

Parameter Reduction and Automatic Generation of Active Shape Models

David Liersch, Abhijit Sovakar, Leif P. Kobbelt

Computer Graphics Group, RWTH Aachen, 52056 Aachen
Email: david.liersch@post.rwth-aachen.de

Abstract. In this paper we propose an alternative method to build Active Shape Models. It avoids the use of explicit landmarks since it represents shapes by normal displacements relative to an average (domain) contour. By this we reduce the redundancy of the model and consequently the number of parameters in our representation. The resulting models have a significantly lower algebraic complexity compared to those based on landmarks. Additionally we show how to automate the generation of ASMs from sets of unprocessed training contours in arbitrary representation.

1 Introduction

Automatic and reliable detection of contours in 2D and 3D image data is an important tool in the field of medical image processing. However, noisy artifacts and low contrast usually complicate this segmentation process and hence, suitable image processing techniques have to compensate these difficulties.

Digital filters can reduce the noise level and extract gradient or edge information from the images [1] but usually they do not provide topological guarantees for the contours since the classification is mostly done on a per pixel basis. Active Contours [2] improve the reliability of the segmentation by exploiting knowledge about geometrical and topological properties: a contour is assumed to be locally smooth and globally connected. Active Shape Models (ASM) [3] go one step further by taking statistical knowledge about the expected shape variations into account. A set of training contours is analysed in a pre-process and the contour detection is then restricted to “plausible” shapes. Consequently, ASMs are particularly effective for medical applications [4] whenever organic structures can be described by a (healthy) average anatomy and a set of typical (pathological) deviations.

ASM is a purely algebraic approach to extract the major shape variations from a given set of training contours. In the standard setup, a set of specific landmarks is (manually) picked on each training contour and the coordinates of the landmark positions are concatenated to build a feature vector. By applying a Principal Component Analysis (PCA) to the set of training feature vectors, we find the major axes of the shape variations. The basis transform induced by the PCA provides a mapping from the space of feature vectors to model parameters.

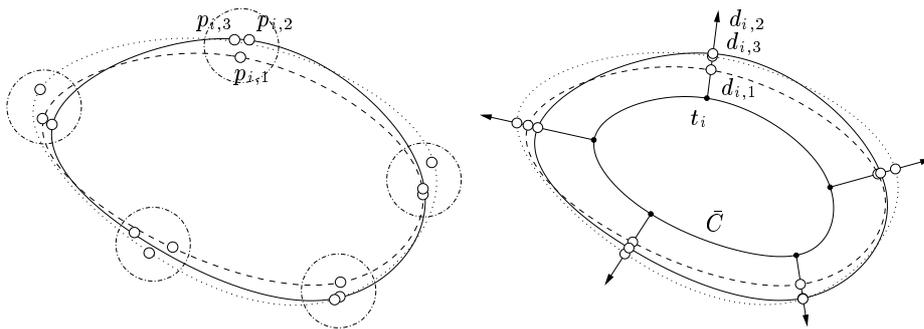


Fig. 1. In the standard ASM setup (left) a set of landmarks $p_{i,j}$ is picked on each contour. The two landmark coordinates enter the model without taking the different nature of normal versus tangential displacement into account. In our new model (right) we do not use individual landmarks but we rather re-sample each contour by shooting rays in normal direction from an average contour \bar{C} .

Since the PCA also provides a ranking of the model parameters according to their shape relevance, we can focus on a small set of leading model parameters while still capturing all significant shape variations.

In this formulation, ASM treats contours like isolated point samples in some higher dimensional space without taking into account the geometric coherence of the landmark positions. The only geometric aspect in the standard ASM setup is that each contour is aligned to a global coordinate system by an affine transformation. This is necessary to avoid the detection of pseudo deformations which happen to be rigid rotations or translations of the contours. Otherwise, the fact that the positions of neighboring landmarks are not completely independent is ignored and true shape variations (where the landmarks move in normal direction to the contour) are treated exactly like insignificant changes of the landmark distribution along the contour (where landmarks move in tangent direction).

As an alternative approach, we suggest to replace the feature vectors in the standard setup by a vector of normal displacements relative to an average contour. By this we can incorporate much more geometric information into the model. Each change in the displacement values represents a true change in the contour shape since tangential movement of the samples is not possible (Fig. 1). In addition we avoid the tedious manual pre-process of picking the landmarks on every training contour since the displacement can be computed automatically by simply intersecting normal rays from the average contour with all training contours.

2 Contour Representation and Model Building

A contour is a closed curve $C(t) : t \in [0,1] \mapsto \mathbb{R}^2$ with $C(0) = C(1)$, that separates the plane into exactly two components (inside and outside). For efficient processing, contours are usually discretized and approximated by a polygon.

Standard ASM relies on landmarks $p_i = C(t_i)$ with $i = 1, \dots, n$, which are placed at suitable locations on the contour. The $2n$ -dimensional feature vector

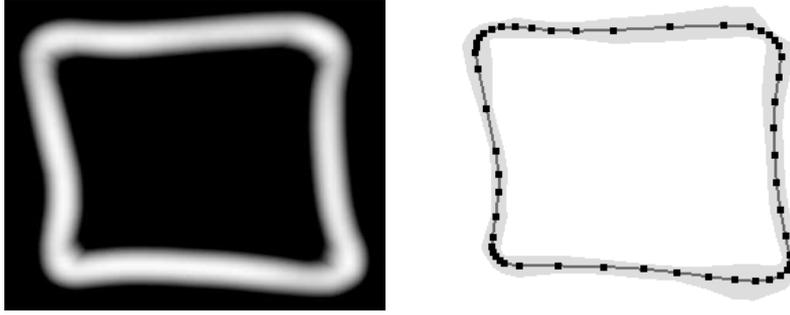


Fig. 2. To generate an average contour, we first sum up the squared distance functions of all training contours in a high resolution grid (left). Then we extract the zero-contour and adaptively decimate it to reduce its point count (right). The minima and maxima of the displacements d_i of the training contours provide additional geometric information about the limits of the shape deformation encoded in the DDM.

used for the model is built by concatenation of the $2D$ vectors p_1 to p_n . Statistical models based on this contour representation are known as Point Distribution Models (PDM). To build a PDM, landmarks must be defined separately on all training contours $C_j(t)$ with $j = 1, \dots, k$. Special care has to be taken to avoid tangential shifts of “synchronous” landmarks $p_{i,j}$ with $j = 1, \dots, k$ (Fig. 1), since these shifts along the contour carry less significant shape information, but still influence the model parameters when applying the PCA.

In contrast, our method initially specifies a smooth contour \bar{C} , which approximates an average shape of the training data C_j . From $\bar{C}(t_i)$ rays are shot in normal direction and intersected with the training contours $C_j(t)$. We call the resulting distances *displacements* $d_{i,j}$ (Fig. 1). In that \bar{C} and the t_i have to be defined only once, each contour C_j is given by the scalar values $d_{1,j}$ to $d_{n,j}$. We call a model based on this type of contour representation a *Displacement Distribution Model* (DDM) and the segmentation method using DDM *Active Displacement Model* (ADM). \bar{C} and $\{t_i\}$ represent the geometric framework for the ADM. Major shape variations are found by applying the PCA to the training vectors $D_j = [d_{1,j} \dots d_{n,j}]$. By definition $\{D_j\}$ contains no tangential components and therefore a DDM encodes only relevant shape information.

The contour \bar{C} is called *domain contour*. We obtain \bar{C} by first summing up the squared distance functions of the training contours in a high resolution grid (Fig. 2). Then we extract the highly detailed zero-contour, which approximates the average shape of all training contours. While decimating this contour to a lower point count, we adapt to local detail by keeping more points in areas of high curvature. The remaining points define the locations t_i on \bar{C} . As long as a distance function can be generated from a training contour, any representation can be used with this method, including implicit functions and discrete images.

The minima and maxima of the displacements $d_{i,j}$ of the training contours are easily obtained and define the bounding hull of the shape deformation encoded in the DDM (Fig. 2).

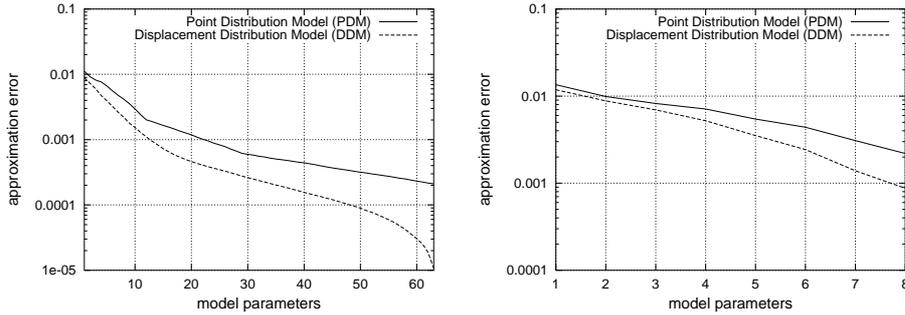


Fig. 3. Created from the same synthetic input data (left), a DDM reduces the approximation error compared to a PDM (vertical axis) and has the same descriptive power with fewer model parameters (horizontal axis). Using real data (right), the DDM again shows better approximation properties. In both cases the DDM uses a feature vector of only half dimension, reducing the cost for the PCA considerably.

3 Results

In our experiments we evaluate the approximation power of a DDM in comparison to a PDM when using the same training data. In any case, the feature vector of a DDM has only half the size of that of a PDM representing the same number of samples of a contour. This considerably reduces the cost of applying a PCA to the training contours while achieving the same approximation quality.

3.1 Approximation Power of Shape Models

In the following we build a PDM and a DDM both with synthetic and real data. Then we sum up the Hausdorff distance between all original training contours and their approximations after mapping to the shape model using a varying number of model parameters. The aliasing error generated by resampling with the domain contour \bar{C} turned out to be negligible.

First we generate 200 variants of a contour with 64 points. For this we start with a contour of 8 points and alternate steps of deformation and subdivision. The maximum amplitude of the deformation is attenuated in each step. The last step is a deformation. The PDM uses the 64 points directly as landmarks. Consequently the PDM feature vector has 128 entries. For the DDM we *automatically* generate a domain contour with 64 points. Hence the DDM feature vectors have only 64 entries. Using the same number of model parameters, our model reduces the approximation error (Fig. 3).

On 10 real radiographs of vertebrae 52 landmarks have been picked by hand (data courtesy by the Department of Diagnostic Radiology of the RWTH Aachen University Hospital). Like above the PDM uses the landmarks directly for model building. For the DDM we automatically generate a domain contour and use 52 displacements independent from the landmark locations. The results are similar to those with synthetic data. Even with the low number of training contours we

observe the same trends in the relation of model parameters to approximation error (Fig. 3).

3.2 Segmentation

The method of extracting contours from images using ASM is described in full detail in [3]. Here we build both a DDM and a PDM for 9 of 10 vertebrae and compare the ASM segmentation of the 10th vertebra with the respective hand-segmented contour (leaving-one-out). Using ADM instead of ASM makes practically no difference once the model of shape is available and we observe comparable segmentation results.

4 Discussion

ADM in comparison to ASM avoids landmarks and therefore circumvents the difficulties related to the reliable detection of landmarks. Although the approximation by displacements is as good as using landmarks, the dimension of the contour representation is halved. A DDM in contrast to a PDM is guaranteed to only store relevant shape information. The generation of domain contours and the measurement of displacements is done automatically and is also automatically adaptable to local detail. This is a big advantage compared to PDM, where model generation requires manual preparation of the raw data. Furthermore the representation of training contours for the DDM is not restricted to polygons. Finally a DDM shows significantly improved approximation power compared to a PDM based on the same input data.

Due to potential aliasing during resampling, a DDM is not very well suited for encoding contours with sharp edges. This problem could be solved by applying a hybrid model using both landmarks and displacements.

In [5] the ADM approach is generalized to 3D, resulting in an even larger cost reduction for applying a PCA on training data, since the feature vector size is reduced by a factor of 3.

References

1. Canny JF: A computational approach to edge detection. *IEEE Transactions on Pattern Analysis and Machine Intelligence* 1:679–698, 1986.
2. Kass M, Witkin A, Terzopoulos D: Snakes: Active Contour Models. *International Journal of Computer Vision* 1:321–331, 1988.
3. Cootes TF, Taylor CJ: Statistical models of appearance for medical image analysis and computer vision. *Procs SPIE Medical Imaging*, 2001
4. Kohnen M, Mahnken AH, Kersten JK, et al.: Ein wissensbasiertes dreidimensionales Formmodell für die Segmentierung von organischen Strukturen. *Procs BVM* 02:197-200, 2002.
5. Liersch DJ: Evaluation of model-based methods for the extraction of organic structures from 2D and 3D image data. *Diploma Thesis, RWTH Aachen*, 2003