

A Novel Explicit 2D+t Cyclic Shape Model Applied to Echocardiography

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Abstract. In this paper, we propose a novel explicit 2D+t cyclic shape model that extends the Point Distribution Model (PDM) to shapes like myocardial contours with cyclic dynamics. We also propose an extension to Procrustes alignment that removes pose and subject size variability while maintaining dynamic effects. Our model draws on ideas from Principal Component Analysis (PCA), Multidimensional Scaling (MDS) and Kernel PCA (KPCA) and solves 3 shortcomings of previous implicit models: 1) cardiac cycles in the data set do not each need to have the same number of frames, 2) the required number of subjects for statistically significant results is substantially reduced and 3) the displacement of contour points incorporates time as an explicit variable. We illustrate our method by computing models of the myocardium in the 4 principal planes of 2D+t echocardiography data.

1 Background

Principal Component Analysis (PCA) [1], also known as the Karhunen-Loève transform, is one of the most popular methods in Statistics for modeling, dimensionality reduction and denoising, and widely employed in biomedical image analysis. It was introduced into the computer vision literature as a dimensionality reduction method for face images [2]. PCA finds a basis of orthonormal vectors that span the data set. The first vector is in the direction of maximum variance of the data. The next component has the direction of maximum variance amongst those orthogonal to the first, and so on. Cootes et al. [3] proposed computing a shape space by applying PCA to Procrustes aligned point configurations, and called it the Point Distribution Model (PDM)

$$x = \bar{x} + V \cdot b \quad (1)$$

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where \bar{x} is the mean shape, V is the shape space matrix, and b is the *coefficient or Principal Components (PC)* vector. In this model, x is a vector with the Euclidean uv -coordinates of $n/2$ points or landmarks

$$x_{2D} = [u(1), \dots, u(n/2), v(1), \dots, v(n/2)]^\top \quad (2)$$

One of the main applications of the PDM in medical imaging is to provide a shape space on which segmentation boundaries can be constrained to physiologically viable organs. In terms of statistical analysis, x is a vector with n random variables. The model is learned from a training set of M examples $X = [x_1, \dots, x_M]$. The mean shape is $\bar{x} = 1/M \sum_{i=1}^M x_i$. The eigenvectors or *loading vectors* $V = [v_1, \dots, v_M]$ are computed using PCA; that is, as solutions to the eigenproblem $Sv = \lambda v$, where λ is an eigenvalue, and S is the covariance matrix $S = \frac{1}{M} \tilde{X} \tilde{X}^\top$ of the centered training set \tilde{X} with elements $\tilde{x}_i = x_i - \bar{x}$.

This formulation is not restricted to 2D, and can be generalized to 3D or higher dimensions. PCA has been used in computer vision to build 2D or 3D deformable models with uncorrelated modes of variation, e.g. in Active Shape Models (ASMs) [4] or Active Appearance Models (AAMs) [5, 6]. Some medical imaging modalities, especially echocardiography, depend strongly on temporal information, and implicit time extensions have been proposed to 2D and 3D PCA models [7, 8]. Such models are implicit because instead of adding a time variable, they are built from the concatenation of shape vectors

$$x_{\text{implicit } 2D+t} = [x_{2D}^{1\top}, x_{2D}^{2\top}, \dots, x_{2D}^{F\top}]^\top \quad (3)$$

where x_{2D}^i is the shape at time $t(i)$. Then PCA is computed in the usual way. This approach, which we call the implicit 2D+t model, has 3 important shortcomings. First, all cardiac cycles in the data set need to have the same number of frames; considering the variability of heart rates in subjects and sampling rates between studies, this is never going to be the case in practice. Thus, it becomes necessary to interpolate the image data to a fixed number of frames, a hard and computationally expensive problem that requires 2D+t volume registration and can introduce new artifacts, e.g. double edges.

Second, even though linear models are relatively immune to the curse of dimensionality problem, in order to start obtaining significant results with PCA, the number of training samples M needs in principle to increase linearly with the number of variables n [9]. When F frames are stacked together, the size of the data set is reduced by a factor F , and the number of variables increases by the same amount. That is, implicit 2D+t models require $\mathcal{O}(F^2)$ times more subjects than simple 2D to approximate the data. With $F \approx 16$ in typical studies, this becomes effectively infeasible. A computational issue also arises, even if there is enough data, as the matrices of the eigenproblem are very large.

Third, implicit 2D+t models assume that consecutively occurring positions of the same landmark are separate independent variables, while it is more realistic and informative to model the variability of each point as a 2-dimensional random variable that changes with time.

The main contribution of this paper is to propose a novel explicit 2D+t cyclic shape model that addresses the above shortcomings. We also propose an extension to Procrustes alignment that removes pose and subject size variability while maintaining dynamic effects. We illustrate our new method by computing 2D+t models from expert traced contours of the myocardium in the 4 principal planes of 2D+t echocardiography data.

2 Method

It may seem that a 3D model [6] could be used for 2D+t, just by replacing the third spatial coordinate by time. But because all the contour points in the same frame share the same value of t , this is equivalent to concatenating the same variable n times to the shape vector. It follows that the determinant $|S| = 0$, and it is not so straightforward to solve the eigenproblem. To avoid this, we propose an extended shape vector with a single time variable $t \in [0, 1]$

$$x_{\text{explicit 2D+t}} = [x_{2D}^{\top}, rt]^{\top} \quad (4)$$

where r is a scaling factor that will be discussed below. The vector in Eq. (4) has important shortcomings of its own for cyclic dynamics. Fig. 1a illustrates the typical horizontal displacement of a 2D contour point in the middle of the left wall of a 2-chamber view. First, the horseshoe-like curve means that any linear model such as PCA will poorly approximate the relationship between spatial coordinates and time. Second, PCA is dual to linear Multidimensional Scaling (MDS) [10], where the distance matrix is defined by the scalar products between the training vectors, i.e. PCA tries to preserve Euclidean distances between training vectors. In Fig. 1a, points near $t = 0$ and $t = 1$ are far apart according to the Euclidean distance for the model; in reality, we know that they are close in the cardiac cycle.

We contend that both the lack of linearity and the distance problem can be tackled with Kernel PCA (KPCA) [11], a non-linear generalization of PCA. The main idea that we borrow from KPCA is that shape+time vectors can be mapped to a higher dimensional space in which the relations between variables are linear, and then we can compute PCA in that space. We propose the transformation

$$x_{\text{explicit 2D+t}} = [x_{2D}^{\top}, rt_1, rt_2]^{\top} \quad (5a)$$

$$t_1 = \cos(2\pi t) \quad (5b)$$

$$t_2 = \sin(2\pi t) \quad (5c)$$

To define r , it should be noted 1) that PCA searches not only for those directions in which relationships between variables are more linear, but also for those with larger variance; and 2) that because there are many more shape than time variables, the model tends to underestimate the temporal effect. We propose

$$r = \sqrt{\frac{\sum_{i=1}^{n/2} \text{Var}(u(i)) + \sum_{i=1}^{n/2} \text{Var}(v(i))}{\text{Var}(t_1) + \text{Var}(t_2)}} \quad (6)$$

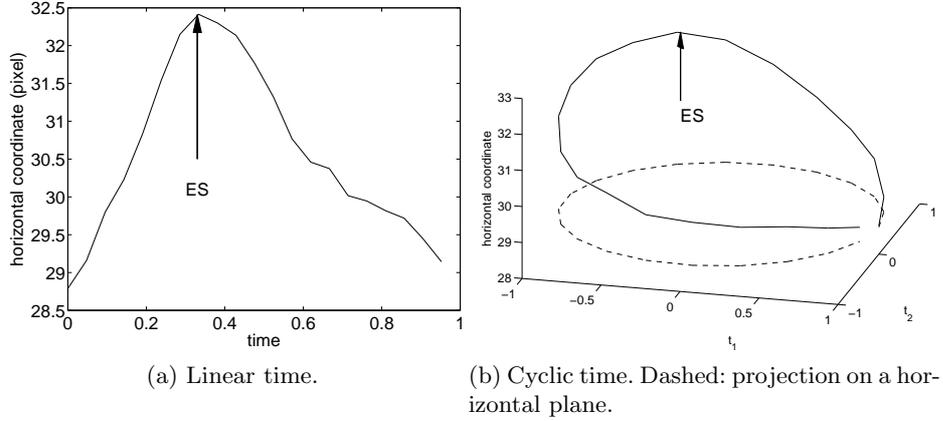


Fig. 1: Mean horizontal coordinate of a 2D contour point in the middle of the left wall of a 2-chamber view (see point marked with a ‘o’ in Fig. 3a). Curve computed as the mean of 21 subjects. Time for the cardiac cycle has been normalized to $t \in [0, 1]$, with $t = 0$ end diastole. The arrow points to end systole (ES). Coordinate units are pixels.

so that the total variance contributed to the model by shape variables is the same as that contributed by time variables, where the variance estimate Var is computed over the sample of size M .

While KPCA usually maps the data to a much higher dimensional space and uses MDS and the kernel trick to make computations tractable, Eq. (5) only increases the dimensionality by 2, so it is possible to work directly in feature space. Fig. 1b illustrates the advantages of the map in Eq. (5). First, the curve and the manifold that contains it can be reasonably approximated by an ellipse and a plane, respectively, which suggests a good linear approximation $u \approx \alpha_1 t_1 + \alpha_2 t_2$ for some scalars α_1, α_2 . And second, the points near $t = 0$ and $t = 1$ are now close in Euclidean distance.

The PDM of Eq. (1) can now be expanded using Eq. (5). In centered block matrix form we have

$$\begin{bmatrix} \tilde{x} \\ r\tilde{t}' \end{bmatrix} = \begin{bmatrix} V_{1,1} & V_{1,2} \\ V_{2,1} & V_{2,2} \end{bmatrix} \begin{bmatrix} b' \\ b_r \end{bmatrix} \quad (7)$$

where $t' = [t_1, t_2]^\top$, $b' = [b_1, b_2]^\top$. An explicit relationship between shape and time can be obtained noticing that

$$\tilde{x} = V_{1,1}b' + V_{1,2}b_r \quad (8a)$$

$$r\tilde{t}' = V_{2,1}b' + V_{2,2}b_r \quad (8b)$$

Substituting $[b_1, b_2]^\top$ from Eq. (8b) in Eq. (8a), and uncentering \tilde{x} , the shape model can be formulated as

$$x = c + A_b b_r + A_t t' \quad (9a)$$

$$c = \bar{x} - A_t \bar{t}' \quad (9b)$$

$$A_t = r V_{1,1} V_{2,1}^{-1} \quad (9c)$$

$$A_b = -\frac{1}{r} A_t V_{2,2} + V_{1,2} \quad (9d)$$

Finally, we propose an extension to Procrustes alignment for 2D+t data. Procrustes alignment is used to remove pose and subject size variability from the training set. But if it is applied to a stack of our 2D+t contours, then temporal variability is removed too. Procrustes alignment could be applied to $x_{\text{implicit } 2D+t}$ vectors, as in AAMM, but then it would be necessary to interpolate each volume to the same number of frames. Instead, we propose applying standard Procrustes alignment (e.g. Least-Squares Fit Generalized Orthogonal Procrustes Analysis [12]) to the mean shape \bar{x} of each cardiac cycle. Procrustes alignment computes a similarity transformation for each mean shape (translation, scaling and rotation) that can be applied to each frame of the corresponding volume. This method is illustrated by Fig. 2.

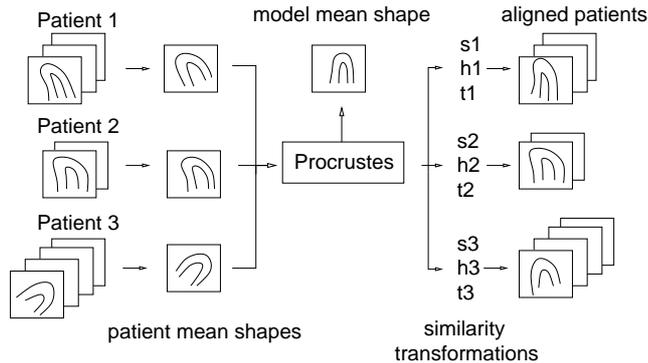


Fig. 2: Procrustes alignment for 2D+t data. Similarity transformations are composed of a scaling s , a rotation h and a translation t .

3 Results

To illustrate our method, we computed 2D+t models using Eq. (9) on 21 contrast echocardiography studies at rest in the 4 standard planes: 2-, 3- and 4-chamber (2C, 3C, 4C) and short axis (SAX). Contours for the endocardium and epicardium were traced by 2 experts, who placed anatomical landmarks (6 in

apical, 2 in SAX). Pseudolandmarks were interpolated at equal arclengths (to a total of 50 in apical, 30 in SAX), and aligned using the method in Fig. 2.

The time effect was studied making $b_r = 0$ and sampling $t \in [0, 1]$ uniformly at 11 instants. For the 2C plane all resulting contours were plotted together in Fig. 3a. A point on the endocardium was selected and marked with a ‘o’ to help visualize its displacement. The modelled horizontal displacement of the 2C point in Fig. 3b is a good approximation of the empirical one in Fig. 1a, and seems to reflect the temporal effect sensibly, although with a limitation: the model does not reflect the asymmetry of the data, so all points in the model show a small phase shift $\Delta t = .07$, with the end systole (ES) peak moving from $t_{\text{ES}} = 0.33$ to $t_{\text{ES}} = 0.40$. Different regions of the endocardium display different degrees of excursion and larger than for the epicardium, as would be expected. Fig. 4 shows results for the other planes. Quite interestingly, the SAX plane model has counterclockwise rotation in the endocardium and clockwise in the epicardium, an indication of torsion.

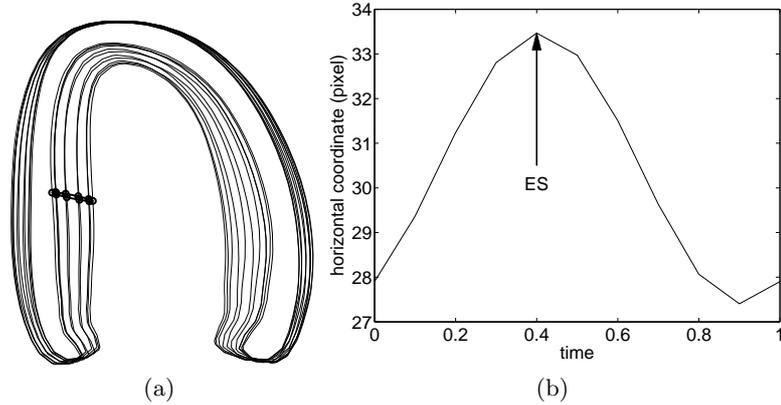


Fig. 3: Endocardium and epicardium in 2C plane cyclic time linear PCA model using Eq. (9). Time variation with $b_r = 0$. The model was trained on the same data as Fig. 1. (a) One cardiac cycle sampled at 11 instants in $t \in [0, 1]$. The ‘o’ marks the point selected to plot the horizontal displacement in (b).

The shape coefficients effect was studied by setting $t = 0$. Fig. 5 displays the first 4 modes of variation for the 2C plane. For the i -th mode we plotted curves for coefficient values in $-3\sigma_i \leq b_r(i) \leq 3\sigma_i$, to point out that extreme coefficient values can generate spurious shapes. The results suggest that contractility dynamics have been largely removed from the shape coefficients, and are modelled by the time variable.

The first coefficients appear to have a physiological interpretation: Mode 1 controls the elongation of the ventricle, while mode 2 controls the thickness of the myocardium.

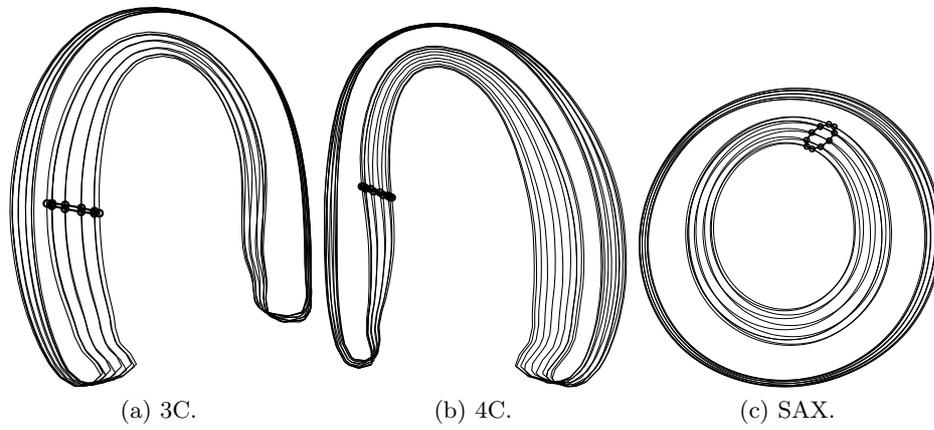


Fig. 4: Similar to Fig. 3a, for the other 3 principal echocardiography planes.

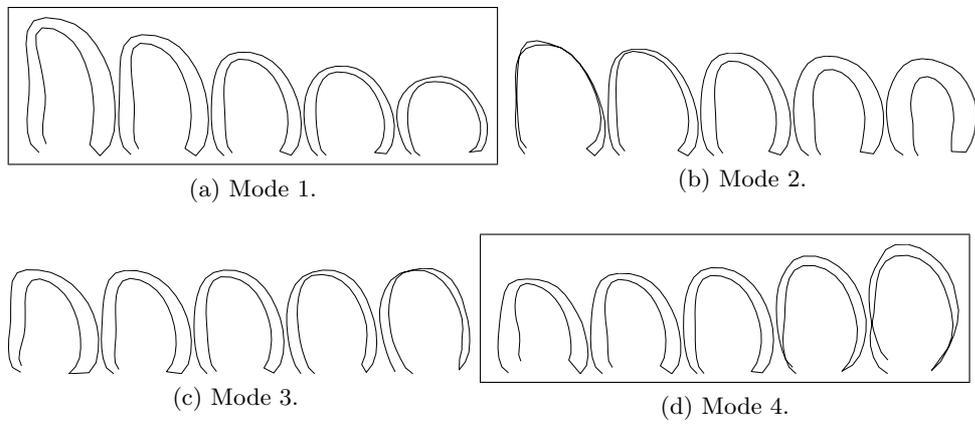


Fig. 5: 2C plane cyclic time linear PCA model using Eq. (9). Shape coefficient variation $\pm 3\sigma$ in first frame ($t = 0$).

4 Discussion

In this paper we have presented a novel explicit 2D+t cyclic shape model that we contend is better suited to cyclic dynamics than previous implicit models. Our model is built on observations drawn from PCA, MDS and KPCA theory to offer a linear approximation of cyclic data. A limitation of the model is that it can not express asymmetries in the displacement of contour points well, and thus suffers from a small phase shift. Future work will be finding a reparameterization of the displacement curve to take into account said asymmetries. Otherwise, it provides a sensible approximation to the expected dynamics of human hearts adding just 2 time variable to shape vectors. We have also presented an extension to Procrustes Analysis that maintains temporal effects in heart dynamics while removing pose and subject size variability. Finally, while our presentation and experiments have been limited to echocardiography 2D+t data, the model itself is not limited in dimensionality or imaging modality, and could be easily extended to 3D+t studies using 3D Procrustes Alignment [6], or applied to data extracted from other modalities, e.g. MRI. It could also accommodate other cyclic effects, e.g. respiration in liver imaging.

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