Point-Based Statistical Shape Models with Probabilistic Correspondences and Affine EM-ICP

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Abstract. A fundamental problem when computing statistical shape models (SSMs) is the determination of correspondences between the instances. Often, homologies between points that represent the surfaces are assumed which might lead to imprecise mean shape and variation results. We present a novel algorithm based on the affine Expectation Maximization - Iterative Closest Point (EM-ICP) registration method. Exact correspondences are replaced by iteratively evolving correspondence probabilities which provide the basis for the computation of mean shape and variability model. We validated our approach by computing SSMs using inexact correspondences for kidney and putamen data. In ongoing work, we want to use our methods for automatic classification applications.

1 Introduction

One of the central difficulties of analyzing different organ shapes in a statistical manner is the identification of correspondences between the shapes. As the manual identification of landmarks is not a feasible option in 3D, several techniques were developed to automatically find exact one-to-one correspondences. In order to automatically establish correspondences between surfaces represented by point clouds, some authors propose elaborate preprocessing methods [1, 2, 3]. Other approaches solve this with a search for the registration transformation using an atlas [4] or the ICP algorithm [5]. More recent methods directly combine the search of correspondences and SSM [6, 7, 8]. All of these enforce homologies between the shapes. However, exact correspondences can only be determined between continuous surfaces, not between point cloud representations of surfaces. Thus, when using imprecise homologies, the resulting variability model will not only represent the organ shape variations but also artificial variations caused by the wrongly assumed exact correspondences. The SoftAssign algorithm tries to solve this problem with an initial probabilistic formulation of the correspondences but it also ends up with one-to-one correspondences [9].

In order to solve for inexact correspondences, we pursue a probabilistic approach and base our work on an affine EM-ICP registration algorithm which proved to be robust, precise, and fast (see [10] for rigid EM-ICP).

2 Methods

The affine EM-ICP algorithm determines the affine registration transformation T to match a point set $M \in (\mathbb{R}^3)^{N_m}$ on $S \in (\mathbb{R}^3)^{N_s}$. Instead of assuming homologies, we focus on the probability of a transformed model point $T * m_j$ being a measure of an instance point s_i. If we knew that point s_i corresponds exactly to point m_j, the measurement process would be Gaussian (see eq. 1).

$$p(s_i|m_j, T) = \frac{1}{(2\pi)^{\frac{3}{2}}|\Sigma_j|^{\frac{1}{2}}} \exp(-\frac{1}{2}(s_i - T \star m_j)^T . \Sigma_j^{-1}(s_i - T \star m_j)) \quad (1)$$

where Σ_j represents the noise as the covariance of m_j.

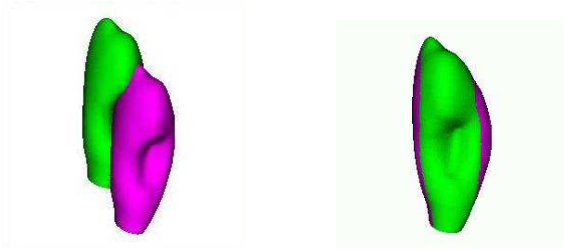
However, point s_i can in fact be a measure of any of the model points, so the PDF of its spatial location is the mixture $p(s_i|M, T) = \frac{1}{N_m} \sum_{j=1}^{N_m} p(s_i|m_j, T)$. Unfortunately, even if we assume that all scene point measurements are independent, no closed form solution exists for the maximization of $p(S|M, T)$. A solution is to model the correspondences $H \in \mathbb{R}^{3N_s \times 3N_m}$ as *random hidden variables* and to maximize the likelihood efficiently using the EM algorithm. We denote $E(H_{ij})$ as the expectation of point s_i being an observation of point $T \star m_j$ (with the constraint $\sum_j^{N_m} E(H_{ij}) = 1$). In the E-step, we fix T and estimate the complete data likelihood $\log\ p(S, H|M, T)$, thus calculating $E(H)$. In the M-step, we fix $E(H)$ and maximize the estimated likelihood with respect to T. This process is iterated until convergence. In order to easily reach the global minimum, we employ a variance multi-scaling. We begin with great variances σ^2 to ensure that shape positions, rotation and sizes are aligned and end with small variances to cover for shape details. We also implemented the EM-ICP for rigid transformations in order to be able to adapt to the data at hand.

The calculation of the mean shape point set M consists of two steps that are iterated until convergence: First, all N instances S_k of the data set are registered with the initial model $M^{(iter)} = M^{(0)}$ using the affine EM-ICP. As initial model we choose one of the instances of our data set which seems to have a 'typical' shape. Next, a new model $M^{(iter+1)}$ is calculated. Using the EM-ICP framework, we have to minimize the associated global criterion

$$C_{\text{global}}(T, E(H), M) = \sum_{k,i,j}^{N,N_{sk},N_m} E(H_{k_{ij}})(s_{ki} - T_k \star m_j)\Sigma_j^{-1}(s_{ki} - T_k \star m_j) \quad (2)$$

where s_{ki} is a point of instance S_k, $E(H_{k_{ij}})$ the correspondence probability between model point m_j and instance point s_{ki}, and T_k the registration transformation from the model to S_k. The criterion is optimized alternately with respect to all T_k and $E(H_k)$ (EM-ICP) and M (which is determined by a simple derivation of equation (2)).

Fig. 1. The original objects S (dark grey) and their transformed versions S_T (light grey) before (a) $d(S, S_T) = 40,3mm)$ and after (b) $d(S, S_T) = 0.5mm)$ registration. For the EM-ICP, the kidney was decimated from 10466 to 510 points, we chose an initial sigma of 8mm, 30 EM-ICP iterations and a reducing factor of 0.9 (which leads to a final sigma of 0.38mm)



(a) (b)

For the variability model we need to compute the principal modes of variation regarding all S_k and M. The usual method is to use the traditional PCA. However, we do not dispose of the exact correspondences between each model point and the instance points. Thus, we generate virtual correspondences $\breve{s}_{kj}$ for each m_j and each S_k by evaluating the mean position of the probabilistic correspondences. In that manner, the PCA results gain a certain independence of the positions of the initially chosen points of the instances.

$$\breve{s}_{kj} = \sum_i \frac{E(H_{k_{ij}})}{\sum_i E(H_{k_{ij}})} (T_k^{-1} \star s_{ik}) \tag{3}$$

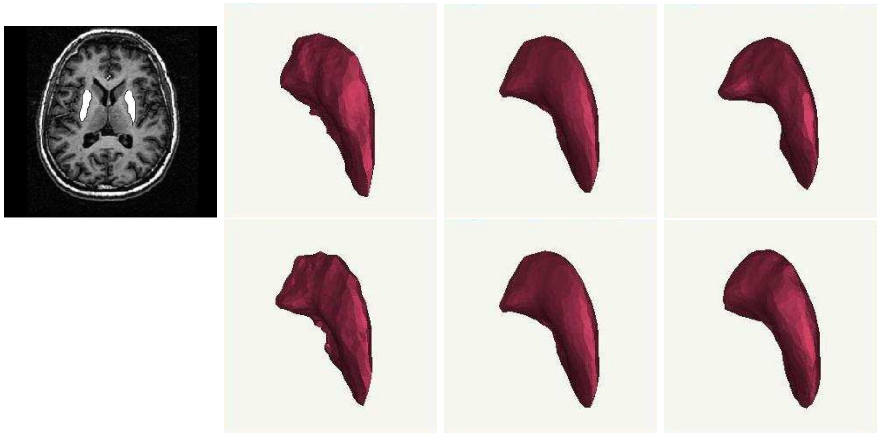
These "virtual surface points" are then used as input for the PCA.

3 Results

In order to evaluate the performance of the affine EM-ICP registration, we applied it to synthetic registration problems. We tested for rigid, similitude, and affine T_{synth} with different numbers of points, variances, and iteration numbers. Our experiment object was a kidney S with $T_{\text{synth}} \star S = S_T$. To evaluate the results, we introduced a distance measure $d^2(S, S_T) = \frac{1}{N_S} \sum_{i=1}^{N_S} \|s_i - s_{T,i}\|^2$. The source S and the deformed version S_T were decimated using different parameters so that no exact correspondences existed between them and the number of points in the clouds were different (for the decimating algorithm see [11]). Thus, real conditions were simulated. We established that the affine EM-ICP finds very good results, needs no previous rigid registration for the affine case and converges quickly. For an evaluation example with distance values before and after registration see the affine case in figure 1.

We computed successfully SSMs for data sets of kidney CTs, brain structure MRs, and sulcal lines. In this article, we focus on the SSM results for the

Fig. 2. First image: Transversal slice of a CT volume of the brain where the putamen structures are marked in white. First and second row: The mean shape (middle images) of the left putamen and the principal deformations according to the first eigenvector ($\boldsymbol{v}_1$) and second eigenvector ($\boldsymbol{v}_2$). The images show a deformation of $-3\sqrt{\lambda_i}\boldsymbol{v}_i$ (left) and $+3\sqrt{\lambda_i}\boldsymbol{v}_i$ (right) respectively (with λ_i being the associated eigenvalues)



putamen, see figure 2. The data set consists of 24 right and left segmented instances (approximately $20mm \times 20mm \times 40mm$) which are represented by about 1000 points. The variance multi-scaling in the EM-ICP registration started with $\sigma_{initial} = 6mm$ and ended with $\sigma_{final} = 0.8mm$. Figure 2 shows the resulting mean shape and the deformations of the left putamen according to the variation modes. We then employ the SSM algorithm for an automatical classification of the putamen. The putamen data consist of 12 healthy and 12 pathological subjects. We want to determine if the disease causes significant shape deformations in the putamen. For the diseased and healthy data respectively, a mean shape and variability model are calculated. Then, the mean shapes and the variations of the shapes are compared. The results seem to show a shape difference between healthy and pathological putamen, but this needs to be confirmed by a statistical test.

4 Discussion

We proposed in this paper an EM-ICP framework to compute statistical shape models. We believe that our approach offers an advantageous method as it provides a resolution to the fundamental problem of homology identification between shapes. We proved that the algorithm is flexible and stable as it comes to good results for different types of organs. Currently, we are investigating the correspondence matrix as an indicator of the quality of the point distribution in the model with respect to the instances in the data set. This might help to choose an appropriate initial model. Secondly, we work on the replacement of the ad-hoc PCA as this approach is not coherent with the initial demand of inexact corre-

spondences. At present, we are developing a proper probabilistic model including the mean shape *and* the variation modes in a global criterion. In future work on the applications, we will intensify our analysis of the putamen variability by extending the data set, conducting more experiments and implementing clustering techniques in order to finally realize an automatic classification. Besides, we plan to apply the algorithm on more complex shapes (e.g. ganglion data) with larger variations. As we want to carefully evaluate our approach, we need to compare its performance to state-of-the-art SSM algorithms.

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