3D Heart Motion from Single-Plane Angiography of the Coronary Vasculature: a Model-Based Approach

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ABSTRACT

In order to complete a thorough examination of a patient heart muscle, physicians practice two common invasive procedures: the ventriculography, which allows the determination of the ejection fraction, and the coronaryography, giving among other things, information on stenosis of arteries. We propose a method that allows the determination of a contraction index similar to ejection fraction, using only single-plane coronaryography. Our method first reconstructs in 3D, selected points on the angiogram, using a 3D model devised from data published by Dodge et al.\textsuperscript{1,2} We then follow the point displacements through a complete heart contraction cycle. The objective function, minimizing the RMS distances between the angiogram and the model, relies on affine transformations, i.e. translation, rotation and isotropic scaling. We validate our method on simulated projections using cases from Dodge et al. data. In order to avoid any bias, a leave-one-out strategy was used, which excludes the reference case when constructing the 3D coronary heart model. The simulated projections are created by transforming the reference case, with scaling, translation and rotation transformations, and by adding random 3D noise for each frame in the contraction cycle. Comparing the true scaling parameters to the reconstructed sequence, our method is quite robust ($R^2 = 96.6\%, P < 1\%$), even when noise error level is as high as 1 cm. Using 10 clinical cases we then proceeded to reconstruct the contraction sequence for a complete cardiac cycle starting at end-diastole. A simple heart contraction mathematical model permitted us to link the measured ejection fraction of the different cases to the maximum heart contraction amplitude ($R^2 = 57\%$ with $P < 1\%$) determined by our method.

Keywords: 3D model, 3D reconstruction, coronaryography, ejection fraction, single-plane angiography

1. INTRODUCTION

The 3D representation of the coronary arteries is an effervescent research topic aiming at morphological and functional analysis. The 3D reconstruction usually involves two or more views, the views can be acquired simultaneously by biplane X-ray acquisition apparatus\textsuperscript{3-5} or sequentially by rotating a single-plane acquisition device.\textsuperscript{6-8} Some reconstructions have also been made by using non-rotating single-plane angiograms only.\textsuperscript{9}

Reconstructions made with multiple views are mainly realized by finding feature correspondences between images using epipolar geometry constraint.\textsuperscript{10,11} With non-rotating single-view reconstruction, since the depth information is lost, the process must rely on other means. In the case of Nguyen et al. the depth information was extrapolated by fitting together features from sequential view of the cineangiogram with a center of contraction constraint. The method we propose, infer depth information by using a 3D coronary tree model. Even if variations exist in the tortuosity and localization of coronary arteries, certain structural characteristics exist, as expressed by the existence of anatomical heart atlas.\textsuperscript{12} These structural characteristics are also used in the 3D reconstruction process.\textsuperscript{13-15} Our 3D reconstruction method relies on inter-patient similarities for fitting the projection of a coronary tree model to selected points along arteries.

Kong et al.\textsuperscript{16} were the first to propose the use of variations in the coronary tree length, measured from 3D reconstruction, to quantify heart contractions. We use the 3D reconstruction to extract a contraction amplitude index from coronaryography, similar to the ventriculography ejection fraction index used in the diagnostic of the overall heart health. The conception of the model and the method used to acquire a contraction index from simulated and clinical data is presented and discussed.
2. MATERIAL AND METHODS

2.1. 3D coronary tree model

The central element in our reconstruction method from single-plane images is the 3D coronary tree model. This coronary tree model is based on the data used in two articles by Dodge et al.\textsuperscript{1,2} where the 3D location of 102 points along the coronary tree of 37 normal subjects using bi-plane angiography were measured. The point locations are based on trisected artery segments. The segments are delimited by anatomical landmarks like artery bifurcations. The different reference points were distributed along the right and left coronary arteries and also along the main branches and their secondary tributaries.

We constructed our 3D coronary tree model using a subset of Dodge et al. data. Only the reference points along the major left coronary branches (LCA) and right coronary branches (RCA) were considered because the selected points had to be present for every subjects. We ended up with 26 subjects matching our selection criteria, the \textit{subject models}. Using the nomenclature defined by Dodge et al. the distribution of the 36 points along the coronary branches is as follows, Fig. 1:

- 12 points on the RCA subdivided as the R1, R2, R3 and R4 segments;
- 3 points on the left main artery (LM), the joint base between the left anterior descending artery (LAD) and the left circumflex artery (LCx);
- 12 points on the LAD subdivided as L1, L2, L3 and L4 segments;
- and 9 points on the LCx subdivided as C1, C2 and C3 segments.

Refining the method described in a previous article,\textsuperscript{17} the model definition of the 3D coronary tree model is realized using global and local components. The global component refers to a transformation that is applied to all the points composing the model, the local component is a more subtle transformation specific to each of the model points.

The global component attenuates inter-subject variations, like heart size, and relative body position during data acquisition. Local component attenuates the specific characteristics caused by the choice of the \textit{reference subject}. 

\begin{figure}[h]
\centering
\includegraphics{figure1.png}
\caption{Reference point locations along the right and left primary coronary arteries. From Dodge \textit{et al.} original data (gray section), only the right coronary artery (RCA), the left main (LM), left circumflex (LCx) and left anterior descending (LAD) arteries were considered in our 3D coronary tree model (dark section). See text for details.}
\end{figure}
Table 1. Clinical cases demographic details

<table>
<thead>
<tr>
<th>Patient</th>
<th>Sex</th>
<th>Age</th>
<th>Ejection fraction (%)</th>
</tr>
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<tr>
<td>JO</td>
<td>M</td>
<td>80</td>
<td>24</td>
</tr>
<tr>
<td>ME</td>
<td>F</td>
<td>58</td>
<td>25</td>
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<tr>
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<td>M</td>
<td>65</td>
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<td>M</td>
<td>61</td>
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<tr>
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<td>F</td>
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<tr>
<td>CH</td>
<td>M</td>
<td>55</td>
<td>75</td>
</tr>
</tbody>
</table>

2.1.1. Global component

The steps involved in the elaboration of the global component can be described as follows:

A well-formed subject is chosen as a reference subject. Well-formed being defined as a subject with clearly defined arterial branches.

The reference subject is fitted, with affine transformations (translation, rotation and scaling), to each of the other subjects, the target subjects. We use a simulated annealing technique to minimize the sum of the Euclidean distances between the reference subject and the target subject corresponding points. The objective function used is \( \sum_{i=1}^{n} ||P'_i \cdot M \cdot P'^i||^2 \), where \( P'_i \) and \( P'^i \) are respectively the 3D reference subject and target subject points and \( n \) is the total number of 3D reference points. \( M \) is the aggregated matrix made of the rotation matrices around the \( x, y \) and \( z \) axes, an isotropic scaling parameter and a translation vector along the 3 orientation axes.

The global component in the definition of our model is obtained by applying on the reference subject the average rotation, scaling and translation parameters found in the minimization process. This gives us the adjusted reference subject.

2.1.2. Local component

The local component in our 3D coronary tree model is obtained by applying a specific displacement for each point of the model. This displacement corresponds to the average residual errors found between the adjusted reference subject and the target subjects.

2.2. Heart contraction simulation

To test our 3D heart motion reconstruction, we did some simulations. To simulate an angiogram, first we used one of the 26 subject models, the simulated case. The 3D coronary tree model use to recover the 3D heart motion was then defined (see section 2.1) using a leave-one-out strategy, excluding the simulated case from the case pool.

The simulated case was then affected by rotation, scaling and translation transformations varying in time, to produce a simulated contraction. Different values were used ranging from \( 0 - 30^\circ \) for rotations, \( 1 - 0.8 \) for the scaling factor and \( 0 - 0.5 \) cm for translation. This dynamic simulated case was projected frame by frame giving the simulated case projection, which was the starting point for our recovery method. To stress our recovery method, random noise varying from \( 0 - 1 \) cm was also added around each reference point.
2.3. Angiographic images

The clinical cases used to test our 3D reconstruction method came from the Montreal Heart Institute, they consist of 7 men and 3 women between 55 and 80 years old (65 average) and with ejection fraction varying from 24% to 75% (50.6% average), see Tab. 1 for details. The single-plane cineangiograms were taken on two different X-ray imaging systems. Three cases were obtained with the Siemens AXIOM-Artis and seven with an Electromed Imaging system. The digital images were saved in the DICOM format. For each case, a complete contraction cycle starting at end-diastole was isolated visually with the help of a custom program, using slow-motion and scrubbing (back and forth) techniques, since no recorded synchronized ECG was available. During a coronaryography examination, the injection of the contrast agent bolus is done separately for the left and right coronary angiogram. To use both the LCA and RCA together, the images must be registered. Since no registering was done with our clinical case angiograms, only images of the LCA were considered.

In all cases, the reference points used to track the epicardial surface movements were located along the LM, LAD (excluding segment L4) and LCx arteries, giving a total of 21 reference points, see Fig. 1. In some angiograms, a camera movement was detected and was corrected by lateral translations.

2.4. 3D heart contraction recovery method

To follow the 3D heart movement from the projected reference points along the coronaries, some assumptions are made on camera parameters. The center of projection is placed at the center of the projection plane, the angiogram. The focal distance $f$, distance between the projection plane and the X-ray source, is estimated using information either from the DICOM format when available or from specifications of the angiography apparatus, see Fig. 2. The projection plane was also scaled to remove heart size differences or magnification adjustments used on the angiographic apparatus. The projection plane scaling value was chosen so that the first frame in the contraction sequence had the same size than the adjusted projection of the 3D coronary tree model.

In order to follow the heart motion, the projection of the model is fitted to the clinical cases with the simulated
annealing technique. The objective function use is

$$\sum_{i=1}^{n} p_i^c - p_i^f = 0,$$

where $n$, represent the number of reference points of a simulated or clinical image, $p_i^c$ is the measured point location of a case, $p_i^f$ is a projected point location of the adjusted model. Two projections models were used, the full-perspective camera model ($p_i^{FP} = [fX_i^c/Z_i^c, fY_i^c/Z_i^c]^T$) and the weak-perspective camera model ($p_i^{WP} = [f/ZX_i^c, f/ZY_i^c]^T$). $Z$ is defined as $\frac{1}{n} \sum_{i=1}^{n} Z_i$ and the points $p_i^f = [X_i^c, Y_i^c, Z_i^c]^T$ are the results of the transformation $P^f = MP_i$. $P_i$ being the 3D coronary tree model point locations. Three combinations of transformations were used: $M^{RTS} = RTS$, $M^{TS} = TS$ and $M^S = S$. $R$ denotes rotations around the three main axes, $T$ the translation along the $x$ and $y$ axes and $S$ represents an isotropic scaling factor. $p_i^f$ can then take the form of the two projection models, combined with the three transformation methods $p_i^{(FP)WP.RTS/TS/S}$. Each combination is studied and discussed.

3. RESULTS

3.1. Heart contraction simulation

As explained in Sect. 2.2, we created simulated case projections. Our goal is to recover the scaling parameter which is our contraction index. Therefore, comparing the scaling factor, used in the construction of the simulated cases, to the recovered scaling parameter found by our method, gives a quantitative evaluation on the efficacy of our reconstruction method. For each of the 25 subject models (one of the subject was constituting the model), we created different simulated case projections. The simulated contractions were spread on 10 frames and were obtained by varying the value in the following parameter ranges: $R_x : 0 - 5^\circ$; $R_y : 0 - 30^\circ$; $R_z : -5 - 0^\circ$; $T_x, T_y, T_z : 0 - 0.5$ cm and $S : 1 - 0.8$. Figure 3 represents the average and the standard deviation of the reconstructed scaling parameter compared to the simulated scaling parameter. The quality of fit is expressed by an $R^2$ of 99.8% ($P < 1\%$).

To stress the reconstruction method we added random noise to every points in the simulated case. Using the same transformation parameters, the noise was spread over increasing circular surface : from 0 to 1 cm in
diameter around the reference points along the coronaries. Figure 4 represents the variation, over increasing noise level, of the regression coefficient between the simulated and the average reconstructed scaling parameter. It can be seen that $R^2$ goes from 99.8% to 96.6% as the noise level goes from 0 to 1 cm.

### 3.2. Clinical cases

The application of our heart motion reconstruction method on clinical cases was similar to the simulated cases except for certain specificities.

During a coronarography examination, the injection of the contrast agent bolus is done separately for the left and right coronary angiogram. To use both the LCA and RCA together, the images must be registered. Since no registering was done with our clinical case angiograms, only the LCA was used when reconstructing the scaling parameter.

With clinical cases, the scaling parameter responsible for the heart contraction, is unknown, hence it cannot be directly compared to the reconstructed scaling parameter. To get an estimation of the clinical case scaling parameter we used instead, the ejection fraction measured by a physician for each case during a ventriculography examination. Using a simple mathematical contraction model we were able to linearize the relation between the ejection fraction and the scaling parameter. In our mathematical contraction model the heart is represented by an hollow ellipsoid and the pericardium volume is kept constant throughout the contraction cycle. Using rotation, translation and scaling transformation parameters, the reconstruction of the clinical cases heart movement was realized, giving satisfactory results for 5 out of 10 cases. In two cases, the scaling was reversed : instead of having a concave curve shape, contraction followed by dilation, the curve was convex. In three other cases, the scaling curve follows an erratic pattern. To alleviate such problems, a second round of reconstructions was undertaken by dropping the rotation and translation parameters, using only the scaling parameters.

Figure 5 represents the relation between the (minimum) reconstructed scaling parameter and the ejection fraction with the theoretical trend based on our heart contraction mathematical model. By linearizing the relation between the reconstructed scaling parameter and the measured ejection fraction, using a mathematical contraction model, we were able to obtain a correlation of $R^2 = 57\%$ with $P < 1\%$. 

![Figure 4](image-url)  
**Figure 4.** Evolution of the reconstructed scaling parameter over different noise level. The regression coefficient between the average reconstructed and simulated scaling parameter is plotted against increasing noise level. The average is done over the 25 subject models. As expected, the trend of the regressions decreases as the noise level increases.
4. DISCUSSION

4.1. Comparison between weak perspective and full perspective projection model

When doing a reconstruction of the isotropic scaling parameter, the minimization process is based on the projection of our heart model, Sect. 2.4. Two geometric projection models were used: the full perspective camera model (FP) or pinhole model and the weak perspective camera model (WP). Contrary to FP, in WP the location of projected points do not depend on individual depth coordinates but rather on the average depth information. Even if this is an approximation, the WP has the advantage of linearizing the FP equation. Besides, when reconstructing the heart movement in FP using rotation, translation and scaling, the depth translation parameter $T_z$ must be set to zero. This is because translating a point away or toward the center of projection gives the same result than applying a decreasing or increasing scaling factor respectively. For these reasons, the WP projection model was preferred over the FP model.

4.2. Heart contraction simulation

As expected, the correlation between the scaling factor used for the simulated contraction and the one obtained by the reconstruction, decreases with the noise level, from $R^2 = 99.8\%$ to $96.6\%$ ($P < 1\%$), see Fig. 4. The average of the scaling parameters over the 25 subject models might explain partially the high correlation even in the presence of relatively high noise, the average smoothing out individual variations.

Since only the LCA was considered in the clinical cases, we tested the effects of reconstructing from the LCA versus RCA-LCA. Without adding noise, the correlation between the average reconstructed scaling parameter and the simulated target is still high ($R^2 = 98\%, P < 1\%$) when using only the LCA, compared to $R^2 = 99.8\%$ ($P < 1\%$) when using the LCA-RCA.

4.3. Clinical cases

The difficulties encountered during the reconstruction process undertaken from clinical cases when using all 6 parameters from rotation, translation and scaling transformations might be explained by the misregistration of reference points. In some cases, anatomical landmarks were difficult to identify. It might also be noted that the spatial distribution of reference points is more concentrated near the root of the arterial tree than the apex, see Fig. 1, probably creating an ill-conditioned reconstruction process.
During the reconstruction process, each of the 6 parameters have the same weight. Although constraints were imposed, for example rotations were limited to ±π/8 radians and the scaling parameter was positive, no a priori information on the behavior of the parameters was given. In specific case, it has been observed that a shift in one parameter, inverse the scaling curve until the system finds a new stable configuration. As if, at certain moments a parameter becomes dominant in the minimization process. This is what happens when over-parameterizing a model. In such cases, it is well known that reducing the number of parameters could improve the conditioning of the problem and the robustness of the solution, this is why we focused on the scaling parameter afterward. Since the minimization process depends on the center of contraction, by placing it in the left ventricle slightly shifted toward the apex of the heart, in concomitance with Potel et al.,3,20 we obtained the best scaling curve shapes and best relation between the scaling parameter and ejection fraction, Fig. 5. Although Potel et al. found that using a moving center of contraction best describes the radial heart wall motion, we used a fixed center of contraction.

5. CONCLUSION

We have presented a model-based method to recover a scaling index, similar to the ejection fraction index, from single-plane coronary cineangiograms. The method relies on the minimization of the RMS distances from reference points along the main arteries and the projected points of a model.

In simulations, our method recover more than 95% of the original contraction, expressed as a scaling parameter. Using 10 clinical cases, we compared our contraction index to the measured ejection fraction and found a coefficient of determination of 57% (P < 1%).

Difficulties were encountered while reconstructing the 3D heart contraction of clinical cases. Some solutions might come from the use of more reference points on the epicardium with more LCA branches and/or a registered RCA. A moving-center-of-contraction model could also mimic more accurately the heart contraction. However, we believe that more complex deformation models (e.g. using torsion amongst others) would probably not be suitable because of the poor conditioning of this problem.

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