CS 766 Midterm Project Report

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1 Current Progress

So far, I have employed a template matching technique based on the method described by Berbeco et al. The idea is, when a live radiograph is acquired during treatment, a simulated radiograph is constructed at each breathing phase from the planning 4D CT. The normalized cross correlation between each simulated radiograph and the live image is computed. The phase is chosen from the simulated radiograph that produced the highest correlation. The tumors live position is chosen from its position in the 4D planning CT at the chosen phase.

While this workflow is very simple at a high level, the implementation of a flouroscopy simulation program was a bit involved. To construct a simulated radiograph, first, I converted the CT volume from Hounsfield units to linear attenuation coefficient mm^{-1} using the following equation:

$$HU_{i,j,k} = (\mu_{i,j,k} - \mu_{water})1000/\mu_{water} \tag{1}$$

Then, using geometry parameters (SID, SAD, detector element spacing, gantry angle etc.) given in the dicom files for each radiograph, I computed the positions of the xray source and each detector element in the CT coordinate system. For each detector element, I sample the CT for the linear attenuation coefficients along the ray that connects the source to said detector element, and integrate to obtain the path length attenuation $\int \mu(l)dl$. The signal falling on this detector element is then proportional to $e^{-\int \mu(l)dl}$ (exponential attenuation). The constant of proportionality is determined from the mean value of the live radiograph.

2 Change in Scope for Direct Method

The template matching algorithm assumes falsely that the tumors motion trace is rigid in time. As such, I plan to develop a direct tumor tracking algorithm capable of segmenting the tumor and computing its centroid. There has been a significant change in how I plan to implement automated tumor segmentation. To this end, I now plan to train a convolutional neural network using the radiologist-labeled planning 4DCT to generate training data. To elaborate, before a patient undergoes treatment, a planning 4DCT is acquired and the tumor is contoured for each phase. This contour defines a 3D logical mask with value 1 for tumor voxels and 0 everywhere else. To generate a labeled training image, I can use my flouroscopy simulation program to generate a projection xray image at some arbitrary angle and phase. I can then project the corresponding 3D tumor mask onto the same plane. The projected mask acts as a label because each 1 valued pixel in the projected mask will correspond to a pixel of the tumors projection. If I construct simulated labeled flourographs with an angular step size of 3.6 degrees, and do so for each of 10 phases, I will obtain 1000 training samples. I will use this training data to train a CNN with SegNet architecture to classify each pixel in an incoming radiograph as either tumor or not tumor, after which calculation of the centroid is trivial. I think this method will work exceptionally well since the CNN will be patient specific, and naturally tuned to the irregularities of this particular tumor.

3 Results

See figure 1

4 Difficulties

Simulated flouro is very computationally expensive. Using my gpu, (Nvidia GeForce GTX 1660) it took 2-3 minutes per radiograph. To implement this in the clinic, we would need to know the angles at which each radiograph will be taken apriori, so that we may prepare the appropriate radiographs ahead of the procedure. Otherwise, significant optimization and/or more parallel processors will be required to construct DRR's as they are needed during treatment.

There are some difficulties with the template matching method. For one, the differences between the radiographs at each phase are subtle. All of the structures maintain a lot of their patterns, resulting in some spurious matches. This leads to all of the simulated images having a reasonably high correlation with the template image. Also, the resolution of the simulated flourographs was limited by the slice thickness of the 4D CT (3 mm). This results in the simulated images having different image quality than the live image. They noticeably have poorer spatial resolution, however they do not suffer from electronic noise as the live image does. All of these compounding factors call in to question the efficacy of using a template matching approach for live tumor tracking. I am hopeful that a direct tracking method using deep learning will be more robust.

5 References

Terunuma, T., Tokui, A. Sakae, T. Novel real-time tumor-contouring method using deep learning to prevent mistracking in X-ray fluoroscopy. Radiol Phys Technol 11, 43–53 (2018). https://doi.org/10.1007/s12194-017-0435-0

Cui Y, Dy JG, Alexander B, Jiang SB. Fluoroscopic gating without implanted fiducial markers for lung cancer radiotherapy based on support vector machines. Phys Med Biol. 2008 Aug 21;53(16):N315-27. doi: 10.1088/0031-9155/53/16/N01. Epub 2008 Jul 25. PMID: 18660557.

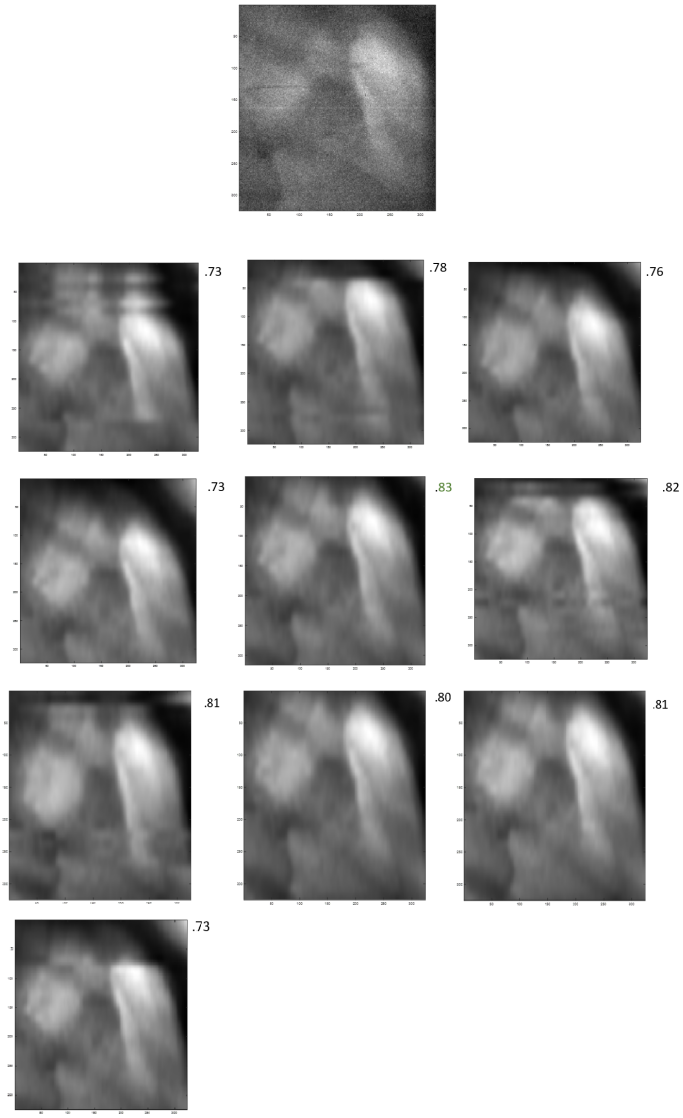

Figure 1: Template Matching: This figure shows an example of template matching for a radiograph taken at a gantry angle of 215 degrees. The top image is the live radiograph, and the lower 10 images are simulated radiographs from different breathing phases. The correlation with the live template is shown to the upper right of each simulated image.