Towards Personalised Aortic Valve Prostheses: A Compact Description of the Individual Valve Geometry

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Abstract

Although the geometry of the aortic valve is highly patient-specific, state-of-the-art prostheses are not capable of reproducing this individual shape. Promising results in the field of tissue engineering move the goal of the fabrication of personalized aortic valve prostheses within reach. However, there is no study on the degree of personalization that is needed, aiming at finding a trade-off between the patient's outcome and economical or logistical issues. One problem in performing such a study is the lack of a compact, unified description of the individual aortic valve shape, which is needed to perform automatic pattern analysis. In this work, we present such a description which is derived model-free and directly from experimental data. For this purpose, we set up a suitable data base of porcine aortic valve shapes. We used principal component analysis for dimensionality reduction and analyzed the minimal number of values in the representation preserving all relevant information. We could show that an accurate representation of the shape of the aortic valve leaflets is possible with no more than 39 values. This representation makes geometrical pattern analysis possible and presents an important step towards personalized cardiovascular prostheses.

1. Introduction

The geometry of the aortic valve is highly patient-specific [1]. The valve apparatus with its three leaflets and the aortic root form a complex biomechanical system where all geometric parameters are interdependant. Especially the size and shape of the three leaflets differs significantly [2]. Studies indicate that even small changes of this specific geometry can cause severe changes in the whole blood cycle, up to an increased short-term mortality [3], [4]. However, state-of-the-art aortic valve prostheses are hardly capable of reproducing this individual geometry. While mechanical prostheses are shaped completely differently, biological prostheses are symmetric, i.e. the three leaflets are equally sized and shaped [5]. Due to this drawback, the field of tissue engineered heart valve prostheses advanced during the last years [6]. The aim is to cultivate cells on an electro-spinned scaffold. By shaping the scaffold, a personalization of the valve prosthesis is possible. Even though the possibility of personalized prosthesis manufacturing seems achievable, there are no studies on the degree of personalization that is necessary to provide an adequate prosthesis for each patient. The question whether a perfect reconstruction of the whole valve shape is superior compared to a specific number of generic valve types that could be provided remains unclear. One way to analyze this question would be to collect a data base containing a significant number of aortic valve geometries, including their leaflet shapes, and perform clustering on this data base. Like this, possible valve types could be found and analyzed. However, clustering in the potentially high-dimensional data, for example imaging data, would suffer from the effect known as the curse of dimensionality [7]. Hence, a compact representation of the individual valve geometry, i.e. the image data, is needed to ensure a suitable clustering quality.

In this work, we present an approach to derive this compact valve representation directly from acquired image data. The method works model-free and completely data-driven. For this purpose, we set up a suitable data base and perform a linear decomposition of the image data using *Principal Component Analysis* (PCA). We analyze the reconstruction quality of the images in dependence of the dimensionality of the representation. Furthermore, we evaluate the model performance concerning the reconstruction of the leaflet shape and the reconstruction of its inner structure, i.e. the location of the prominent collagen fibers [8].

2. Material and Methods

Biological aortic valve prostheses can be stented or unstented. What both types have in common are the three leaflets, that, in case of a personalization, should be shaped according to the patient's individual geometry. Hence, the focus of this work is to describe the shape of the three

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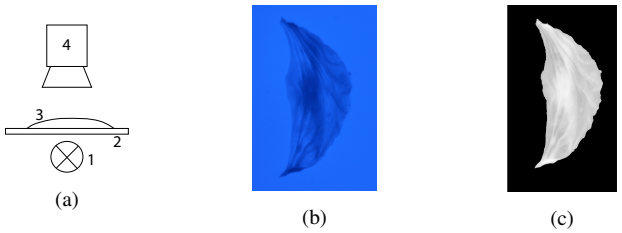

Figure 1: Data base setup. (a) Sketch of the imaging procedure with light source (1), diffusing plate (2), leaflet (3) and camera (4). (b) Example of raw leaflet image. The collagen fibers are clearly visible. (c) Preprocessed leaflet image.

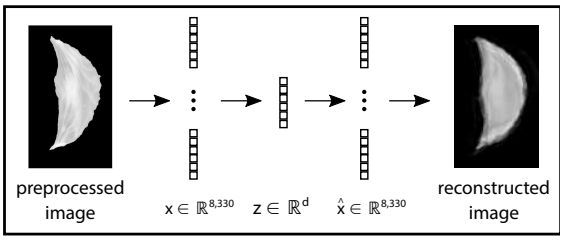

Figure 2: Outline of the proposed method. The raw image is preprocessed and represented as a vector x. This vector is decomposed using PCA and represented by d values in its compact representation z. From this representation, the image can be reconstructed.

leaflets in a compact way. To simplify the description, we measure the planar shape of the leaflets. This allows data acquisition with a high resolution, including the imaging of the inner structure of the leaflets, which is not possible with classical volumetric imaging modalities. Our work is divided into three steps: The generation of a suitable data base, the image decomposition to derive a compact representation and the evaluation of this representation. The single steps are described in more detail in the following paragraphs.

2.1. Data Base Generation and Preprocessing

In this initial study, we analyzed the shape of ex-vivo porcine aortic valves. The pig hearts were bought at a slaughterhouse, so there are no ethical concerns arising from this study. From the whole heart, the aortic root was extracted and opened by a vertical cut through the aorta. This cut was positioned right in between the right-coronary and non-coronary sinus to not damage the leaflets. Afterwards, the leaflets were cut off the aortic root wall along the commissure lines. The leaflets were spread on an optical diffusion plate (see Fig. 1 a). Special attention has been paid to the preservation of the natural shape with minimal deformation. The plate was backlit with blue light (470 nm) and we took a photograph from above (see Fig. 1 a). The diffusing plate provides homogenous illumination. The blue light is absorbed in collagen tissue, resulting in a high contrast of the leaflet and its inner structure. Especially, the prominent collagen fibers on the leaflets are clearly visible (see Fig. 1 b). This method was performed on 10 porcine aortic valves, resulting in images of 30 leaflets, i.e. 10 right-coronary, 10 left-coronary and 10 non-coronary ones.

The data acquisition was followed by a preprocessing pipeline. Aiming at a suitable, unified representation of the leaflets, the steps of this pipeline are described in the following. First, the images were cropped manually to extract images of the single leaflets. Each image was converted to grayscale (ranging from 0 to 255) and inverted, resulting in an image corresponding to a thickness profile. To avoid noise around the leaflet, a mask was created. For this purpose, the leaflet was segmented using thresholding. The threshold was defined manually and was set to 167. Because very thin areas of the leaflet could result in holes in this segmentation, a morphological closing was applied. The structural element was a circle with a radius of 10 pixels. The resulting leaflet segmentation served as a mask and all pixels in the image outside of the segmented region were set to 0. Like this, noise around the leaflet is cut away while the inner structure of the leaflet is preserved. The images were downsampled to the unified size of 119 x 70 pixels with a resolution of $0.37 \frac{mm}{pixel}$. Finally, the leaflet was translated such that its center of mass lies in the center of the image (see Fig. 1 c).

2.2. Derivation of Compact Representation

The images were represented as vectors of $119 \cdot 70 = 8,330$ elements, respectively. The transformation between the image space and the compact representation should be unique in both directions, i.e. image compression as well as image reconstruction from the compact representation should be possible. Hence, a dimensionality reduction technique with an embedded model is needed. The *Principal Component Analysis* (PCA) is such a technique.

As the images in our data base are represented as vectors, we could construct a data matrix $X \in \mathbb{R}^{8,330 \times 30}$. We performed a PCA on the whole data set, receiving a mapping U_d depending on d, the number of principal components taken into account for the reconstruction. This number is limited by the number of training data points, i.e. the maximum number of principal components we can derive from our dataset is 29, which is one less than the number of images in our data base. Fig. 2 shows an overview of the decomposition and the reconstruction.

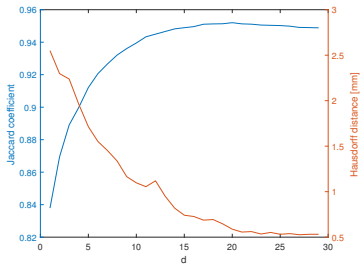

Figure 3: Reconstruction accuracy of the leaflet shape, given as mean Jaccard coefficient (blue) and mean Hausdorff distance (red) over all leaflets.

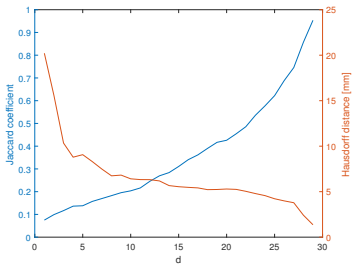

Figure 4: Reconstruction accuracy of the prominent collagen fibers, given as mean Jaccard coefficient (blue) and mean Hausdorff distance (red) over all leaflets.

2.3. Evaluation Method

As described above, we are able to derive a compact representation of the leaflet images using PCA. We examined the influence of the parameter d to find a trade-off between dimensionality reduction and reconstruction accuracy. The aim of this analysis is twofold: First, we want to examine whether it is possible to reconstruct the shape of the leaflet from the compact representation. Furthermore, we want to analyze whether the inner structure of the leaflet, i.e. the location of the prominent collagen fibers, can be reconstructed. As the principal components are sorted by the percentage of variance in the data set explained by the component, respectively, we can assume that there is a number of d_{shape} components that carry enough information to reconstruct the leaflet shape (this also holds for a value d_{fibers}). Of course, these conditions only hold if the linear decomposition itself is sufficient for these problems. To find the values for d_{shape} and d_{fibers}, we analyzed the reconstruction accuracy depending on the number of principal components included in the reconstruction. For this purpose, we reconstructed each leaflet in the data base with a number of included components ranging from 1 to 30. To analyze the capability of the model to represent the shape of the leaflets, the images, i.e. the ground truth as well as the reconstruction, were segmented using thresholding. This segmentation threshold was set to 65 manually. Like this, the inner structure of the leaflet is ignored and artifacts around the leaflet arising from the linear composition are removed from the reconstruction. To compare the two segmentations, we used the Jaccard coefficient and the Hausdorff distance. Both are commonly used metrics to evaluate the segmentation overlap (Jaccard coefficient) and the distance between two contours (Hausdorff distance). Additionally, in a second study, we applied a segmentation threshold of 197 to the ground truth and the reconstruction to extract the prominent collagen fibers. The treshold was adjusted manually. By comparing these segmentaion, an analysis of the capability of the model to represent the inner structure of the leaflet was possible. Once again, the Jaccard coefficient and the Hausdorff distance served as error metrics.

3. Results and Discussion

We performed a PCA on the whole data set of 30 leaflet images. Fig. 3 shows the reconstruction accuracy of the leaflet shape. At about $d_{shape} = 13$, the Jaccard-coefficient saturates at a level of about 0.95, while the Hausdorff distance is below 1 mm. The reconstruction accuracy for the collagen fibers is shown in Fig. 4. The Jaccard-coefficient is significantly smaller than for the shape reconstruction, while the Hausdorff distance is higher. There is no sign of a saturation of the metrics. Fig. 5 shows examples of reconstructed leaflet shapes and the ground truths. In this case, the reconstruction was performed using 13 principal components. The blue coloured overlay are the segmented collagen fibers.

As described above, a saturation of the Jaccard coefficient is clearly visible for the reconstruction of the leaflet shape. This saturation starts at about $d_{shape} = 13$ and indicates that this number of principal components carries enough information to describe the shape of an individual leaflet. The Hausdorff distance falls a little with increasing d_{shape}, but it is below $1mm$ at $d_{shape} = 13$ which is a maximal distance of less than three pixels. Hence, it lies in the range of inaccuracies of the imaging and preprocessing methods. The absolute error values in the saturation (Jaccard coefficient: about 0.95, Hausdorff distance: below $1mm$) are acceptable. The qualitative analysis shows that the shape of the individual leaflets are matched very well and that the algorithm is capable of identifying specific leaflet types, for example slender, bulbous or sheared leaflets. Hence, a linear decomposition of the images seems to be sufficient to describe the shape of the aortic valve leaflets in a compact way.

The analysis of the capability of reconstructing the inner structure did not yield appropriate results. There is no sign

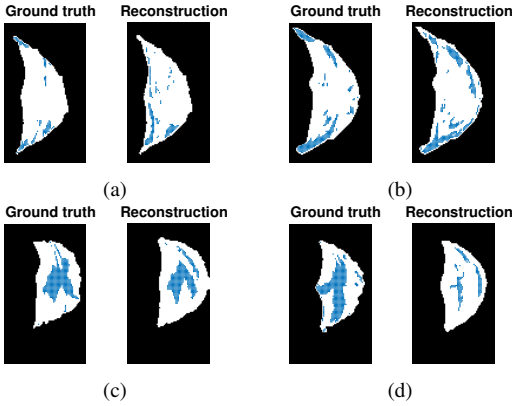

Figure 5: Example results of the reconstruction of right-coronary leaflets with $d_{shape} = d_{fibers} = 13$, listed from (a) to (d) with the ground truth and the reconstruction, respectively. The blue coloured areas are the location of the prominent collagen fibers.

of saturation visible, both error metrics are on a rising or falling edge, respectively. Even the smallest error values reached by the maximum number of d_{fibers} are poor. This indicates that the location of the prominent collagen fibers can not be represented with a linear decomposition technique. This might be due to the fact that the course of the fibers seems to appear non-linear. However, the qualitative analysis reveils that in some cases, a rough estimation of the prominent fibers position on the leaflet can be made even though an exact localization seems impossible.

Our study shows that a model-free derivation of a compact representation of the aortic valves leaflet's shape can be performed using PCA. Hence, an analysis of the inter-patient variability of the valve geometry as well as clustering studies to find patterns in this variability are possible. For this purpose, we could show that the individual geometry of an aortic valve, defined by the shape of its three leaflets, can be represented by $3 \cdot 13 = 39$ values. In such a dimensionality, clustering is possible without facing the curse of dimensionality. However, this initial study is limited by the size of the data base. Future work should aim on an increased data base to receive representative sample of the valve geometry variability to enable clustering techniques. Another limitation of this study is the linearity of the image decomposition technique. Especially the inner structure of the leaflet seems to be of non-linear nature. Unfortunately, many methods for non-linear dimensionality reduction face the problem that the reconstruction of the image data from its compact representation is not trivial or even impossible [9]. One possibility to find a non-linear decomposition while the transformation is known are deep autoencoders However, this method is not trustworthy on a data base of this size, which in turn underlines the necessity to increase it.

To the best of our knowledge, we proposed the first model-free, data driven compact representation of the individual geometry of the aortic valve. For this purpose, we set up a data base consisting of images of the leaflets of 10 ex-vivo porcine aortic valves, resulting in 30 leaflet images. We presented an image decomposition for dimensionality reduction. Our analysis shows that the shape of the aortic valve can be described with 39 values. This work represents the basis for the analysis of the demand for personalization of aortic valve prostheses. Hence, our study is an important step on the way towards personalized cardiovascular implants.

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