Chicken Heart Movement Modeling

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BACKGROUND

Research about congenital heart disease is at the forefront of many health initiatives. Both valve defects and holes in the heart's walls can make daily living a struggle. The best way to find a solution to heart defects is through rigorous study and extensive research. Since the heart is a vital organ, it can be difficult to study without causing harm to the patient. Computer graphics modeling provides a unique environment to study the heart: it is a relatively inexpensive and safe way to gain insight about the human heart. It can also provide for a more exact comparison between healthy hearts and hearts with defects.

A human heart is incredibly intricate and complex. In order to obtain an accurate and effective model, a better understanding of how it functions is necessary. The first step for us is to understand how blood flows through the heart. For my project, I worked with Dr. Cindy Grimm to make models of chicken hearts. Chicken hearts are unique because they are the simplest heart we can use but still apply the results to human hearts. When the chicken is still developing inside of the egg, its heart is barely more than an elliptical tube. This is much simpler to model than a human heart, and it allows us to explore curvature and reconstructions.

HOW WE GOT OUR DATA

This project involves the heart of eight different chickens. Four chickens had bands placed around their hearts to simulate valve defects and holes in the heart's walls. Four additional chickens with normal hearts were used as the control group. The chicken hearts were scanned continuously while they were beating at three different points along the heart. The contours of the hearts were traced from the scans using sketch based path design (McCare and Singh, "Sketch Based Path Design"). Once the coordinates were placed into matrices, the next step was to have Dr. Cindy Grimm build models of the data.

CURVATURE

The contours were analyzed by finding their radius of curvature at given points along the contour. The curvature was measured by finding the radius of a circle that is tangent to a curve. Taking this measurement over multiple time steps provides a simplified matrix for reconstructing the curve. Once the data from all the curves were combined, we were able to build a reconstruction of a chicken heart. For a circle, the curvature is inversely proportional to the radius (Weisstein).

$$\kappa = 1/r$$

Curvature can also be measured by the change in the angle over the change in length. Three points are read in and two vectors (V1 and V2) are formed around the central point. The change in angle, $d\Theta$, is approximated by the exterior angle between V1 and V2, using properties of the dot product (Weisstein).

$$\kappa = \text{acos}\,[\frac{V1 \cdot V2}{||V1|| * ||V2||}]$$

For our contours, the curvature was measured at 19,600 points. This was done at all three contours per heart in all eight chicks. In order to make the code more efficient for reconstruction, we approximated the curvature values using various functions determined by previous research conducted by Dr. Grimm (Liu, et al. "Ecient postacquisition…"; Liu, et al. "Biomechanics…"; Xin, et al. "Extracting…"). The approximations were enhanced by automatic neatening of sketched strokes (McCrae and Singh, "Neatening …"). The next step was to determine which curvature fitting methods yielded the most accurate reconstructions.

We experiment with multi-basis functions and single basis functions that are represented in Table 1.

Table 1. Basis types used to approximate curvature

Single Basis	**Multi-basis**
Piecewise linear	Mexican hat wavelet
Piecewise quadratic	Haar wavelet
Piecewise quadratic with matched derivatives	Laguerre polynomials
Piecewise quadratic spline	Hermite polynomials
	Sinusoid basis
	Combination of multi-basis functions

An example of how the curvature was approximated is shown in Figures 1-3.

Figure 1 shows the original contour and the original curvature from the measured data set.
Figure 2 shows the curvature approximated with a piecewise linear fit (black).
Figure 3 shows the reconstructed contour plotted on top of the original curvature (black).

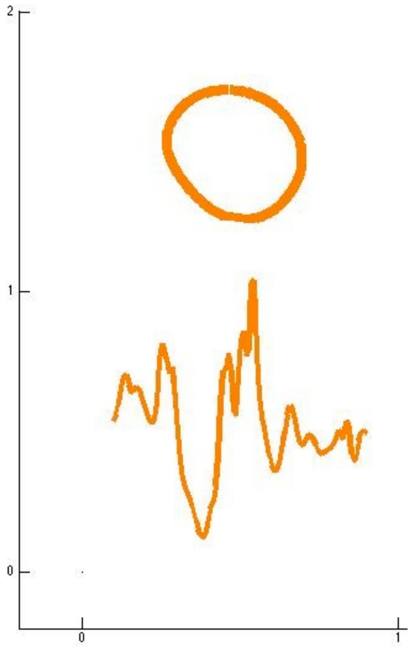


Figure 1.

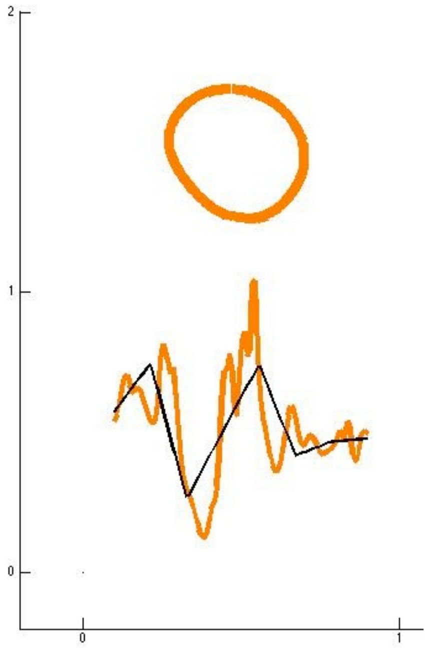


Figure 2.

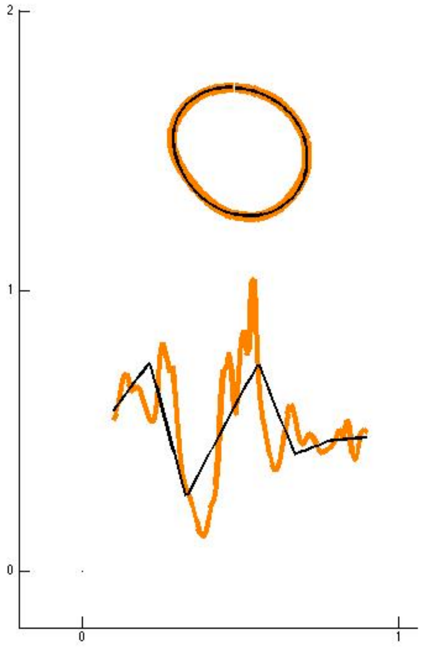


Figure 3.

One of the big questions was to see if a single basis or a multi-basis curvature fit would yield the best fitted points. The single basis fits are faster and are the most efficient way to create a basis for reconstruction. However, they are a very rough estimate and may not yield an accurate reconstruction. Multi-basis fits take slightly longer to run, but generally fit the curvature values better. The reconstruction process uses elements from the curvature data, and many not require a fit as rigorous as the multi-basis options. The best reconstructions come from the best overall approximation of the curvature.

An example of one of the multi-basis fits is the Mexican hat wavelet, which is illustrated in Figure 4.

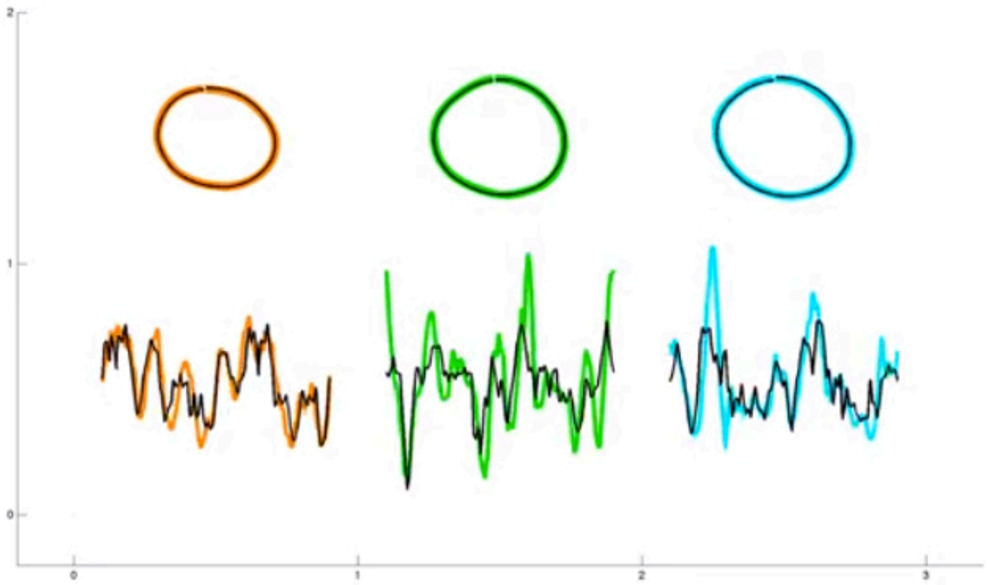


Figure 4. Three contours of one chick with fitted curvature using the hat wavelet fit

After every contour of every chick had been run through each fitting method, animations were constructed to simulate a chick heart while it was beating. When animations are running in a continuous loop, it gives us an idea of what the contours of the heart look like while it is beating. Animations also allow us to observe which fit gives the best reconstruction over the entire time sequence instead of just at one time step.

RECONSTRUCTION

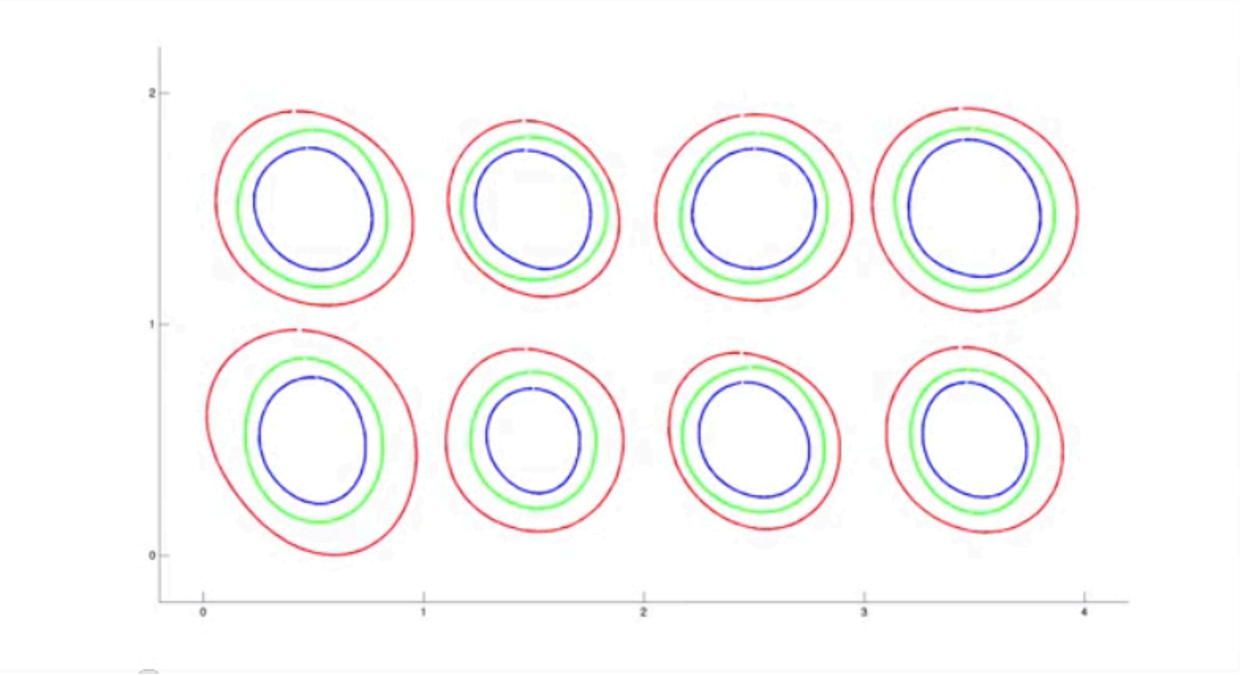
Curvature reconstruction is essentially undoing the process that was used to calculate the curvature ((Liu, et al. "Ecient postacquisition…"; Liu, et al. "Biomechanics…"; Xin, et al. "Extracting…"). The original curvature was fit with an approximation function, and output the data for the fitted curvature. If a multi-basis function was used, the weights for the fit function were also output. For the single basis functions, the number of segments used to approximate the function could be modified. The weights and the fitted curvatures were then run through a function that would build the curve. The bases were summed after multiplying the base times the weight, and then integrated over each time step. The reconstructed contour values were generated using the following:

$$FittedPoints = \int_{0}^{ts} \sum_{0}^{s} (Weights * BasisFunctions(s))$$

The fitted points were plotted against the original data to see how closely the reconstruction and the original curve matched. The single basis functions overall generated a better reconstruction than the multi basis functions. The contours are a relatively simple shape and did not require the complexity of a multi-basis fit to yield and accurate reconstruction.

In order to make comparison between different chicken hearts easier, the contours needed to be plotted side by side. The ability to view all of the data at one time helped determine the overall best analysis. However, finding a way to show all eight chicken hearts and every contour cleanly in one space proved a challenge. After several different models, the best way to show the data was with various scaling on one large plot. For each chicken, the contour at the top of the heart was shown as the largest, the contour in the middle was shown in the middle, and the contour at the bottom was shown in the center. After the data was plotted at ever time step, the images were combined to create an animation.

Figure 5. All contours and all chicks, reconstructed using the quadratic spline fit. The first row of contours shows normal hearts, and the bottom row shows banded hearts.



RESULTS OF 2D CODE

After the analysis of each set of fitted data, it was determined that the single basis typically yielded a more accurate fit. Although the multi-basis seemed to accurately fit the curvature better, the most accurate reconstructions were yielded from the single basis fits. This was actually a very beneficial result because single basis functions take less computational time to run during curvature fitting and contour reconstruction.

THREE DIMENSIONAL MODELING

The next challenge is to make a code that will perform all of the functions in the 2D code while also accounting for a third dimension. There are now two different curvature values, one for theta, the in plane curvature, and one for phi, the out of plane curvature. The points are vectorized, and the curvatures are calculated along with the rotation matrices. The curvature is fit using two different calls, one to fit the curvature in the xy-plane and one to fit the curvature in the yz-plane.

The fitted curvature and weights are then formatted into a structure to make it easier to conceptualize the data. When analyzing 3D data there are three possible directions of movement: torsion, lateral and dorsal. In order to simplify reconstruction and analysis, one of these directions can be held constant. In our model, we opted for a torsion free fit and only analyzed the lateral and dorsal movements.

The data is then combined based on the weights and the basis functions, then integrated over small time steps to receive the desired fitted points. Both the original data and the fitted data are centered around the origin. We used an additional script to make sure the reconstructed code is plotted near the original code for ease of comparison in the plots.

I worked with relatively simple original contours in order to test the integrity of my code. As a result, I was able to develop a reconstruction method that worked for simple 3D curves whose curvature had been determined using the methods in the 2D data.

NEXT STEPS

The 3D points for the chicken heart data are still being generated. Generating 3D points from the scanned images poses an interesting challenge. When the data is ready it can be run through my 3D code and be compared to the original points.

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