any drawing, or supplemental information you feel relevant.
- Also to remember:
 - Submit all in one zip file named LastName_hw3.zip
 - Put all .m files in the same folder
 - Always include a main.m that calls all other files in order to test. Do not expect me or the TA punch in parameters from the command line. Clearly identify the input and output.
 - Always include a PDF report answering all questions and providing the required analysis of the results. (No long essays are needed, all questions can be answered in a couple of sentences.)