

3D Statistical Shape Model Building using Consistent Parameterization

Matthias Kirschner, Stefan Wesarg

Graphisch Interaktive Systeme, TU Darmstadt
matthias.kirschner@gris.tu-darmstadt.de

Abstract. We propose a new correspondence optimization algorithm for building 3D statistical shape models (SSMs) of genus-0 shapes. The main contribution of our work is the use of parameter space propagation to generate consistent spherical parameterizations of the training shapes. We present evaluation results for two data sets: A set of 30 liver shapes from different patients, and a set of 25 left ventricles covering the cardiac cycle of a single patient. Our evaluation shows that the use of parameter space propagation improves the robustness of correspondence optimization algorithms and leads to fast convergence.

1 Introduction

In medical imaging, statistical shape models (SSMs) are mainly employed in segmentation algorithms like the active shape model (ASM), which shows good performance in terms of both segmentation accuracy and running time [1]. SSMs are learned from a set of training examples, which have to be provided in a landmark representation, that is, each training shape has to be represented with the same number of points, and points with same index on different shapes have to describe the same anatomical feature. The challenging optimization problem of computing a landmark representation automatically from a set of unnormalized training meshes is known as the correspondence problem.

To tackle the correspondence problem, Kotcheff and Taylor [2] introduced a general optimization scheme, which we follow in our work: Each training shape is mapped to a suitable parameter space, and correspondence is then optimized by reparameterization. The correspondence of the reparameterized shapes can be assessed with various objective functions, for example the Minimum Description Length (MDL) objective function [3].

The natural parameter space for the construction of 3D SSMs of shapes with genus-0 topology is the unit sphere. Davies et al. [4] construct area-preserving spherical parameterizations of the training shapes, whereas Heimann et al. [5] use conformal mapping to generate angle-preserving spherical parameterizations of liver shapes. We concentrate on area-preserving parameterizations, because they allow for an easy reconstruction of the shapes using uniform sampling. It is crucial to parameterize the shapes consistently – that means to map the same anatomical features to similar regions in the parameter spaces – in order

to decrease the convergence time and to prevent that the optimization process gets trapped in a poor local optimum [6]. Recently, we introduced parameter space propagation [7] to generate consistent parameterizations more efficiently and without a complex optimization process as proposed in [6, 8]. The key idea of our method is to propagate the parameterization of a reference shape to all other shapes.

In this paper, we propose a new optimization algorithm that automatically establishes correspondence of shapes with genus-0 topology. The main novelty is the use of parameter space propagation in order to generate consistent parameterizations. Our evaluation shows that the use of parameter space propagation avoids that correspondence optimization algorithms get trapped in poor optima and leads to a fast convergence towards a good solution.

2 Materials and Methods

2.1 Consistent Parameterization by Propagation

We use parameter space propagation [7] in order to consistently generate spherical parameterizations of the training shapes. In this method, an area-preserving parameterization of an arbitrarily selected reference shape S_{ref} is computed. Every other shape S is aligned to the reference shape using the ICP algorithm in order to derive a common coordinate system. Based on the Euclidean distance in this coordinate system, a fuzzy correspondence between points in S and S_{ref} is established. The points of S are then mapped to the unit sphere by interpolation of the parameter space coordinates of the corresponding points of S_{ref} . A subsequent correction method handles triangles that are inverted or overlap on the unit sphere. Parameter space propagation is a heuristic method, but works robustly for typical organ shapes. By computing surface normals of the triangles of the generated parameterizations, we verified that only valid parameterizations were generated for our test data sets.

2.2 Optimization Algorithm

In this section, we present our optimization algorithm, which minimizes the objective function $\mathcal{L} = \sum_{i=1}^t \log(\lambda_i + \epsilon)$, where the λ_i are the eigenvalues of the $t \times t$ covariance matrix of the shapes, which is determined by numerical integration [3, 8]. We set the regularization constant ϵ to 0.005. The correspondence measure \mathcal{L} is (up to a constant term) the so-called DetCov function [2].

Our algorithm follows the general minimization approach with parametric regularization [8]. We start with generating sampling points for each shape which are initially uniformly distributed over the sphere. The optimization works iteratively: In each iteration, we select a shape uniformly at random and re-parameterize its sampling points using two kinds of re-parameterizations:

- *Uniform rotation:* We consider rotations of the sampling points around the x, y and z-axis, one after another, in randomly determined order. For each

axis, we choose the optimal rotation angle between -15° and $+15^\circ$ using a line search algorithm.

- *Clamped plate spline warps*: We map the sampling points of a randomly selected spherical cap to the unit circle using orthographic projection, manipulate them using a clamped plate spline warp [8] and project them back to the sphere. The optimal parameters for the spline transformation are found using gradient descent optimization, with numerically estimated gradients.

Additionally, we optimize the pose parameter rotation directly. The other pose parameters are handled prior to the optimization process, by scaling the shapes to same size and translating them to the origin.

2.3 Evaluation Method

With our evaluation, we want to show that 1) our optimization algorithm is able to generate SSMs for different sets of genus-0 shapes and that 2) the use of parameter space propagation enables us to compute SSMs of high-quality. To show 1), we tested our algorithm on data sets with different organs: A set of 30 liver shapes from different patients, and a set of 25 left ventricles (LVs) which cover the whole cardiac cycle of a single patient with a myocardial infarction. To verify our second hypothesis, we started our algorithm with three different kinds of parameterizations: Parameterizations generated with our propagation method, parameterizations generated using Davies’s method (see [7] for implementation details) and parameterizations which are generated independently from each other. We used a fixed number of iterations ($n = 3000$). Prior to the parameterization, the liver shapes are aligned into a common coordinate system, to ensure

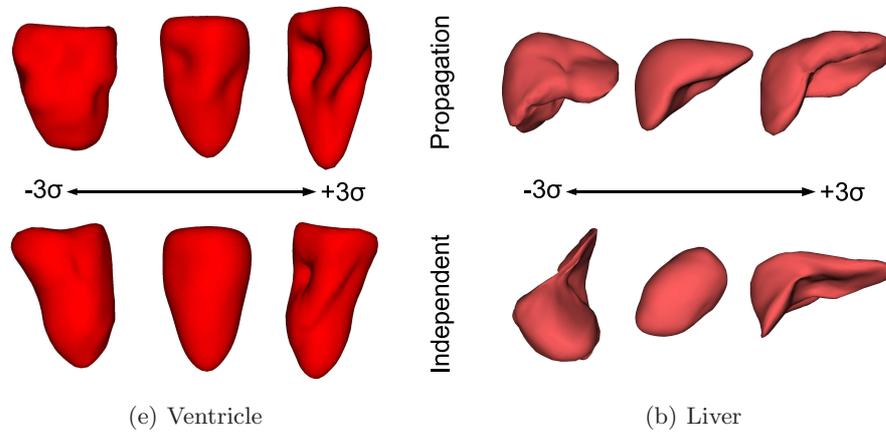


Fig. 1. The first mode of variation of the ventricle and liver models, optimized using parameterizations generated with our method (top row) and independently computed parameterizations (bottom row). $\sigma = \sqrt{\lambda_1}$ denotes the standard deviation of the first mode of the respective SSM.

that our results are not tampered by poor initial alignment. The meshes in the LV data set are already aligned, as they were generated from a single 4D MRI volume. In order to compare the quality of the generated models, we calculate the standard measures specificity and generalization ability as described in [8], by sampling 10000 shapes randomly from the respective probability distribution.

3 Results

Figure 2 shows the evolution of the objective function during the execution of the algorithm. The figure shows that the algorithm converges quickly towards a local optimum in case of consistent parameterization. But the final objective function value after 3000 iterations is smaller in case of independently computed parameterizations. However, only the shapes of the models generated with consistent parameterization look plausible, as illustrated in Fig. 1. This visual impression is confirmed by evaluating the models using the specificity and generalization ability measures. On both data sets, our optimization algorithms produces significantly better models in case of consistent parameterization. A comparison between the two different methods for consistent parameterization shows that the parameter space propagation generates better models on the ventricle data set (Fig. 3). On the liver data set, the differences between the two approaches are very small. Here, initialization with parameter space propagation leads to models with slightly better generalization ability, but which are also slightly less specific than the models generated using initialization with Davies’s method. The required optimization time for a liver model was approximately 300 minutes, and 210 minutes for a ventricle model on a 2.4 GHz CPU.

4 Discussion

We presented a new algorithm for correspondence optimization, which employs parameter space propagation to generate consistent spherical parameterizations.

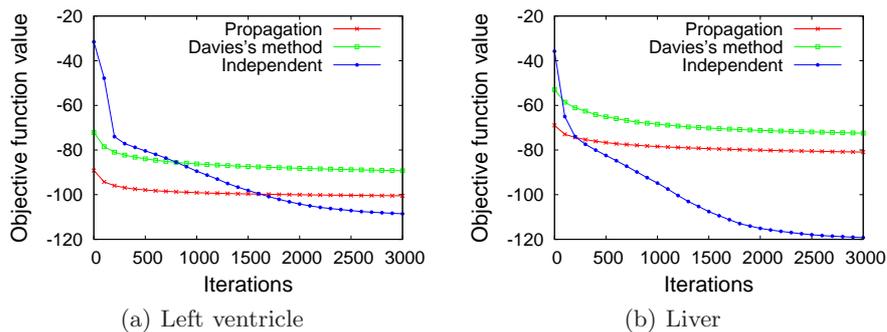
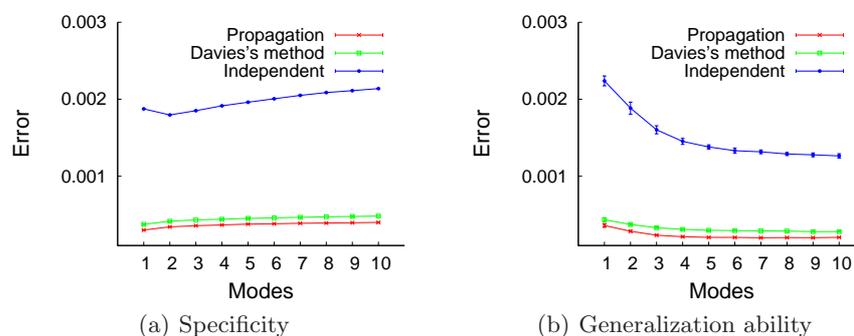


Fig. 2. The evolution of the objective function during execution of the algorithm using different methods of parameterization.

Fig. 3. Specificity and generalization ability of the generated ventricle models.

Using this technique, the algorithm quickly converges to a SSM which captures the variation of organ shapes present in the training set well. Our evaluation shows that the use of parameter space propagation improves the robustness of the correspondence optimization process. In comparison to Davies's method [6], initialization with parameter space propagation produces models which are more compact, but have comparable if not better quality in terms of specificity and generalization ability.

Possible directions for future research are an extended evaluation of our approach on other organ shapes, a comparison of different objective functions as well as algorithmic techniques to decrease the computation time of the algorithm.

References

1. Heimann T, van Ginneken B, Styner M, et al. Comparison and evaluation of methods for liver segmentation from CT datasets. *IEEE Trans Med Imaging*. 2009;28:1251–65.
2. Kotcheff ACW, Taylor CJ. Automatic construction of eigenshape models by direct optimization. *Med Image Anal*. 1998;2:303–14.
3. Davies RH, Twining CJ, Cootes TF, et al. A minimum description length approach to statistical shape modeling. *IEEE Trans Med Imaging*. 2002;21(5):525–37.
4. Davies RH, Twining CJ, Cootes TF, et al. 3D statistical shape models using direct optimisation of description length. In: *Proc ECCV*; 2002. p. 3–20.
5. Heimann T, Wolf I, Williams TG, et al. 3D Active shape models using gradient descent optimization of description length. In: *Proc IPMI*; 2005. p. 566–77.
6. Davies RH, Twining CJ, Taylor CJ. Consistent spherical parameterisation for statistical shape modelling. In: *Proc ISBI*; 2006. p. 1388–91.
7. Kirschner M, Wesarg S. Construction of groupwise consistent shape parameterizations by propagation. In: *Proc SPIE*; 2010. p. to appear.
8. Davies RH, Twining CJ, Taylor CJ. *Statistical Models of Shape: Optimization and Evaluation*. Springer; 2008.