Correspondence based 3D reconstruction requires time-synchronous imaging from multiple views. Single plane imaging provides images during the same cardiac cycle- not time-synchrnous views. It is not clear from the paper how this fundamental problem handled in this work.

He points out that we did not make how we do reconstructions with asynchronous angiograms clear.

What he says is right. Actually, our reconstruction is done on asynchronous angiograms. This is a problem already known.

There are three ways to solve this problem:

1. The most exact method is to use the mono-plane X-Ray machine which can take two views of angiograms at the same time, but we don’t know whether we can get the DATA!
2. The second way is to use the electrocardiograms. This is also a classical method. I wonder maybe this is what he wants. But we are in short of electrocardiograms data along with the angiograms I got from Beijing Union Hospital last time. The doctor says that they do not take electrocardiograms while taking angiograms. Because we were short of time when we sent the CAD/CG paper last month, I had not spent much time on this thing. But, we actually will achieve better and more convincing results if we have the data.
3. The third way is we want to find a method to calculate the cardiac cycle in image space. This has not been done during any other prior papers. This way may lead to the registration between two adjacent angiograms and we do not know what precision it can reach.

With the problems mentioned in the Clarity session, it is difficult to evaluate the details of the technical quality. The pipeline looks reasonable, though. The results of synthetic data appear to be promising. However, I would like to see more results of real data to judge it. Also, it will be greatly helpful if the authors can figure out some way to analyze the results of real data.

There is no conclusion and discussion of limitation.

What he says is actually what we need to do.

1. We need more experiments on real data and more analysis on both real data and synthetic data such as error analysis, reconstruction effects analysis.
2. For real data, we can project the reconstructed skeleton onto the angiograms for the evaluation.
3. For the diameters of vessels, we can use the smoothness and other known issues to evaluate.
4. Also, after we have an entire CUDA edition of our method, we should do the time consuming analysis and comparisons between our method and other methods.

One reviewer points out that our work is similar with the well known variant of the classic voxel carving method.

While, another says the similar pipeline has been employed to many other applications of other fields involving 3D reconstruction based on 2D input images like cell movement tracking visualization.

For the first one, I guess what he says is the space division and ray tracing step in our method, but that step is just the preparation step, not the core. Anyway, I will spend some time to look into the *classic voxel carving method.* Also, I will have a look at the *cell movement tracking visualization* mentioned by the prior reviewer.

All other mistakes such as spelling and grammar mistakes have been corrected now.