

## A numerical 3D coronary tree model

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### Abstract

We present a method that defines a numerical 3D model of the main coronary arteries of the human heart at end-diastole. The data used in this article are a subset of the data used in two articles by Dodge et al. [1, 2]. 26 subjects with normal hearts, having measures for the 3 main arteries (right coronary artery, left anterior descending artery and left circumflex artery), were chosen. The method used to obtain the heart model can be summarized as follows: A well-formed subject is chosen as the reference. Subsequently, each of the other subjects is fitted to the reference with affine transformations (translation, rotation and scaling). The model is obtained by applying the mean of the inverse affine transformations back on the reference coronary tree. This model is the first step for the 3D construction of an atlas of the structure and motion of coronary arteries for cardiac contraction analysis.

**Keyword:** 3D, coronary, model

### 1. Introduction

When confronted with the task of recovering 3D information of the coronary arteries from angiographic images, one can use multiple views [3, 4], but due to the structure of the coronary tree, there exist a large number of possible ambiguities. The use of a priori knowledge in the form of a qualitative model [5], quantitative model [6], or a combination of both [7], helps alleviate these ambiguities. The use of a model can also help in the reconstruction of coronary arteries from a single view cineangiogram [8, 7]. Qualitative models can contain information in the form of a graph structure used for labeling purposes, quantitative models can be expressed with global shape descriptors as in a parametrically deformable model [9] or with more local attributes, like the location and variation of branching points [1]. It is an accepted fact that the location of the coronary arteries is variable, nonetheless certain constancy exists. And even if numerical models do not capture all the subtleties of the coronary tree, they offer certain advantages over the qualitative models, if only for anatomical visualization purposes.

In 1988 Dodge et al. published an article in which they describe the 3D location of branching points, among others, of the coronary tree [1]. An article published in 1992, added information about the lumen diameter at the different reference points [2].

Dodge's articles are often cited in the literature (32, 54 respectively [10]) and a phantom called *Coronix* [11], used in various simulation studies, has also been constructed based on Dodge's data.

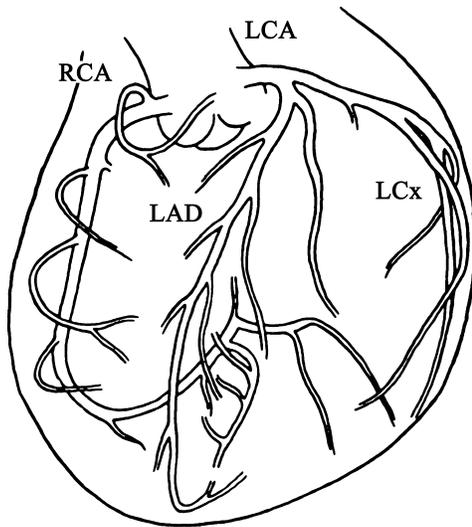


Figure 1. Right coronary artery dominance anatomy. RCA: Right coronary artery; LCA: Left coronary artery; LAD: Left anterior descending; LCx: Left circumflex. From Dodge [1]

Starting with Dodge’s data we made some transformations in order to obtain a model less dependent on certain parameters like the absolute position of the coronary tree or the relative heart size. We are interested in the spatial location of reference points along the coronary tree in order to construct a model that will be used for tracking the motion of coronary arteries.

Each of these main arteries divides themselves into smaller ramifications. The artery that irrigates the heart’s anterior wall is said to define the dominance anatomy. There are three dominance anatomies: the right dominance, left dominance and the balanced anatomy.

## 2. Data

The coronary tree present itself as a hierarchical structure divided in 3 main sections according to the heart region irrigated. We use here a nomenclature devised by Dodge et al. [1], see Figure 1. The left coronary artery (LCA) starts at the left of the aorta as the left main artery (LM) and divides itself into the left anterior descending artery (LAD) and the left circumflex artery (LCx). The right coronary artery (RCA) starts at the right of

the aorta and irrigates the right side of the heart. Each of these main arteries divides themselves into smaller ramifications. The artery that irrigates the heart’s anterior wall is said to define the dominance anatomy. There are three dominance anatomies: the right dominance, left dominance and the balanced anatomy.

The original data comes from the 3D location of 102 points along the coronary tree of 37 normal subjects. The measurements were taken at the end diastole by a biplane angiographic apparatus and were corrected for optical magnification and X-ray beam divergence, see Dodge’s et al. articles for more details [1, 2].

For the elaboration of our model, a subset of the original data was selected, based on certain criteria. We kept only the subjects where the three main arteries were present. Also, the reference points from secondary branches and those having sporadic presence were dropped. We ended up with 26 subjects having a coronary tree composed of 36 reference points. See Table 1 for the demographic description of the subjects.

Age	Gender		Coronary dominance		
	M	F	Left	Balanced	Right
26 to 77 (mean, 48)	23	3	2	22	2

Table 1. Demographic summary

## 3. Methodology

In order to construct a *coronary tree model* that is immune to certain influences, we allow some transformations of the selected subset data. For example, scaling attenuates the inter-subject variation of the overall size of the coronary tree, translation and rotation

bring the coronary tree in a reference space that is less dependent on the relative position between the body and the measuring apparatus.

In a way similar to Guimond et al. [12], the method used for obtaining the heart model can be summarized as follow:

- First, a well-formed subject is chosen as a reference, the *reference subject*;
- Subsequently, the reference subject is fitted to each of the other subjects with affine transformations (translation, rotation and scaling);
- An average of the affine transformations is then computed;
- Finally, the *coronary tree model* is obtained by applying the average transformation on the *reference subject*.

The choice of the well-formed subject is based ... on its well-form! Without large variations to what could be described as an ideal normal subject.

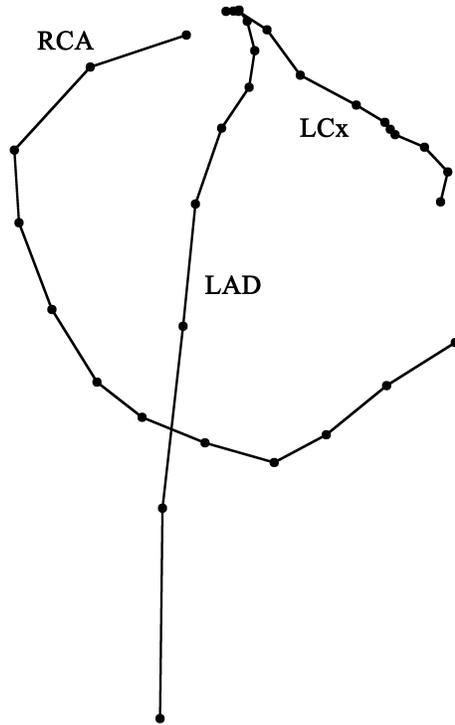
Next, to find the affine transformations we consider this problem as a classic computer vision problem known, among various aliases, as *model-based object location*. It can be stated as follow: knowing the correspondence between two 3D points sets and their locations, find the best geometric transformation that minimize a cost function with respect to certain constraints. Different analytical and numerical techniques exist that solve such problems. Closed form solutions solved by singular value decomposition [13] or represented by orthonormal matrices [14] or unit quaternions [15] exist and they all give similar results [16].

The problem can be formulated as follows: given the relation between two point sets  $\{m_i\}$  and  $\{d_i\}$ ,  $i = 1..N$  as  $d_i = s\mathbf{R}m_i + \mathbf{T} + \mathbf{V}_i$  where  $s$  is a scaling factor,  $\mathbf{R}$  is a  $3 \times 3$  rotation matrix,  $\mathbf{T}$  is a translation vector and  $\mathbf{V}_i$  is a noise vector. We want to find  $\hat{s}$ ,  $\hat{\mathbf{R}}$  and  $\hat{\mathbf{T}}$  that minimize the sum of the Euclidean distances between corresponding points  $\sum_{i=1}^N \|d_i - (\hat{s}\hat{\mathbf{R}}m_i + \hat{\mathbf{T}})\|^2$ . We solve the scaling factor using Horn method [15] and the translation and rotation using the Arun method [13]. The three transformation components can be solved independently. By expressing the points sets by their respective centroids  $\bar{m} = 1/N \sum_{i=1}^N m_i$  and  $\bar{d} = 1/N \sum_{i=1}^N d_i$  as  $m'_i = m_i - \bar{m}$  and  $d'_i = d_i - \bar{d}$ , the translation component is simplified and we are left with the scaling and rotation components only. The scaling is independent from the rotation and can be defined as  $\hat{s} = \sqrt{\sum_{i=1}^N \|d'_i\|^2 / \sum_{i=1}^N \|m'_i\|^2}$ . The solution to the rotation matrix is  $\hat{\mathbf{R}} = \mathbf{V}\mathbf{U}^t$  where the singular value decomposition of the correlation matrix  $\mathbf{H} = \sum_{i=1}^N m'_i d'^t_i$  is  $\mathbf{H} = \mathbf{U}\mathbf{L}\mathbf{V}^t$ . The translation component can then be found by using the rotation matrix on the centroids  $\hat{\mathbf{T}} = \bar{d} - \hat{\mathbf{R}}\bar{m}$ .

As previously stated, the *coronary tree model* results from the application of the average transformations on the *reference subject*.

## 4. Results

After applying the outlined method on the 26 coronary trees, we obtain the *coronary tree model*, see Figure 2. The average coefficients of transformation found after fitting the *reference subject* to the other subjects are:



- for the scaling factor,  $s = 1.08$ ;
- for the rotation expressed as the angles of rotation about the  $x$ ,  $y$ , and  $z$  axes respectively,  $\alpha = -0.04$ ,  $\beta = 0.09$ ,  $\gamma = -0.31$  and
- for the translation component,  $\mathbf{T}_x = 0.59$ ,  $\mathbf{T}_y = 0.18$  and  $\mathbf{T}_z = -0.04$ , corresponding to the translation on the specific axes.

The average distance between the matching points of the *coronary tree model* and the other subjects is 0.84 cm (0.15 SD). This average distance was 1.42 cm (0.45 SD) before applying the mean transformation.

## 5. Conclusions

We have presented a method that composes a model of the main coronary arteries of the human heart based on 3D reconstructions of 26 normal hearts. Although the reference system used by Dodge et al. was adequate for their study, the proposed method focuses on the morphological variations and considerably reduces the variability observed by their group by eliminating heart size, orientation and position

Figure 2. Wire-frame of the *coronary tree model* with an angle of view similar to Figure 1. See Figure 1 for definitions.

variations. This model is the first step for a more general 3D atlas of the structure and motion of coronary arteries that will help cardiac contraction analysis and understanding.

## Acknowledgements

The authors express their gratitude to Dr J. Theodore Dodge Jr. for having so generously shared his data.

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