Shape 2014

The annual SICAS conference on statistical shape modeling.

Symposium on Statistical Shape Models & Applications

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Proceedings
Preface

In his seminal work nearly hundred years ago D'Arcy Thompson was the first drawing attention to the problems of mathematically characterizing biological shapes. While Harry Blum significantly contributed to the development of formal tools to address the related questions, it was not before the early nineties of the last century when this issue has become a major research focus within the emerging new field of medical image computing.

A broad spectrum of methods has been developed since, allowing to use shape information as a priors for solving different problems in patient care, ranging from improved automatic segmentation to predicting individual organ shape from sparse information. These approaches did not only sustainably change radiological diagnosis by providing efficient support for the interpretation of the vast amount of images acquired today routinely, but also contributed to greatly improve therapeutic procedures by enabling more efficient surgical planning and improved outcome prediction.

The Swiss National Competence Center of Competence in Research on Computer Aided and Image Guided Medical Intervention (NCCR Co-Me) has greatly contributed to this vigorous progress during the past 12 years. Shape modeling was one of the major scientific foci of the work of this Swiss-wide collaborative research and clinical network, resulting in major contributions to the international state-of-the-art. After these years of highly successful work, the recently founded Swiss Institute of Computer Assisted Surgery (SICAS) has taken over the coordination and support of the related continuing efforts of numerous Swiss research groups, in order to finally establish a Swiss network center for statistical shape modeling in the Canton Jura. As part of this, computing infrastructure has been installed and related personnel has been hired to run a medical image repository (Virtual Skeleton Database) which was used in the SHAPE 2014 challenge and will serve as an open lab for the scientific community.

The current Symposium is a first major initiative of SICAS, and is intended to become an annual pillar of the center, to further promote the exchange on the field of shape modeling and characterization, not only within the Swiss research community but in an international context. It has been a great pleasure to welcome leading scientists from all around the world, presenting their most recent results and shaping the future of this exciting research area through intensive discussions within the numerous sessions and podium discussions, covering many important aspects of recent research. It is our hope that this meeting is just a first step in maintaining the great traditions of the NCCR Co-Me and will serve as a basis and foundation for a series of similar events in the future.

Gabor Székely, President of the SICAS Foundation Council
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Conference Abstracts
Background: The majority of statistical shape analysis methods are based on point-based shape representations. These representations, however, have a notion of correspondences between a set of exemplar shapes, since (1) the order of the points can modify freely, and (2) the points are allowed to slide over the boundary surface of the shape while still representing the same shape. Ideally, the intrinsic distance metric of the shape space is invariant with respect to these modifications. Therefore, certain constraints on the position of the points are enforced, as to ensure corresponding points that identify the same point on all exemplar shapes to exist. A variety of approaches exist to solve this constraint [1]. A common approach is to employ point-cloud to point-cloud registration algorithms. More effective approaches formulate the constraint as an optimization problem whereby a certain quality criterion is optimized over the correspondences [2].

Aims: The aim of this abstract is to present an algorithm for the construction of Principal Component Analysis (PCA) shape models using point-based shape representations, while solving the correspondence problem at the same time. This algorithm extends the work of Hufnagel et al. [3].

Methods: Similarly to Hufnagel et al., a probabilistic point-based shape representation is used to construct Principal Component Analysis (PCA) shape models. This probabilistic representation assigns to each point a probability for that point to belong to the boundary surface of the respective shape, and helps to overcome the correspondence problem. This representation is estimated using Kernel Density Estimation (KDE) with a Gaussian kernel. Different from Hufnagel et al., an additional outlier distribution is added to the KDE representation in order to improve the robustness to outliers. For constructing the PCA model a distinction is made between three sets of parameters. The first set of parameters corresponds to the actual PCA model parameters, consisting of the mean shape, modes of variation, and corresponding standard deviations. The second set corresponds to the observation parameters, consisting of a rigid transformation and deformation coefficients with respect to the modes of variation. These observation parameters fit the PCA model to each of the exemplar shapes. The third set of parameters corresponds to the exemplar shape specific bandwidth parameters of the KDE representation. The PCA models are constructed by minimizing an energy function, obtained from a maximum-a-posteriori approach. This energy function consists of two terms; the first term originates from the exemplar shape likelihood, while the second term originates from the observation parameter likelihood. In contradiction to Hufnagel et al. the Expectation-Maximization (EM) algorithm is used for optimizing the energy function. In the E-step probabilistic correspondences are estimated. These probabilistic correspondences naturally arise from the probabilistic shape representation. However, in contradiction to Hufnagel et al., they are obtained using Sinkhorn iterations on the probabilistic correspondence matrix, leading to more accurate correspondences. In the M-step the PCA model parameters, observation parameters, and, different from Hufnagel et al., bandwidth parameters are estimated. Closed form expressions are obtained for all parameters except the modes of variation due to their orthonormality. This property is enforced via additional Lagrange multipliers, estimated in an iterative manner and different from Hufnagel et al., leading to better estimates for the modes of variation.

Results: The algorithm presented above is used to construct PCA models for different types of teeth. This task is complicated by the large anatomical variability observable over a population, as well as noise and outliers present in the exemplar shapes. The resulting models are compared to the models resulting from the original method of Hufnagel et al. using model specificity, generalization ability and compactness. This comparison shows improved values for compactness, specificity and generalization ability.

Conclusions: This approach overcomes the requirement for explicit correspondences while still using a compact point-based shape representation. Compared to the original method of Hufnagel et al., our approach provides more accurate (probabilistic) correspondences, better robustness to outliers, automated estimation of the exemplar shape specific bandwidth parameters, and a better estimation of the modes of variation. This results in an improved compactness, specificity and generalization ability.

ROBUST IMAGE ANALYSIS BY FITTING A 3D MORPHABLE FACE MODEL FOR PORTRAIT MANIPULATION

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Background: A 3D Morphable Model (3DMM) is a dense generative parametric statistical model [3]. The model encodes our facial shape and texture prior based on a Probabilistic Principal Components Analysis of 200 exemplar faces. It is used to generate a 3D reconstruction of human faces from a still image. The 3D face reconstruction can be used for facial attribute analysis, face recognition, psychophysical experiments and many more. Here, we present an application of portrait manipulation, changing the strength of perceived social attributes, such as trustworthiness, aggressivity or competence.

Aims: Our goal is to manipulate perceived facial attributes in portraits robustly, fully automatic, in a psychologically validated and photorealistic manner.

Methods: In order to manipulate the input image, the 3DMM is used to gain a machine-understandable face representation. The manipulation is based on psychological studies where the model space has been charted with respect to ascribed social attributes. We use the probabilistic model combined with a Data-Driven Markov Chain Monte Carlo fitting algorithm [1] to integrate model-based and image-based cues to robustly find the best set of parameters for a given image. The stochastic algorithm is able to handle unreliable face and feature point detections and can thus work without user interaction.

The detections are obtained by Random Forests which are learned on the features known from Viola and Jones [4]. Combining the Random Forest with a sliding window approach yields a probability map for each feature depicting the belief of the Random Forest to see the feature at the particular position. We use the ten best locations after overlap elimination as face candidates.

To attain the desired new attribute value, the obtained model representation is manipulated with a linear model. To update the face shape the input image is warped, whereas the appearance changes due to color and shading are additively rendered into the target image.

Results: The probabilistic interpretation of the detection stage in the sampling-based fitting increases robustness and fitting quality. The dense correspondence is exact enough for portrait manipulation.

Conclusions: The integration of detection into the model-based fitting process [1] leads to the first fully automatic 3DMM fitting pipeline. Using the final fit, we have a dense correspondence of the image to our model and are able to manipulate the portrait with photorealistic results. The manipulation itself is validated by psychological experiments [2].

Acknowledgements: This project is partially founded by the Swiss National Science Foundation

References:

The outer images are manipulated to be perceived less or more trustworthy than the original image.
Background & Aims: The single-figure discrete quasi-medial skeletal representation of anatomic objects called the s_rep (Fig.), capturing position (via skeletal samples), orientation (of the quasi-boundary-normals forming the s_rep spokes), and width properties (spoke lengths), has been used for a variety of goals of or using shape statistics. We summarize the performance of these statistics and compare them to those on the more prevalent object representation of boundary point distribution models (PDMs).

Methods: Methods for probability distribution estimation, classification, and hypothesis testing have been developed using s_reps. All involve recognizing that for both s_reps and PDMs, many of their geometric properties abstractly live on spheres and thus, when analyzing them statistically, the method of Principal Nested Spheres (PNS) [2] is needed to statistically preprocess these properties before applying methods designed to work in Euclidean spaces.

1) Estimating a probability distribution on objects, incl. modes of variation, principal variances, and total variance, using (Euclidean) PCA. We show how to transform incommensurate shape variables into comparable units, needed for PCA and allowing comparison of methods as to total variance. Also, we show the necessity of fitting s_reps to primary object descriptions in correspondence, which requires estimating the probability distribution. In our method the correspondence was produced by a final stage of s_rep fitting that initialized from a common mean and was fitted over common modes of variation, followed by spoke length refinement.

2) Training and execution of classification between 2 classes of objects using (Euclidean) DWD [3], less sensitive to noise than SVM. Histograms in DWD's separation direction in the Euclideanized feature space were used by a Bayesian approach to produce the function P (schizo | position along the separation direction). Varying the prior probability of being schizophrenic yielded a curve: true positive rate vs. true negative rate.

3) Hypothesis testing to discriminate geometric properties that differ significantly between two classes of objects, using (Euclidean) permutation tests on geometric properties with locality, via family-wise error rate to correct for multiple tests. The permutation subclass means were computed from the backward means implied by PNS, and the inter-mean distances for the subclasses were computed geodesically for sphere-resident geometric properties.

Results: Our data consists of hippocampi segmented from MRIs. 221 are from first-episode schizophrenics, and 56 are from controls. The PDMs were constructed as the boundary points at the end of the s_reps spokes. We made the following comparisons:

1) Classification into schizophrenic and normal classes, comparing via Area under ROC, using iterated cross-validation [Hong]. Results: s_reps with Euclideanization: 0.65, s_reps without Euclideanization: 0.56, PDMs with Euclideanization: 0.63, volume only (the common neuroscience approach): 0.58. Visualization of the s_reps falling along the separation vector through the population mean of the pooled classes yields comprehension of the inter-class shape differences.

2) Estimating a probability distribution [1]. First, we found s_reps to have 9% more total variance per dimension than the PDMs. Second, PDMs required 10 eigenmodes to obtain an accumulated variance per dimension equal to 80% of the s_reps’ total variance per dimension, whereas the s_reps required only 4 eigenmodes. When doing the statistics without correspondence, 25 eigenmodes were required.

3) Hypothesis testing on the s_reps [4] showed significant global differences between the classes. It also showed significant differences in skeletal position and s_rep spoke orientation for specified spokes.

Conclusions: With respect to this data, statistical analysis via Euclideanization of s_reps is superior.


Figures. A mean s_rep for a hippocampus and its implied boundary. Balls = skeletal points. Spokes proceed from the balls.
CONSISTENT DENSE CORRESPONDENCES FROM PAIR-WISE NON-RIGID REGISTRATION

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Background: Establishing correspondences is a crucial step in generating statistical shape and deformation models. In this abstract we present a technique to compute dense correspondences across a set of images. In contrast to group-wise registration, where images are iteratively registered to an evolving mean image, our method explicitly uses all pair-wise registrations among the set of images by minimizing their group-wise inconsistency using a regularized least-squares algorithm. The regularization controls the adherence to the original registration, which is weighted by the local post-registration similarity. This allows our proposed method to adaptively improve consistency while locally preserving accurate pairwise registrations. We show that the rectified registrations are not only more consistent, but also have lower average deformation error (ADE) when compared to known deformations in simulated data, and lower target registration error (TRE) in clinical data.

Aims: Establishing dense consistent correspondences between images with minimal error.

Methods: We assume that a non-rigid registration method has been used a-priori to compute pair-wise registrations between all images in a set of images. Our method then takes this set of images along with their registrations as input, and outputs new registrations with improved consistency. We formulate an inconsistency-based optimization criterion based on the sum of the squared norms of the transitivity errors. Transitivity error is defined as the vector difference between a direct registration $T_{ab}$ between images $a$ and $b$, and the composition of $T_{ac}$ and $T_{cb}$. By including all possible intermediate images $c$ in the criterion a redundancy is created which allows us to avoid ambiguities. We additionally add a similarity-weighted adherence to the input registration to avoid degenerate solutions, i.e. the set of identity transforms. We find a solution to the optimization problem by casting it as a linear least-square problem, which is solved multiple times to improve necessary approximations. In order to efficiently solve for all pair-wise registrations at the same time, we solve only for displacements of a coarse displacement control grid with a spacing of about 8 pixels. For the weights, we use local normalized cross correlation [1] with a window size of 4mm.

Results: We evaluate our method on two datasets: (i) A set of 19 2D MR images of the head (481x374 with 0.3mm res) generated from one template by deforming it with anatomically estimated deformations. These images were then re-registered using Demons- and MRF-based registrations [2,3], and each resulting set of registrations was used separately as input to our algorithm. An example result can be seen in Fig.1. Average dense deformation accuracy was improved by 35-40%. (ii) A set of 15 3D CT scans of the head (160x160x129 with 1mm res) with manually delineated jawbone and 12 landmarks placed on bone features. These images were similarly registered pair-wise using Demons and MRF registrations, and then processed separately by our algorithm. Average TRE was improved by 12-28%, and average Dice coefficient between deformed source and target manual segmentation was improved by 2-15%.

Conclusions: A novel method for improving dense pair-wise correspondences between images in a set was proposed. As the resulting registrations have improved consistency, they could further be used to estimate statistical deformation models, which will be the focus of our future work.

Acknowledgements: This work was partly funded by the Swiss NCCR Co-Me.

References:

Figure 1: From left to right: target image, source image deformed by input registration, visualization of dense deformation error (hue=direction, saturation=magnitude), deformation error after our algorithm, source image deformed by new registration.
**A BILINEAR MODEL FOR TEMPORALLY COHERENT RESPIRATORY MOTION**

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**Background:** Modelling respiratory organ motion is an active field of research. Having an accurate model of respiratory motion is desirable for many practical applications including motion segmentation, registration, tracking and reconstruction as well as tumour tracking in a clinical scenario. While respiratory motion is very similar from cycle-to-cycle, there are variations that must be taken into account. On the other hand, we wish the model to produce only valid motion patterns. Recently, statistical motion models which are learned from data, typically by employing Principal Component Analysis (PCA) techniques, have been proposed in various studies. However, they often do not take into account the temporal regularity of respiratory motion.

**Aims:** To build a bilinear motion model that compactly represents the temporal regularity within the training data and apply an efficient reconstruction algorithm for sparse observations.

**Methods:** We apply the bilinear model from [1] to respiratory organ motion. We augment the model with a Bayesian algorithm for reconstruction from sparse and noisy measurements [2], leading to a variety of interesting possible applications. The bilinear model is learned from a sequence of 40 respiratory cycles represented by a set of 84 2-dimensional landmarks uniformly distributed along the liver obtained from non-rigid registration of MRI images under respiratory motion. One cycle $X$ is represented by a $p \times t$ matrix, where $p$ equals the number of coordinates and $t$ equals the number of frames per cycle. Based on the training data, we optimise for two bases $X = B_s C B_m^T$, one for shape and one for motion. Fig(a) shows how the coefficients $c_{ij}$ are related to the outer product of shape and trajectory basis vectors $b^s_i$ and $b^m_j$, respectively.

**Results:** On a test set of 80 cycles, we performed two types of experiments. First, individual landmarks were removed through the entire sequence. Second, entire frames were removed, i.e. all landmarks of a particular time point were dropped. The advantage of the bilinear model is that it can cope with both of these cases, as compared to a linear PCA model of respiratory states. Although it is possible to build a PCA model of entire cycles with similar properties, the bilinear model represents the training data more efficiently and, in our experiments, gives comparable reconstruction results.

**Conclusions:** We presented a novel model for modelling respiratory motion that respects the temporal regularity of the underlying data. Shape and motion information is separated into individual bases and a coefficient matrix defies weights of the basis vectors’ outer products. This separation leads to more compact models compared to conventional PCA. The model can potentially be used as a regulariser in registration algorithms as well as for motion compensation.

**References:**


$$
B_s : \text{shape basis} \quad C : \text{coefficient matrix} \quad B_m^T : \text{trajectory basis}
$$

Figure (a): Illustration of bilinear multiplication. The coefficients $c_{ij}$ define a weighting of each outer product between shape basis vectors $b^s_i$ and trajectory basis vectors $b^m_j$. 
**Background:** Apart from their robustness in medical image segmentation, Statistical Shape Models often exhibit limitations in boundary search coverage and detection, resulting in segmentation errors. That is, during their search for meaningful organ boundaries, many techniques are restricted to a narrow search direction normal to the model boundary [1]. This leads to segmentation errors if no candidates or only misleading ones are within search scope. Consequently, a-priori knowledge on boundary appearance for proper target candidate identification is mostly based on anisotropic descriptions like boundary normal profiles, where learning is achieved involving basic machine learning techniques (e.g. kNN-Classification) or organ-specific heuristics. Recently, classification and regression forest techniques have shown to be particularly robust in object detection, such as 2D boundary landmarks in radiographs [2]. Not only do such techniques provide higher detection robustness, but they also take into account isotropic spatial feature description for more ubiquitous landmark detection.

**Aims:** For the first time, we have developed a surface appearance model based on 3D regression voting in order to provide robust and isotropic target surface detection, successfully encountering weak boundaries and misleading background structures.

**Methods:** For each true surface landmark position on all training images, a regression forest is trained that learns the spatial deviation from surrounding voxels based on an infinite set of 3D random Haar-like descriptors. Randomness is introduced in the learning process by bagging of training samples and by feature randomization. Node split decisions minimize the determinants of sample deviation covariance. During candidate landmark search, voxels in a cube around SSM surface landmarks vote for target candidates. That is, the relative target landmark displacements are estimated voxel-wise derived from the covariance-measure weighted mean of all per-tree estimates, resulting in voting maps indicating meaningful targets at local maxima.

We have trained our system for 2562 SSM liver surface landmarks on 45 CT volumes. For qualitative evaluation, 5 volumes were randomly excluded from training. Voting maps have been created for each surface landmark in a 31×31×31 cubic search space around the real landmark positions. Candidates have been determined at the weighted mean of smoothed voting map maxima.

**Results:** Our results show an excellent surface detection capability. Votings enclose target boundaries while being constraint on the target surface by the respective true landmark positions.

**Conclusions:** Both search space flexibility and strong detection capability of our method are very promising in terms of better segmentation accuracy, especially on low-quality images and for complex target structures.

**Acknowledgements:** This work was funded by the German Research Foundation (DFG), as part of the collaborative research centre for Cognition-guided Surgery (SFB/TRR125).

**References:**

**Figures:** Black patches represent the cubic search space. Inside, voting maps indicate meaningful candidates, represented in red. Right figure: Candidate landmarks in yellow, ground truth in red.
GEODESICALLY DAMPED SHAPE MODELS

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Background: Statistical shape models are well established in medical image segmentation. On the basis of sample shapes, a segmentation is sought within the span of these samples. If the given samples do not cover the full variation of the desired object class, the statistical model bias might be too restrictive. We present a method for model bias reduction. This is achieved by damping the empirical correlations between points on the surface which are geodesically wide apart. This yields locally more flexibility of the model and a better overall segmentation performance.

Aims: Statistical model bias reduction by geodesic correlation damping for more flexible shape models.

Methods: Our method is based on the Gaussian process framework of [1], where empirical covariances are combined with a generic shape prior \( k_{\text{comb}} = k_{\text{emp}} + k_g \). Performing a low-rank approximation of the resulting kernel function yields a generative linear model \( \mathcal{M}[\alpha] = \mu + \sum_{i=1}^{n} \phi_i \alpha_i \), where \( \phi_i \) are the main \( n \) orthogonal basis functions of the kernel. In our method, we propose to damp the point correlations with respect to their geodesic distance on the reference surface. Let the reference shape be represented by a label map \( L_R : \mathbb{R}^3 \to \{0,1\} \), where the value 1 indicates object and 0 the background. We define the reference surface as \( \Gamma_R := \{ x \mid x \in \partial L_R(x) \neq 0 \} \subset \mathbb{R}^3 \). The geodesically damped kernel becomes \( k_{G_{\text{comb}}} = k_{\text{emp}}, k_g \), where

\[
k_g(x,y) = \exp\left(-\frac{\psi(L_R, x, y)}{\sigma^2}\right)
\]

and \( \psi \) returns the geodesic distance on the surface.

For the object segmentation, we follow the approach of [2], to estimate the object probability map \( P_T : \mathbb{R}^3 \to [0,1] \) of the target image. However, instead of integrating over the full image domain, in our approach we solely consider the object boundary

\[
\arg \min_{\alpha \in \mathbb{R}^n} \int \frac{1}{1 + |\nabla P_T(x)|} L_R(x + \mathcal{M}[\alpha]) \, dx + \lambda|\alpha|^2
\]

where \( \lambda \) is a trade-off parameter.

Results: We tested our method with a CBCT dataset containing 47 images of the jaw region, where we segmented the wisdom tooth shape. We compare the following variants of our approach: the combined geodesic \( k_{G_{\text{comb}}} \) and the combined Gaussian model \( k_{\text{comb}} \). The pure empirical model serves as baseline. The separate Gaussian \( k_g \) resp. geodesic kernel \( k_g \) are provided as well. We evaluate the results using the bidirectional local distance (BLD) measure between the fitting results and the ground truth target shapes (see Table 1). Both of the combined models perform better than the empirical and the generic models. Figure 1 serves as a qualitative example to show the expressiveness of the \( k_g \) and \( k_f \) model.

Conclusions: Combining statistical shape models and generic shape priors greatly improves the expressiveness of the model as well as the segmentation performance. In particular, the geodesic model performs well in case where points are close together in an Euclidean sense but topologically wide apart.


<table>
<thead>
<tr>
<th>Model</th>
<th>BLD (mm)</th>
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<tr>
<td>( k_{\text{emp}} )</td>
<td>0.288/0.390</td>
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<tr>
<td>( k_f )</td>
<td>0.256/0.391</td>
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<tr>
<td>( k_{G_{\text{comb}}} )</td>
<td>0.240/0.301</td>
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<tr>
<td>( k_g )</td>
<td>0.269/0.337</td>
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<tr>
<td>( k_{\text{comb}} )</td>
<td>0.251/0.301</td>
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Table 1: Numerical results, format: median/mean

Figure 1: For this specific example, the ground truth target label map has been used as \( P_T \).
Towards a Practical Clinical Workflow for Cardiac Shape Modeling, with Application to Atrial Fibrillation and Stroke

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Background: The scientific and clinical motivation for this work comes from research at the University of Utah in atrial fibrillation (AF). AF is characterized by uncoordinated electrical activity and contractions in the left atrium (LA). AF is associated with increased mortality and several morbidities, the most notable of which is that due to stroke. Shape change in the LA and other heart chambers in AF is not well understood, but is hypothesized to be an indicator of the AF pathology and to play a role in the formation of thrombus (precursor to stroke) in the left-atrial appendage (LAA). In addition, cardiac shape atlases, particularly of the LA, will allow us to study the spatial patterning of fibrotic tissue changes due to AF.

Aims: To develop a practical shape modeling workflow for cardiac anatomy with the eventual aim of supporting large-scale research trials. The motion of the heart chambers, their open surface topologies (e.g. valve and vessel openings), and their highly variable appearance all present special challenges.

Methods: Pre-treatment and follow-up cardiac MR imaging is performed on AF patients presenting at the University of Utah Hospital EP Clinic. Image sequences include a respiratory and ECG-gated MR angiography acquired during continuous gadolinium contrast agent injection, followed by a 15 min. post-contrast LGE sequence [1]. Endocardial borders of cardiac structures are segmented semi-automatically from the MRA image. Fibrosis in the LA wall is segmented from the co-registered LGE image. For shape modeling, we use the particle-based modeling (PBM) framework developed by Cates, et al. [2], with extended functionality for masking out surface openings (vein ostia and valves). PBM models compute dense sets of correspondences points and we use PCA for dimensionality reduction.

Results: Preliminary results of applying our modeling workflow to problems in AF research include the following studies: (1) An AF population atlas of fibrosis distribution (N=160), which suggests fibrosis develops mainly in the posterior region of the LA near the pulmonary veins (see Figure 1); and (2) Description of significant shape differences (independent of volume) in the opening of the LAA for age and gender-matched patients with and without history of stroke (N=30, p < 0.01, Figure 2).

Conclusions: Our approach is proving effective for the study of AF and is currently in use for several clinical investigations. However, future work remains to incorporate modeling of valve and vein annuli directly and to reduce computation time to allow scaling from hundreds to thousands of subjects.

Acknowledgements: Marrrek, Inc. and the National Alliance for Medical Image Computing (U54 EB005149)


Figure 1: Shape atlas of the LA, showing fibrosis in mainly centered in the PA region of the LA

Figure 2: Significant shape differences are found narrowing of the LAA opening in a population of sufferers with history of stroke
Background: Magnetic resonance guided high intensity focused ultrasound (MRgHIFU) therapy is a promising new technology to ablate tissues non-invasively. Exact knowledge of the location of the target organ as well as the risk structures on the beam path is crucial to a successful therapy. One particularly important structure is the ribcage due to its vicinity to the liver, and bones’ absorption and reflection of ultrasound energy causing harm to themselves and the surrounding tissues. Therefore, it is necessary to detect ribs in MR images.

Aims: We tackled the problem of rib detection in MRI. This is a challenging task, as bones do not emit sufficient magnetic signal and are relatively small structures.

Methods: We used two independent datasets from healthy volunteers. A CT dataset including 20 end-inhale images and an MR dataset of 21 end-exhale MR images with spatial resolution of 1.37×1.37×1.37mm³, and 1.33×5×1.33mm³, in anterior-posterior, left-right, and inferior-superior directions, respectively.

Our method is based on combining a ribcage geometric model generated from CT images and a rib appearance model from MRIs. It requires the definition of one landmark per rib, and 2 extra landmarks per subject. For the ribcage geometric model, ribs were segmented in CT images using a region growing algorithm. Correspondence between ribs was established by dividing each rib into two segments at its angle point (most posterior point) and uniformly subdividing each segment by a fixed number of points (100 in total). The geometry of each rib was initially defined by its shape (3D locations of 100 points), length and orientation (3 angles). Since these attributes have a high degree of correlation in a ribcage, we built statistical population models based on principle component analysis (PCA) to find their main modes of variation for ribs 7-10, which enclose the liver. First the shape parameters were reduced to 2 principle components (covering 96% shape variability) per rib. Then further PCAs were performed for 8 = 4 × 2 rib shape parameters (2 PCs), 12 = 4 × 3 Euler angle values (5 PCs), and 4 length values (2 PCs), keeping enough PCs to cover 95% variability.

The appearance model was based on 4 region-specific random forest classifiers [1], which were trained to discriminate between rib and non-rib patches, see Fig. 1. The classifiers employed normalized intensity based features.

The aforementioned 9 PCA coefficients, (2 for shape, 2 for length, 5 for angle), were used to generate rib centerline hypotheses, consisting of 4 centerlines, each having 100 points. The hypotheses were generated by uniformly drawing samples from the interior of a 9-D hyper-ellipsoid, which covers 95% of the multidimensional Gaussian distribution associated with the PCA models. Finally, the most likely rib location was determined by accepting the hypothesis whose corresponding image patches provided the highest probability of rib appearance.

Results: The RF classification accuracy was 89% on average. The extracted centerlines from 21 volunteers had a mean (90%) distance of 8.1mm (17.96mm) from the manually selected centerlines.

Conclusions: We have shown that, despite their poor visibility, ribs can be detected in MRI by taking advantage of the accuracy of CT images in observing the ribs. This was achieved by learning a statistical ribcage shape model from CT and combining it with an MR appearance model.

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AUTOMATIC EXTRACTION OF HAND-BONE SHAPES USING RANDOM FOREST REGRESSION-VOTING IN THE CONSTRAINED LOCAL MODEL FRAMEWORK

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Background: The ability to accurately detect feature points of deformable models is important for a wide range of algorithms and applications. A widely used approach is to apply a statistical shape model (SSM) to regularise the output of independent feature detectors trained to locate each point. Examples include Active Shape Models (ASMs) [1] and Constrained Local Models (CLMs) [2]. The task of the feature point detector is to compute a probability that the target point occurs at a particular position, given the image information. Local peaks in this correspond to candidate positions (e.g. ASMs), or the probabilities for each point are combined with the SSM shape constraints to find the best overall match (e.g. CLMs).

Aims: To show that Random Forest (RF) [3] regression-voting is a powerful technique that leads to fast, accurate and robust feature point detection results when used in the CLM framework, and to demonstrate its accuracy and robustness by applying it to the annotation of the joints of the hands in radiographs.

Methods: During training, we randomly sample features from patches around each point and train a RF regressor to cast votes for its optimal position. We also build an SSM over the point positions of all training images. During search, we apply the RF regressors over a grid of the estimated position of each point, and accumulate the votes to obtain a 2D histogram of votes for every point. Using the shape constraints of the SSM, we then combine the votes of all histograms by maximising the number of votes over all points and update the point positions accordingly. We evaluate the technique in detail by applying it to 564 hand radiographs of children aged between five and eighteen years, aiming to annotate the joints of the hands using 37 points. Here, we apply RF regression-voting as part of a fully automatic shape model matching system: We use our own implementation of Hough Forests [4] to estimate the position, orientation and scale of the object in the image, and use this to initialise the shape model matching. We follow a coarse-to-fine, multi-stage approach where every RF regressor is trained on Haar-like features [5] and uses 10 trees. The fully automatic system can process one hand radiograph in less than a second.

Results: In Figure (a), we show that our approach outperforms alternative techniques and that it achieves a mean point-to-point error of within 1.1mm for 99% of 564 images (assuming an average wrist width of 50mm). Figure (b) gives the first mode of the SSM to demonstrate the shape variation present in the dataset, and Figures (c-d) show the 95%ile annotation result and superposed 2D histograms of votes.

Conclusions: RF regression-voting in the CLM framework outperforms alternative feature point detection techniques, achieving what we believe to be the most accurate hand joint annotation results yet published.

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Figures: Fully automatic hand joint annotation system (using 37 points): (a) performance comparison to alternative shape model matching techniques; (b) first mode of shape model; (c) 95%ile annotation result (mean point-to-point error: 0.8mm); (d) superposition of 2D histograms of votes over all points.
Background: Research on segmentation methods of the right ventricle has for a long time been neglected in favor of the left ventricle. However, as the right heart’s role in cardiovascular diseases is being more widely recognized, interest in right ventricle segmentation is growing. Modeling of the right ventricle is inherently more challenging than the left ventricle, because of increased anatomical complexity and larger inter-patient variations. For echocardiography in particular, weak myocardial borders and a challenging acquisition makes the problem even harder.

Aims: To develop a geometrical model of the right ventricle that will support a robust and computationally efficient automatic segmentation method for 4D echocardiographic images.

Methods: We propose to use a Doo-Sabin subdivision surface as the underlying geometrical representation of the right ventricle. This enables an anatomically accurate model with a compact parameterization, and inherently enforces regularization and C1 continuity. The surface is parameterized by 35 control vertices; 9 on the septum, 12 on the free wall, 5 at the tricuspid annulus, 8 at the outflow tract, and one at the apex. We derive the statistical modes of variation from manual segmentations of 12 short axis cine-MRI recordings each with 20 phases, including healthy subjects and patients with heart disease from an open access database [1]. For each patient and each phase, the endocardial borders in all slices were traced manually. The Doo-Sabin surface was then fitted by minimizing the sum of Euclidean distances between surface points and endocardial borders using gradient descent optimization.

Results: The dice similarity coefficient between the fitted subdivision representation and manual segmentation were 0.90 ± 0.030. Using the first 24 modes of variation, constituting at least 95 % of the total variance, the leave-one-out reconstruction absolute volume differences were 12.87 ± 10.7 % and point-point distances were 3.1 ± 1.4 mm.

Conclusions: The proposed Doo-Sabin surface is well suited to represent the right ventricle.

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AN AUTOMATED STATISTICAL SHAPE MODEL DEVELOPMENTAL PIPELINE: IMPLICATIONS TO SHOULDER SURGERY PARAMETERS

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Background: Being able to represent 3D structures with high sample variability, use of Statistical Shape Models (SSMs) of bones has been proven effective in surgical planning and biomechanics research [1]. Despite its importance, SSMs of shoulder bones (scapula (S) and humerus (H)) have not been evaluated – primarily due to the complexity involved.

Aims: To build an automated and unbiased global SSM of S and H bones from a set of CT scans using open source tools (VTK, ITK, and Statismo) and to evaluate the method for generality, specificity, and compactness criteria.

Methods: CT scan images of dry bones of 27 S and 28 H were acquired using Siemens SOMATOM scanner. The CT scans were segmented in Amira (v5.4.3, Visage Imaging) and a smooth 3D surface mesh was extracted. This surface was remeshed to acquire an isotropic vertex count of N = 15000 for each bone sample. Using an Iterative Median Closest Point (IMCP) algorithm, an intrinsic consensus shape was established. In this groupwise rigid registration based algorithm [2], each sample was registered on its virtual form representing the consensus of the correspondence information in all the data. For each point in the data, robustly matching neighbor points were used to calculate a virtual corresponding point leading to the virtual shape building. By using a Tukey W-estimator to weight the reliability of each point, a consensus emerged as a dense unorganized point cloud. This process eliminated the need for manual landmarking, region building and reference selection that induce bias. Making the intrinsic consensus shape as a reference, a non-rigid registration of the original data on the intrinsic consensus shape was performed using point set registration method called Coherence Point Drift (CPD)[3]. The 3D mean of the outcome of the CPD algorithm was called mean virtual (Mv) shape. We iteratively used the CPD algorithm to transfer and optimize one-to-one correspondences of the Mv shape on the original datasets to form Mv estimates. The trade-off between data fitting and smoothness of the deformation field was empirically determined. Each of the Mv estimates was a 15000 vertex mesh in dense correspondence with other instances and the respective Mv shape. SSM of S (Figure 1(a)) and H was derived by conducting a probabilistic Principal Component Analysis (PCA) on Mv estimates using Statismo toolkit [4].

Results: The quality of the Mv estimates was tested in terms of 3D shape approximation of the original data (surface distances). The anatomic correspondence transference quality checked using the anatomical landmarks on the basis showed 95-100% correspondence. For S, first seven principal components accounted for 90% of variation (Figure 1(b)) and for H, first two accounted for more than 90% of variation showing a good compactness. This method was compared with 1) Expectation Maximization-Iterative Closest Point algorithm (EM-ICP)[5], and 2) groupwise Gaussian mixture model (GMM)[6] based registration on hippocampi data (n = 42) and performed equal to or better than these two methods based on generality (Figure 1(c)), specificity and compactness criteria.

Conclusions: This methodology successfully developed SSMs of three bony structures of varying complexity. The automatic segmentation, unbiased reference selection, and the use of probabilistic PCA makes this methodology a robust and accurate pipeline to develop SSMs. Future work aims at using the SSMs on real patient data to evaluate shoulder morphological and clinical analysis.

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Figure 1: (a) Shape variation pattern for the first three principal components of the scapula (without size). (b) Cumulative contributions of the first principal component for scapula SSM. (c) Hausdorff generality measurements (mm) from three methods for the hippocampi data.
Background: Human bone cortical thickness and in the particular case of this study, humeral cortical thickness, plays an important role in clinical diagnosis, bone fracture treatment, prosthetic design, finite element simulations involving the shoulder, forensics and paleontology [1-3]. Despite all these well documented uses, there are no statistically relevant published results of the full humeral shaft (diaphysis and proximal metaphysis) cortical thickness.

Aims: To analyze in detail humeral shaft cortical thickness in three dimensions. To produce a statistical cortical thickness map with average thickness and main modes of variation and to create a model capable of extracting detailed humeral shaft thickness maps based on limited or noisy medical image data.

Methods: Sixty nine humeri obtained from cadavers, CT scanned at high resolution (0.5x0.5x0.5mm). Each scanned bone data was segmented and reconstructed (both endosteal and periosteal surfaces) in 3D, the bone shaft (Metaphysis and Diaphysis) was cut in a direction perpendicular to the humeral shaft axis with one hundred cut slices and one hundred thickness measurements per slice resulting in ten thousand measurements per bone. Correspondence, geodesic unwrapping, parameterization and principal component analysis is used to produce a mean thickness map and the main modes of variation. A statistical shape model is created and validated using measures of compactness, reconstruction ability, generalization ability, specificity, interpolation and extrapolation abilities and robustness to noise.

Results: Observed humeral shaft cortical thickness varied between a minimum of 1 mm to a maximum of 12 mm. Higher thicknesses values are always observed more distally and lower thicknesses more proximally. The mean goes from approximately 5 mm to 3 mm with a standard deviation of 1.5 mm distally and 1 mm proximally, with an overall mean of 4.2 mm. Cortical thickness does not follow a normal distribution, but a mixture of simple unimodal distributions (2 unequal normal distributions with p=0.2731, mean 1 = 2.6786, mean 2 = 4.7719, sigma 1 = 0.5816, sigma 2 = 1.1645) can model the data well. The statistical shape model is compact (the first 3 modes account for 89.32% of the variance). For potential real world applications like the derivation of full thickness maps from planar X-rays, high inter slice spacing CTs, noisy data or incomplete data from bone fragments, the model shows good performance in the required characteristics, namely inter and extrapolation abilities and robustness to noise, the mean absolute error never exceeds 13% of the average cortical thickness.

Conclusions: This is the first full description of humeral cortical thickness. This model opens the door to the creation of detailed, individualized 3D thickness maps of the humeral shaft using only planar x-rays, low resolution CT data or even incomplete data. The developed methodology is applicable to other long bones with an intramedullary canal e.g. femur.


Figures: (a) Humeral Shaft Cortical thickness color mapped to the bone and unwrapped (b) example of parameterized thickness map
SSM-BASED 3D CUP PLANNING FROM TWO CONVENTIONAL X-RAY IMAGES

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Background: Preoperative planning is an important means for the clinician to optimally prepare the surgical intervention [1]. The conventional planning of Total Hip Arthroplasties (THAs) relies on plain X-ray images. As these images only provide two-dimensional (2D) projections of the three-dimensional (3D) bony anatomy and the radiographic magnification is normally not precisely known, the best fitting cup implant can only be approximated. An incorrectly selected implant size could lead to bone fractures, limb length inequality or implant instability.

Aims: In order to optimize the cup planning, we propose an integrated approach for X-ray calibration, 2D/3D reconstruction and automatic cup planning.

Methods: Our approach requires the acquisition of minimally two X-ray radiographs (e.g. anterior-posterior (AP) and outlet view) of the patient’s pelvis. The spatial relationship of the images is determined by integration of a specifically designed calibration phantom into the X-ray acquisition process [2]. For a set of minimum two calibrated radiographs the 2D/3D reconstruction pipeline as presented by Zheng et al. [3] was applied. This pipeline non-rigidly deforms a statistical shape model (SSM) of the pelvis to the contours extracted from the X-ray images, resulting in a patient-specific surface model of the pelvis. This reconstructed model was further matched to a combined statistical atlas as developed by Otomaru et al. [4]. This statistical atlas consists of pelvis surface models extracted from computed tomography (CT) scans and manually planned cup implant data. The proposed approach was evaluated based on digitally reconstructed radiographs (DRRs) from CT-datasets of Japanese patients scheduled for THA. Our presented pipeline was applied to these datasets and the resulting cup plan was compared to the manually planned cup using the original CT-datasets.

Results: In total 16 DRR datasets (AP & outlet view) were generated. On average the pelvis was reconstructed with a Euclidean distance error of 1.60 ± 1.51 mm. The automatic planning approach using the X-ray reconstructed surface model predicted the correct cup size with a success rate of 87.5%.

Conclusions: The proposed pipeline of X-ray calibration was evaluated based validated in a pre-clinical trial using DRR datasets, demonstrating higher prediction rates than conventional X-ray based plantings.

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Figures: (a) Checkerboard visualization of reconstructed pelvis superimposed on AP radiograph (b) Reconstructed pelvis model with surface-distance map indicating the surface reconstruction accuracy (c) Comparison of automatically planned cup (yellow) versus manually planned (green). Contour of reconstructed pelvis is shown on top of CT slice in red color.
Background: It is crucial to understand the anatomy and anatomical variability of the inner ear in order to improve the design and functionality of implantable hearing devices such as Cochlear Implants (CI). Statistical shape modelling of the inner ear provides a versatile tool that can aid numerous interesting Cochlear Implant applications, in particular implant design optimization and surgical planning. The spiral-shaped cochlear of the inner ear presents an anatomy with small important features that can only be properly perceived in high resolution micro-CT scans of cadaveric specimens. The complex anatomy and the large data sizes make it a challenging dataset to handle and to build a shape model from.

Aims: To build a statistical shape model of the inner ear from high resolution micro-CT data.

Methods: 17 temporal bones excised from human cadavers were dried and scanned with a micro-CT system (Scanco Medical, Switzerland). The region of interest in the datasets was reconstructed in 24 micron isotropic voxels (resulting in approximately 6GB of data per scan). Segmentation: The inner ear (cochlear and vestibular system) was segmented manually using ITK-SNAP[1]. The surfaces of the segmentations were extracted using Marching Cubes and post-processed using MRF surface reconstruction[2] to provide smooth and well-formed surface meshes. Registration: One dataset was chosen as a reference. An initial rigid transformation aligning the center of mass and the principal directions was calculated. The principal directions are consistent due to the asymmetric shape of the inner ear. This was followed by a deformable registration using elastix[3]. A multi-level B-spline grid minimizing sum of squared differences with bending energy regularization was used. The registration was between the segmentation images to reduce the influence of the noise in the micro-CT data.

Model Building: The transformations were applied to the reference surface model, to create surfaces representing the anatomy in the individual datasets with point correspondences. Using Statismo[4] a point distribution model (PDM) was built (Figure 1-3).

Evaluation: The quality of the model is constrained by the accuracy of the registration which is evaluated against the ground truth segmentation using Dice score and Hausdorff distance (the latter calculated with the ‘ground truth’ surface model).

Results: A PDM of the inner ear containing 466k vertices and 16 modes of variation (Figure 1-3). The average Dice score was 0.96 ± 0.01 and average Hausdorff distance 0.69 ± 0.24 mm.

Conclusions: An inner ear shape model has been built using open source libraries and tools. The model has more anatomical detail and modes of variation than what has previously been reported.

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Background: The identification of one-to-one correspondences between point clouds is the weak point of model-based methods. We extended the method of Hufnagel et al. [1,2], that proposed the use of probabilistic correspondences instead of one-to-one correspondences for statistical shape models, by incorporating appearance information for shape and appearance models (SAMs).

Aims: The purpose of this work is to open up new directions for SAMs without one-to-one correspondences, where position and appearance feature are modeled at the same time using one global optimization criterion.

Methods: We introduce a point-based representation of image data, which enables an image registration using a variation of the Expectation Maximization-Iterative Closest Point (EM-ICP) [3] for multidimensional feature vectors. The image is represented by a set of vectors assembling position and appearance features at (randomly located) sampling points. Then, we use a maximum a-posteriori approach with probabilistic correspondences between these vector sets of different image representations (observations) to derive a single global optimization criterion with respect to the model parameters (the mean shape and appearance and its variation modes) and the observation parameters (transformations and weights of variation modes). The same optimization criterion maximizes the a-posteriori probability of the parameters given a set of observations during the model generation as well as the model fitting.

For segmentation purposes additional information e.g. label information can be included into the model and then transferred during model fitting onto unseen images.

Results: In a first evaluation on 2D lung CT slices the feasibility of the model generation method and the model-based segmentation is shown. An example of a model instance after model generation is visualized in Fig(b).

Conclusions: The use of point-based representations and probabilistic correspondences between them increases the efficiency of SAMs: no (accurate) landmark determination is necessary, no warping step to align the image intensities is needed, and one global optimization criterion is minimized. The method also shows high flexibility, because the approach is independent of the choice of appearance features and of the number of additional information (labels) opening up the method for multi-object segmentation.

Furthermore, using probabilistic correspondences the number of sampling points has not to be the same in different images.


Figures: (a-b) point-based representation of mean model (a) and one model instance after model optimization (b): only the first feature (mean gray value of a neighborhood of each sampling point) is visualized. The red and green contours are the contours of the additional label information. (c) shows the corresponding input image with the contour of the mean model (red) and the adapted segmentation after model-generation (green). It is notable that the features as well as the sampling point positions are adapted during the optimization.
Background: The native aorta in newborns with hypoplastic left heart syndrome (HLHS) is typically underdeveloped, thus requiring surgical reconstruction and enlargement with a homograft patch to enable systemic blood flow from the single right ventricle. However, morbidity and mortality in these patients remain high after surgery. The shape and size of the reconstruction are important factors affecting the hemodynamics in the aortic arch, as well as likely impacting on ventricular performance by inducing changes in afterload. In order to better understand the physiology of repaired HLHS and potentially facilitate the diagnosis of abnormal or high-risk cases, an average reference model of the aortic arch is desirable. Such a representative mean shape of the patient population (the “atlas”) helps to quantify shape variations in 3D and allows for statistical correlation of shape features with clinical outcomes.

Aim: Calculating a 3D shape atlas of the surgically reconstructed aortic arch in patients with HLHS in order to describe shape features for correlation with clinical parameters.

Methods: This is a retrospective study based on a patient population of n=40 children with HLHS who underwent surgical arch reconstruction and subsequent cardiovascular magnetic resonance (CMR) examination. Three-dimensional surface models of the surgically enlarged aortic arches, excluding the brachiocephalic arteries, were reconstructed from the CMR 3D whole-heart sequence and served as input data for the atlas calculation. The surfaces were encoded as currents allowing pair-wise registration without assuming a parameterisation of the surfaces. The atlas and its registration toward each subject were estimated using an alternate minimization strategy based on a forward approach [1]. Principal Component Analysis (PCA) was applied to the resulting shape vectors to determine the dominant shape modes in our population. Non-parametric bivariate correlation analysis was used to correlate shape modes to clinical parameters.

Results: The resulting 3D shape atlas is shown in (a). Ten principal deformation modes from PCA accounted for 90% of the shape variation. Remarkably, shape mode 7 – describing the shape variation from a straight aortic arch to a more skewed arch with distinct size-mismatch between ascending and descending arch (b) – showed a significant correlation (p < .05) with ejection fraction (EF), which is a clinically relevant parameter related to cardiac systolic function (c).

Conclusions: We present a 3D shape atlas of the reconstructed aortic arch in patients with palliated HLHS. Our data suggest that clinical outcomes can be associated with shape features. Fluid dynamics simulations may provide further insight into the relation between shape and flow patterns in the aortic arch. Results from such analyses can improve risk assessment and potentially affect the surgical approach and technique adopted for completion of aortic arch reconstructions.


Figures: (a) 3D shape atlas, (b) variation of shape mode 7 around the atlas (green), and (c) correlation of shape mode 7 and clinical parameter ejection fraction, EF.
Background: Accurate diagnosis of prostate cancer relies on an accurate biopsy procedure. A biopsy must be performed on the center of a suspected malignant region in order to reliably diagnose the patient's condition. Tissue taken from the edge of this region, or outside the region altogether, can result in a negative test or misdiagnosis. The difficulty is that regions of interest (ROI) are identified on MRI images of the prostate, while image-guided biopsy is done using ultrasound. The great differences in appearance between these two modalities as well as shape deformations caused by the transrectal ultrasound transducer makes identifying these ROIs in the ultrasound image difficult.

Aims: To produce a method that can segment the prostate in 3D transrectal ultrasound and transfer identified ROI information from MRI images into 3DUS.

Methods: We introduce a method to segment the prostate in ultrasound using 1) a statistical model of prostate shape deformation caused by the transrectal ultrasound transducer and 2) regional ultrasound texture classifiers. Over a set of training data consisting of pairs of segmented MRI/3DTRUS images for each patient, we learn an average deformation and modes of variation of the prostate's shape between the MRI and TRUS images. We use skeletal representations (s-reps) to represent the prostate shapes [1], and build regions using corresponding locations of and near the object boundary across the training population. Using these, we learn regional classifiers of ultrasound tissue appearance (intensity and texture) using Distance-Weighted Discrimination[2] to yield probabilities of being inside the prostate.

For a target case, we apply the learned mean deformation to an s-rep fit to the patient's manually-segmented MRI image as an initialization. We deform the prostate shape along its modes of variation to match the image data. This image matching is performed by computing, for every voxel, the probability that it came from inside the prostate, based on its texture and location relative to the prostate boundary. Local s-rep boundary regions whose classification was shown reliable in training are adjusted in a refinement stage.

Results: We present results on a data set of 16 training and 13 target cases. We show the power of our appearance model in distinguishing between voxels from the interior and exterior of the prostate. Our segmentation results show good performance, with average MAD between our surfaces and ground-truth manual segmentations of 1.73mm and an average DSC of 0.892.

Conclusions: Regional classification via intensity and texture to yield probabilities together with a shape space on MRI-to-TRUS s-rep shape change results in attractive prostate segmentations.

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References:

Figure: Selected segmentation results, shown left against a slice of the TRUS image and right against the manual segmentation.
**Background:** We present a Quasi-conformal Geometry framework for genus-zero closed surface registration. We introduce a new energy functional involving Beltrami equation, which controls the conformality distortion and smoothness of the quasi-conformal map. The optimal diffeomorphic registration satisfying the prescribed landmark constraints is then obtained by minimizing the energy. We apply the framework to develop a pipeline of algorithms for statistical shape analysis on Brainstem surfaces.

**Aims:** To introduce a new landmark-based registration method for statistical shape analysis.

**Methods:** The two genus-zero closed surfaces $\Omega_1$ and $\Omega_2$ to be registered are first mapped conformally to spheres $S_1$ and $S_2$ using the fast spherical parameterization method proposed in [1]. For simplicity, we denote the conformal map to be $g_1 : \Omega_1 \rightarrow S_1$ and $g_2 : \Omega_2 \rightarrow S_2$ respectively. Secondly, we apply the least square Mobius transform to initialize the landmark-aligned registration. We then propose an iterative scheme called Quasi-conformal iteration [2] to minimize the follow energy:

$$\min_\mu \int_{S_1} \left( a |\nabla \mu|^2 + \beta |\mu|^2 + \gamma |\mu - f^0| f^0|^2 \right) \, dA,$$

where $f : S_1 \rightarrow S_2$ is the Quasi-conformal map between the spheres, $\mu$ is the Beltrami coefficients to be minimized. The optimal $\mu$ corresponds to the unique diffeomorphism which minimizes the proposed energy and satisfies the prescribed landmark constraints. The overall registration can then be obtained by $F : g_2^{-1} \circ f \circ g_1$. To evaluate morphological changes between registered individual brainstems and the mean surface model, we define the Shape Index:

$$\rho |\mu|^2 + \delta |H_2 - H_1|^2 + \sigma |K_2 - K_1|^2,$$

where $H_1$, $H_2$, $K_1$, $K_2$ are the mean and Gaussian curvature of $\Omega_1$ and $\Omega_2$ respectively. Discretely, vertex correspondences between $\Omega_1$ and $\Omega_2$ are established and each vertex contains the index value. By using the Hotelling’s T-squared test, we can then apply the p-values from shape index of both normal and abnormal groups of brainstems.

**Results:** Figure (a) shows the pair of brainstems $\Omega_1$ and $\Omega_2$ to be registered. (b) shows the spherical conformal parameterization $S_1$ and $S_2$ of the brainstems. (c) shows the registration result and (d) shows the shape index (left) and the p-values (right) on $\Omega_1$.

**Conclusions:** We propose a new landmark-based registration method and a pipeline of algorithms for genus-zero closed surface statistical shape analysis. We also apply this to brainstem morphometry to show the effectiveness of our method.

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**References:**

Figures: (a) Original brainstems pair. (b) Spherical conformal parameterizations of the brainstems. (c) Registration result. (d) The shape index (left) and the p-values (right) on the brainstem.
INFLUENCE OF CORRESPONDENCE METHOD ON STATISTICAL MODEL BASED SHAPE PREDICTION

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Background: Since the introduction of statistical shape models (SSMs) [1] in the mid-'90s, shape modelling has been used in a broad range of applications such as automated segmentation, target tracking and shape analysis. One of those applications is the prediction of shapes based on partially known information. These predictions would enable the use of medical images of confined field of view around the knee in preoperative surgical planning by estimating, e.g., the mechanical axis.

Aims: We evaluate the influence of the correspondence method on shape prediction of the proximal part of the femur. Five different correspondence methods are evaluated on 90 femurs. To our knowledge, no research has been done on the impact of the correspondence method on model based shape prediction.

Methods: Our shape prediction method is based on concepts introduced in [2]. The shape prediction is computed as the conditional expectation of a joint distribution composed by the shape space of the training set separated in a known and unknown part, conditioned on the object under consideration. This approach assumes both an adequate correspondence in the training set as well as with the object.

In total, 90 cases were used to train the models. The cases were segmented from two sets of images: the first set consisted of CT scanned dry bones (GE LightSpeed VCT; 0.813 x 0.813 x 0.625 mm), the second set consisted of clinical CT scans (GE LightSpeed VCT; 0.625 x 0.625 x 0.625 mm) from which symptomatic bones were excluded.

Five different correspondence methods were considered in this experiment. The first method employs a non-rigid morphing strategy (MORPH) to establish correspondence. The next two methods are based on non-rigid iterative closest point registration [4] regularized by an elastic stiffness parameter (WARP), which can be extended with model based regularization (MBWARP). The final two methods start by parameterizing the femurs as cylinders [5], followed by a rigid (RCyP) or non-rigid (NRCyP) minimum descriptor length (MDL [3]) optimization, generally considered as the optimal correspondence criterion.

Results: We performed a full leave-one-out experiment to test the influence of the different methods. Fig. 1 illustrates that the accuracy of the prediction largely depends on the correspondence method used. Both warping methods and the non-rigid MDL-optimized cylindrical parameterization outperform all other methods significantly. Fig. 2 shows that the influence of the correspondence method on accuracy cannot be compensated by increasing the training set, a resolution that is often proposed in literature.

Conclusions: We conclude that an adequate correspondence is not only important for the quality of the model, but also has an impact on its application in statistical model based shape prediction. Errors introduced by the correspondence methods are thus likely to propagate through the prediction of shapes.

References:

Fig. 1 - Root mean square (RMS) error of fitted versus original bone (point to surface) for all correspondence methods. The inset shows a paired left-tailed t-test with significant p-values in bold (α = 0.05), skewness of data is resolved using the log10 transform

Fig. 2 - Root mean square (RMS) error of fitted versus original bone (point to surface) in function of the size of the training set. For each set, random cases were taken from the full training set.
Background: Delineation of ocular anatomy in 3D imaging involves a big challenge for ophthalmologists, mostly when developing the treatment planning for ocular diseases. Magnetic resonance imaging (MRI) is used today in clinical practice as a complementary source of information, together with fundus imaging or ultrasound, in diagnosis and treatment planning for retinoblastoma in children. Here we present a novel 3D statistical Active Shape Model (ASM) to automatically segment the eye anatomy in the MRI.

Aims: To develop an Active Shape Model (ASM) based on 3D MRI for precise children eye segmentation.

Methods: Our data set is composed of 12 healthy eyes from children aged 3.2±1.7 years old. Imaging was performed a 3T Siemens TimTrio machine (Siemens, Erlangen, Germany), with a 32-channel surface head coil attached. The images are T1-Weighted GE VIBE (TE/TR, 3.91/20 ms). The Dataset has images which were acquired at two different spatial resolutions of 0.416x0.416x0.399 mm and 0.48x0.48x0.5mm. All the volumes were resampled to a common space 0.416x0.416x0.399 mm for constructing the model. The eye model comprises the regions of the lens, the vitreous humor, the sclera and the cornea. Manual delineations were done for all subjects and structures. They were corrected for all orthogonal planes by a senior radiation oncologist. The model construction is done by combining all the surfaces extracted from the manual delineation, generating a shape variation model, and coupling it with the intensity information to build the ASM as suggested in [2,3]. The segmentation of a subject works as follows. We first automatically detect the position of the center of the eye, the lens and the optic nerve, using the algorithm proposed in [4] for aligning the model. Afterwards, we proceed to do the fitting by minimizing the Mahalanobis distance between the ASM and the subject until convergence. We quantitatively validate our segmentation method with a leave-one-out cross validation test. The resulting segmentation is assessed by the overlapping measure (Dice Similarity Coefficient, DSC) with the manual segmentation used as the ground truth (GT). Additionally, we provide a measure of the mean distance error of the given segmentation wrt. the GT for every region in the eye.

Results: Through the leave-one-out test for the ASM fitting, we obtain an average DSC of 96.68±1.24% for the sclera and the cornea, a 95.88±1.73% for the vitreous humor and 84.41±3.4% for the lens. The mean overall distance error is 0.20±0.09mm for both the sclera and the cornea and the vitreous humor. For the lens we reach an average error of 0.21±0.1mm. The entire segmentation process takes in total 8 s.

Conclusions: We have shown a reliable and accurate segmentation tool that enables clinicians to automatically delineate the sclera, the cornea, the vitreous humor and the lens in MRI. This tool will contribute to reduce the time spent in the tedious task of eye shape delineation and will eventually help clinicians during ocular tumor treatment planning and diagnosis confirmation.

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Figures: (a) Pre-processed MRI. b) Model Initialization c) Automatic Fitting. d) Final Segmentation.
ANATOMIC SEGMENTATION OF STATISTICAL SHAPE MODELS

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Background: Shape segmentation is one of the fundamental tools in shape processing and analysis, and it provides a starting point for building part based shape models. A multitude of methods for segmenting static and dynamic shapes has been developed over the last decades [1] based on various intrinsic and extrinsic geometric features. Interestingly, so far no method seems to make explicit use of a statistical shape model, as the method presented here does. Considering additional model information, a segmentation based on (co-)variation of individual parts can be derived. This allows defining meaningful shape parts in the sense that all points in a part behave similar according to the model, while different parts show distinct variation patterns. This is a desired property for instance in biological morphometrics, where independent modules are sought relating to an underlying independent evolutionary development of corresponding sub-structures. Another application area is motion analysis, where correlation between part movements is relevant for motion understanding and compression.

Aims: To introduce a novel automatic shape segmentation method driven by covariance analysis.

Methods: We use a recent variant [2] of the anatomic covariance tensor [3] to capture covariant behavior between points in a shape model. An inter-point covariance is defined via the model based deformation framework of Blanz et al. [4], i.e. given a perturbation at a specific point the most likely shape according to the PCA model is predicted. It turns out that this relationship can be summarized by a symmetric 2nd order tensor [2]. Based on this tensor we perform a k-medoids clustering of the shape points such that tensors in one cluster are similar to each other. As dissimilarity measure for clustering we use a weighted average of a metric for covariance matrices and the Euclidean distance between corresponding points on the mean shape. Increasing the distance weight allows to enforce spatially connected clusters. In the experiments described here we utilize a covariance metric induced by Frobenius norm, although other well-known metrics like Log-Euclidean could be employed depending on the application.

Results: Segmentations of two different datasets are illustrated together with underlying tensor fields, visualized as in [3]. A volumetric segmentation of a Biological structure is shown in Figs(A-D) using a non-zero Euclidean distance term to yield a strict anatomic segmentation. Figs(E-H) demonstrate the application to a mesh animation, omitting the Euclidean distance term to uncover correlated movements.

Conclusions: The presented clustering based on covariance statistics facilitates automatic anatomic and correlation based shape segmentation, potentially supporting part based shape analysis in future work.

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References:

Figures: (B,E) Illustration of datasets, (A,G) inter-point covariance fields, (D,H) our segmentation results, (C,F) k-means clustering of points for comparison. Note in (D) how clusters a to e nicely correspond to anatomical substructures of teeth, processes and incisor, while clusters i, j, k reflect interior structures.
Background: We aimed to identify shape change in the human mandible associated with age. We addressed the issue of changes associated with tooth-loss as well as general aging. Our data consist of 115 surface meshes representing the human mandible. Using CT-scans, automated landmark and surface mesh extraction was performed on 115 individuals, of which are 37 Chinese female, 43 Chinese male, 23 European female and 12 European male. As the Chinese were only little affected by tooth-loss, even at very old age, they were used as control set for age-related changes not attributed to tooth-loss. The European sample, however, showed severe tooth-loss for older individuals.

Aims: Estimating age related shape changes with and without effect of tooth-loss based on surface meshes registered deploying statistical models.

Methods: The automatically extracted landmarks were used to identify the individual closest to the sample’s average (Procrustes distance). The surface mesh of this individual then was deformed onto all other meshes using an elastic ICP-Algorithm consisting of two parts: An iterative Gaussian smoothed deformation is performed [1] with the resulting deformation being additionally regularized by minimizing deformation energy as defined in [2]. The matched vertices were registered by Procrustes registration, outliers were removed based on Mahalanobis distances and a statistical model was generated from these data. The surface mesh, with the mean shape’s coordinates as vertices, was set as template in the second run of the registration. Additionally, we included the statistical model. We applied the matching process with the additional constraints from that model: After each iteration the resulting shape was restricted to (increasing) boundaries estimated from the sample’s probability distribution (cf. [3]). Due to bad quality of the CT-data in the condylar region and the coronoid processes, as well as the inconsistent presence/absence of teeth, these areas were excluded from further statistical analyses.

Results: The resulting set of registered coordinates were statistically evaluated for effects of aging. The PC-scores of the first 20 PCs were, after correction for sex and population, regressed onto age. The predictor age was found to be highly significant in the European sub-sample and only mildly significant in the Chinese data. Visualizations show a similar pattern in both populations in the gonial region. But, while these are the only shape differences among Chinese, Europeans exhibit a significant “shrinkage” of the corpus mandibulae, when compared to the rami (Figures b, c).

Conclusions: We can conclude that age related shape changes of the mandible (excluding the condyles and coronoid processes) are only small when ruling out changes associated with tooth-loss loss and subsequent atrophication of the alveolar processes and only the shape of the gonial region seems to be affected – which is a consistent finding in both populations. The changes related to tooth-loss are those to be expected by atrophication with the consequent shift in mandibular shape and static properties making it more prone to deformations from masticatory forces, which might cause an outward drift of the rami.


Figures: (a) vertex references between template and target. Age-related differences in Europeans (b) and Chinese (c). Red: estimated at age 80; cyan: estimated at age 20.
Background: The generation of a statistical shape prior often starts with a set of rigidly (with regard to rotation, translation, and scale) aligned training shapes. Here, we use an implicit shape representation where the shapes are given as the zero level set of a higher dimensional signed distance function. A common approach to obtain a statistical shape prior for a certain shape class from this set of training shapes is to assume that all shapes, which belong to this class, are given by weighted linear combinations of the training shapes. The distribution of plausible shape weights is usually assumed to be Gaussian and can be obtained by a covariance analysis of the training shapes. In order to remove redundancy from the prior, it is common to additionally perform a principal component analysis on the set of training shapes. Using this approach to build a statistical shape prior, all shapes that can be modelled by the prior have to lie in the low-dimensional vector space spanned by the training shapes. Other shapes are not possible. The thus obtained prior works pretty well when the number of training shapes is sufficient to model the full intra-class shape variability. However, for simple shapes with limited intra-class shape variability, fewer training samples are needed then for complex shapes with high intra-class shape variability. The result is that in practice the prior is often too restrictive for complex shapes.

Aims: To obtain a good prior for complex shapes with only a limited amount of training shapes.

Methods: A common approach to cope with the problem of limited training data is to partition the shapes and use the prior to model them independently across the predefined segments. However, it is not always straightforward how to choose the segments. So, we propose another approach to handle the problem of limited training data without the need for any predefined segments. Our idea is to generalize the low-dimensional vector space of feasible shapes to a space that better represents the information which is available from the training data. This is achieved by replacing the linear combination of training shapes, where each training shape is weighted by a scalar factor, by a more general multiplication with smooth functions that may have a different scalar weight value in each pixel/voxel of the data domain. Thus, instead of a set of scalar weights that describes a modelled shape, we now have a set of smooth weight functions. The requirement that the weight functions have to be smooth ensures a continuous shape representation without discontinuities. Also, by controlling the degree of smoothness of our weight functions, we can obtain a smooth transition from a single global adaptation of the shape prior to pixel/voxel-wise local adaptations of the prior, where the final degree of locality is controllable.

Results: The benefit of our new formulation can be seen in figure (a). With only two training shapes available, it is not possible to model the partially occluded test shape with a global prior (blue line) but with our new global-to-local prior (red line). Furthermore, we recently showed the excellent performance of our new approach in an image segmentation task [1] and a shape reconstruction task [2]. Some exemplary results from these experiments can be seen in figures (b) and (c), respectively.

Conclusions: We introduced a new formulation for a global-to-local statistical shape prior that allows us to model complex shapes with only a limited amount of training data. This is achieved by replacing the set of scalar weights, which is used to describe a modelled shape, by a set of smooth weight functions.


Figures: Benefit of the global-to-local shape prior (a) and some exemplary approximation results (b-c).
**Background:** Shape and size of the left ventricle (LV) are routinely assessed to inform clinical diagnosis in several cardiovascular diseases such as hypertrophy or heart failure. Traditional metrics including end diastolic volume or wall thickness provide a gross characterization of variations in LV anatomy. Statistical atlases of computational anatomy have the potential to enhance the analysis of LV shape by introducing a further level of anatomical detail and discriminative power, and thus to improve patient stratification.

**Aims:** To investigate the comparative performance of conventional clinical vs atlas-based shape metrics of the LV in a classification problem.

**Methods:** 224 MRI studies of the LV (both long and short axis views), corresponding to three subgroups (preterm-born young adults, term-born young adults, and term-born older adults), were selected from a previous study [1]. Two classification tasks were defined in terms of gestational age (preterm vs term birth) and aging (young vs. older controls, with 10 years of difference). All cases were manually characterized by five metrics obtained in 2D views: LV length, endocardium and epicardium diameters, cavity volume and mass. Segmentation of the short axis stack needed for the estimation of volume and mass was used to generate a computational atlas. Computational meshes with high order interpolation were fitted to each case [2-3]. Atlas-based metrics were obtained by a projection of 3D meshes into three orthonormal directions of anatomical change defined a-priori (taking into consideration only mesh node coordinates), accounting for ventricular elongation, eccentric remodeling (changes in the epicardium) and concentric remodeling (changes in the endocardium) [Fig(a)]. The performance in a linear discriminant analysis by either the clinical or the atlas-based metrics was compared based on sensitivity and specificity statistical measures.

**Results and discussion:** Atlas-based metrics outperformed conventional clinical metrics in both classification tasks (preterm vs term-born and younger vs older controls), and with different number of clinical metrics used in the analysis [Fig(b-d)]. This result can be attributed to the capacity of the 3D meshes to capture a higher level of anatomical detail available in the images, and to a reduction of observer-dependence in the extraction of manual clinical metrics.

**Conclusions:** An automatic and robust pipeline for the segmentation, meshing and construction of atlas of the LV has the potential to improve patient stratification.

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**References:**

**Figures:** (a) Mean LV shape model (dark/blue mesh) and directions of anatomical shape change superimposed (top: elongation, middle: eccentric remodeling, bottom: concentric remodeling); (b-d) pairwise classification results between preterm-born young adults, term-born young adults and term-born older adults.
Background: The increased use of 3D models of organs or bones by the surgeon has lead to rapid development of new methods to automatize model generation. 3D models are generated from computerized tomography (CT) scans of patients with segmentation mainly done manually using appropriate software such as 3D Slicer [1]. The process takes about 1-2 hours and this time delay makes it unsuitable for some procedures, especially emergency surgeries. There is a real need therefore for rapid and precise automatic segmentation methods, the main challenge for computer-assisted medical applications, and this is where statistical shape model (SSM) is leading the way. Our case study focuses on segmentation and 3D model generation of the second cervical vertebra (C2). The C2, (or axis), presents very specific challenges to the surgeon during C1-C2 screw placement. Its unique shape is the most complex in the entire spine and renders it the most risky for implant placement. Screws are placed in the isthmus, which measures about 6mm while the screw diameter is 4mm so that maximum variation in implant placement is ±1mm (Fig(a)). A C2 3D model will optimize screw placement and provide rapid automatic planning for the surgery procedure.

Aims: Here we describe how to use a SSM generated from CT scans of the C2 to generate the C2 3D model for use in spine surgery.

Methods: To generate the C2 3D model, a SSM-based segmentation is performed on the input CT scans. A Statistical Shape Model of the C2 (C2-SSM) was created and used to fit it to the C2 of the patient. A constrained SSM is then computed using landmarks placed by the user on the input CT scans and the C2-SSM. These landmarks allow improving robustness of the method but also dealing with patient specificity. The constrained model is employed to obtain the 3D model from the CT scans by performing registration. The SSM-based segmentation is implemented using Statismo [2].

Results: The 3D model generation of the C2 was tested on 31 CT scans from anonymous patients. Using the 3D Slicer software (manual segmentation), generation of a realistic 3D model takes about 1 hour. In contrast, using our SSM method, a mean of 2min is required for all steps; from landmark placement on the CT scans to 3D model generation. The Euclidean distance and Dice coefficients computed from the manual model and the model obtained using our segmentation algorithm to give a mean distance error of 0.90mm ± 0.12 and a mean Dice coefficient of 0.85 ± 0.1 (Fig(b)). The shape differences between the manual and generated model are mainly located in the inferior articular facet of the vertebra, a zone where the distinction between two vertebrae is difficult to identify even by direct viewing of the CT scan (Fig(c)). These results are demonstrated the advantages of 3D generated models for surgery planning.

Conclusions: Until now, C2 segmentation was done manually slice-by-slice and is very time consuming. Using a SSM automates the process and rapidly generates the corresponding 3D model. User interaction is simplified and the time the surgeon has to wait for the 3D model is greatly reduced. Notably, using SSM-based segmentation, the surgeon will obtain the 3D model of the vertebra almost instantaneously after the patient CT scan, enabling rapid planning or adaptation of planning for spine surgery. The robustness of the SSM segmentation process can be improved by focusing the landmark to the region of interest depending on the problem: the isthmus for this application. Fitting can also be enforced in particular zone such as the inferior articular facet to become closer to the manually segmented vertebra. In conclusion, SSMs are invaluable tools for rapid and precise 3D model generations in surface merge algorithms, diagnosis (scoliosis, trauma modeling of broken vertebrae elements) and robotic surgeries.

Acknowledgements: The Swiss National Science Foundation (SNSF) supported this study.


Figures: (a) Screws placement, (b) Euclidean Distance and Dice Coefficient and (c) Euclidean Distance.
**DIFFERENCES IN LEFT VENTRICULAR SHAPE BETWEEN ECHO AND MRI: A PRELIMINARY ANALYSIS**

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**Background:** The left ventricle experiences remodeling of its shape and size after myocardial infarction, which has been characterized by bulk metrics like end diastolic volume. The use of computational atlas has the potential to improve this characterization particularly by encoding and quantifying shape differences. However, it is not clear which imaging modality is more suitable to detect the subtle changes after infarction.

**Aims:** To investigate the feasibility using two imaging protocols, 3D echo and short axis MRI, to detect changes in ventricular shape after myocardial infarction.

**Methods:** 8 patients with myocardial infarction were assessed at the acute and follow-up (6 months) stages after myocardial infarction. Each assessment included a 3D echocardiography and a MRI study. The end diastolic frame of each sequence was extracted, manually segmented, and automatically fitted to a mesh topology using high order interpolation [1,2]. 3D echo was also segmented to emulate the domain captured with a set of short axis slices (base anatomy was cropped). Principal component analysis was performed to identify modes of variation and differences between groups. The 16 3D echo and MRI meshes were analysed independently in order to study the effects of remodelling in each modality, and the complete set of 32 meshes was used to characterise inter-modality discrepancies.

**Results:** Inter-modality difference was much larger than the difference between acute and follow-up stages (see Fig.1). This result could be caused by the fundamental differences between the two imaging protocols despite of our efforts to capture the same topology (cropping the base), and also by methodological limitations on our meshing step. On the other hand, only some of the anatomical models of variation from 3D echo led to statistically significant differences between infarction stages (Student's T-Test, P<0.05). This finding is attributed to the higher spatial resolution and lack of inter-slice shift in 3D echo as compared to MRI short axis slices.

**Conclusions:** 3D echocardiography seems more suitable to identify anatomical changes due to myocardial infarction than a stack of 2D MRI short axis slices.

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**References:**


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Fig.1: (a) Average echo vs. average MRI shape of the left ventricle. Acute vs. 6M post-infarction stage with MRI (b) and with US (c).
Background: The human face is a complex 3-dimensional (3D) structure varying in shape and size with different demographics. Analysis of face shape variation from a large cross-sectional population of over 10,000 standardised 3-dimensional facial photographs gives surgeons a measurable, objective normative outcome at which to aim facial reconstructive surgery. This depends on the accuracy of facial landmarks for converting ‘normal’ facial surfaces into sets of points in 3D space for statistical shape analysis. These landmarks must be homologous and provide good surface description, where predicted faces generated match actual ones in surface contour to produce ‘recognizable’ human faces. Landmarks must be reliable with a low intra-landmarker error to preserve homology. ‘Homologous points’ are more easily identified at well-defined facial features like the eyes and more difficult to define in subtle contour regions like the cheeks. This requires a combination of techniques to optimize facial landmark development for accurate human facial shape description.

Aims: To develop and validate a reliable set of facial landmarks to accurately capture facial variation across a population using thin plate spline (TPS) warping and principle component analysis (PCA).

Methods: 6 ‘test’ faces age 18-35 years of different demographic were selected for landmark development from a cohort of 10,000 of the general public in London. 27 landmarks based on facial surface anatomy were identified initially. A TPS was applied to each landmarked face producing 15 predicted face shapes from the original 6. Each predicted face shape was compared to the actual face shape with surface differences measured on a colour gradient scale. New landmarks were added (iterations) until there was a good overall and regional facial surface match with the predicted face resembling the actual face. Intra-landmarker variability of each landmark was also assessed. The difference in facial surface correspondence was sampled globally (whole face) and in 8 defined and standardised regions (forehead, brow, nose, lips, chin, malar, jaw, and temporal) at every 3rd or 4th iteration for the 15 predicted facial shapes. A root mean squared (RMS) analysis of the difference in surfaces in all regions was performed and compared 1) across regions, 2) with increasing iterations of landmark placement, and 3) between different faces. The results guided further refinement of the landmark set and produced models of facial variation by PCA.

Results: 116 facial surface landmarks were identified in total. Similar trends were noted over 15 predicted faces with the greatest improvement in RMS difference from 27-41 landmarks. The RMS of the difference in facial surfaces globally improved from 1.52 to 0.74mm from 27 to 116 landmarks (intrinsic camera error is 0.3mm). The RMS difference improved from 1.00 to 0.51mm (Forehead), 1.18 to 0.63mm (Brow), 0.90 to 0.57mm (Nose), 0.88 to 0.60mm (Lips), 1.06 to 0.44mm (Chin), 1.30-0.55mm (Malar), 1.16 to 0.59mm (Jaw) and 1.14 to 0.49mm (Temporal). Landmarks placed in one region were found to improve remote surface differences. Those added from 86-116 caused an obvious improvement in predictive to actual facial likeness without measurable surface RMS improvements. Good repeatability was shown for all landmarks appropriate to the regional topography of the face. The first, second and third principle components of facial variation were performed successfully by PCA of the landmarks on 96 faces of the same cohort.

Conclusions: A reliable set of facial landmarks which adequately capture facial shape variation within the test cohort has been developed using a thin plate spline warping technique. PCA models have been successfully created using the landmarks. Validation of this set on a large cohort of over 10,000 faces is currently being undertaken in a semi-automated fashion.

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NON-RIGID REGISTRATION OF SURFACES FOR STATISTICAL SHAPE MODEL LEARNING IN AMIRA SOFTWARE

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Background: A critical aspect of statistical shape modeling [1] is the data preprocessing, including segmentation, meshing and the establishment of correspondences between the training samples. The software Amira already proposes various automated and interactive tools for image segmentation and meshing. The correspondence establishment step can be performed using non-rigid registration, but is currently not implemented in this software.

Aims: We propose a variant of the Iterative Closest Point algorithm [2] for automated non-rigid registration of surfaces in Amira.

Methods: First, pairs of corresponding points are estimated by associating vertices from one mesh to the closest point on the other surface, not necessarily a vertex, but any point on a triangle. Then, a deformation model is fitted to these sets of points (or a subset), and applied to the reference. The deformation model can be either Bookstein thin-plate-splines [3], or a Radial Basis Function [4] of the form:

\[ f(p_1, p_2) = \exp\{-d(p_1, p_2) \beta\} \]

Where Beta is a stiffness factor controlling the smoothness of the deformation field, and the distance metric which can be the L1 or L2 norm:

\[ d(p_1, p_2) = |x_1 - x_2| + |y_1 - y_2| + |z_1 - z_2| \]

or:

\[ d(p_1, p_2) = \sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2 + (z_1 - z_2)^2} \]

The process of correspondence estimation and deformation is iterated until convergence.

The proposed implementation allows the selection of the source and target surfaces for the correspondence establishment step independently of which surface is to be transformed and which is the target surface. Typically, if one surface is expected to be a subset of the other, it should be used as the source for the estimation of correspondences. The implementation also offers the possibility to select a (possibly randomized) subset of vertices from the source uniformly distributed over the source surface to accelerate the computations, at the cost of bias or automation of the convergence.

Conclusions: An automatic non-rigid registration algorithm is proposed for the Amira software, which can be used for aligning surface datasets prior to learning a statistical model of shapes, e.g. using the Statismo library.

Acknowledgements: FEI.

References:

Figure: Illustration of the non-rigid warping of surface samples.
Background: Statistical shape models are essential in several medical imaging algorithms and applications. These models are able to capture not only the mean topology of a structure, but also to encode deviations from this average. We developed a method to compute an average shape from a set of 3D meshes.

Aims: To develop a method that can be used to compute and validate an average 3D anatomical shape from a selected set of closed and orientable 2-manifold boundaries in Euclidian 3D space. An implicit surface representation is used to increase the method's robustness with respect to local shape variability.

Methods: Each input mesh (closed and orientable 2-manifold boundary Ω) was represented as a set of vertices and faces. The meshes were normalized with a scale derived from a length of their largest principal component. The meshes were translated to the origin of a common coordinate space and further aligned using 2-step rigid registration. Procrustes analysis was applied to a set of strategically selected landmarks to compute the initial registration. To finalize the inter-mesh alignment, we considered mesh vertices as point clouds and used the iterative closes point algorithm in the second registration step. For each mesh, we defined an implicit representation based on a signed distance field (SDF). The 3D discrete signed distance field was represented as a uniform voxel grid. For a voxel with position v, the signed distance value is defined by the equations in Fig. (a), and as described in [1]. The SDF representations of input meshes were averaged and a zero distance isosurface (mean mesh) was extracted using the marching cubes algorithm (similar steps were used in [2]).

The method was used to compute a mean cardiac Right Ventricle (RV) mesh from a database of 90 manually segmented CT volumes. The k-fold cross validation technique was used to assess the accuracy of using an average RV mesh instead of a patient specific mesh. The meshes were randomly divided into 6-subgroups. One group was left-out as test data and the others were used to compute the mean mesh. To determine test-to-mean shape distances, the test meshes SDF values were sampled at the mean model’s vertices. This way we could measure the signed Euclidian distance between the mean mesh vertices and the test mesh surface. The same process was repeated for each group and the results were combined. The test-to-mean SDF error metric for a randomly selected patient is presented on Fig. [b].

Results: Combined mean distance between the test RV meshes and the average RV mesh, expressed as (mean ± SD mm), was found to be 0.0±2.3 mm. Max distance value was +10.6 mm and min was -11 mm.

Conclusions: The results suggest that the average RV mesh could be clinically acceptable for certain applications. The extreme max and min distance values, for some applications, could be considered as outliers in regions of little clinical importance. The same method can be applied to other cardiac chambers. A 4-chamber average cardiac model may bring even more value for some clinical applications.


\[
f(v) = \begin{cases} 
-d(v,\Omega), & v \text{ inside } \Omega \\
d(v,\Omega), & v \text{ outside } \Omega \\
0, & v \text{ on } \Omega 
\end{cases}
\]

where \( d(v,\Omega) = \inf_{p \epsilon \Omega} ||v - p|| \)

Figures: (a) SDF equations, and (b) signed distance error for a random test mesh.
DEVELOPMENT OF A MULTI-MODAL, MULTI-COMPONENT, ARTICULATED MODEL OF THE LOWER LIMB. A LABORIOUS WORK IN PROGRESS

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Background: The introduction of 3D and 4D imaging modalities has had a dramatic impact on understanding the complexity of human anatomy and physiology by facilitating detailed non-invasive exploration of the human body. With improved modalities, such as Multi-Detector/Multi-Slice Computed Tomography (MD/MSCT) and Magnetic Resonance Imaging (MRI) to visualize and describe skeletal anatomy, an increasing interest in the description of anatomical variation has emerged and research findings have been translated in numerous areas including anthropology, evolutionary biology, forensics, anatomy, epidemiology and last but not least clinics, for the distinction of physiological versus pathological anatomical variation. This area of research has grown exponentially since the invention of geometric morphometrics. This has led to the introduction of statistical shape models (SSM) that realistically describe anatomy and its variation in any population by conventional multivariate statistics of sets of homologous landmarks representing the shape of the underlying structures. Further, it has become apparent that this type of data can be reliably related to other data modalities such as kinematic and mechanical information.

Aims: To introduce a framework and current progress in the ongoing development of a multi-modal, multi-component articulated model of the lower limb.

Methods: Angio-CT images, with a slice thickness below 1mm of the lower limb serve as data for the skeletal model of the lower-limb, the basic layer of the model, whereas MRI is used as input for the definition of relevant soft tissues (mainly cartilage) of different sub models of the specific joints. In addition; a group of volunteers is being recruited to obtain a library of kinematics of activities of daily living following detailed 3T MRI imaging of their respective lower limb joints. All will finally be merged into one single hyper-model of the lower limb, consisting of several layers of complexity that can be added from submodels of local anatomy and mechanical information. As such, the model will be applicable to personalize a subjects musculoskeletal profile, even from sparse data.

Results: Variation of skeletal anatomy has been established from CT datasets of currently 120 cases. Each anatomical segment was separately aligned with his anatomical peers, before further PCA analysis of the dataset. Reassembly of the segments to a full lower limb was than performed with respect of the mechanical properties of the connecting joints using mutual anatomical information between segments during the construct of the aligned segmental models e.g. hip joint center. The model has already been applied to serve different scientific purposes such as classification, analysis and diagnosis of disease among others. Detailed results are presented in fig 1.

Conclusions: The present project has important application possibilities among which to advance image analysis techniques by the development of algorithms for automated segmentation, clinically the models will be readily applicable in surgical planning, probabilistic disease recognition as for the development of detailed personalized mechanical models and finally, the project will allow the further evolution of anatomical science and teaching towards virtual applications. Nevertheless the quantity and quality of data is the major limitation to success. Therefore multicenter collaborations seem mandatory to maximize the models’ potential

References:
Background: Segmentation approaches based on statistical shape models (SSM), such as the Active Shape Model (ASM) framework, are a family of powerful methods for image segmentation [1]. The general idea of these methods is that a weak contrast at object boundaries, partial occlusions or high noise that make a proper segmentation very difficult can be compensated by employing a-priori knowledge of the shapes of the structures that are to be segmented. However, deploying SSMs for practical image segmentation tasks is non-trivial, as a vast amount of configurations of the algorithm has to be chosen, such as shape representation, appearance descriptor, model fitting method, etc., each having a substantial impact on segmentation quality.

Aims: The objective is to simplify the application and evaluation of ASMs for tackling individual segmentation tasks and to provide an extensible framework including a graphical user interface (GUI) for the efficient exploration of various parametrisations and alterations (such as in [1,2]) of the ASM method.

Methods: A prototype of a development environment (DE) for the application of ASM-based segmentation methods has been developed in MATLAB. As a particular segmentation task has its individual requirements and peculiarities it is not possible to provide a general framework that is suitable to all thinkable scenarios. Thus, our focus lies on providing a robust object-oriented (OO) software architecture that can easily be tailored to specific tasks. Core components of this architecture, which directly translate to OO classes, are: training set, shape representation, image representation, active shape model (comprising a point distribution model and an appearance/profile model), search method, segmentation result and cross-validation setting. Customisations of these components are enabled by class inheritance. A simplified UML class diagram including some provided customisations is shown in Fig (a).

On top of this OO framework a GUI has been developed in order to interact with the core components. It comprises four modules (training module, ASM inspection module, search module and evaluation module).

Results: The developed software is currently used for applying ASMs for the 3D segmentation of deep brain structures [3] and has proven to be a highly valuable tool for evaluating various ASM configurations.

Conclusions: Due to the large number of improvements of the ASM framework proposed in the literature it is non-trivial to find the appropriate alterations including their optimal parametrisations for a given segmentation task. Thus, finding a good configuration is in general tackled manually by a combination of heuristics and trial-and-error. In order to improve the efficiency of this procedure the proposed prototype DE for ASM-based segmentation has been developed. The extension of the proposed DE to other approaches based on SSM, such as the Active Appearance Model, is straightforward and can be implemented by class inheritance.

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SHAPE MODELS IN RADIATION THERAPY PLANNING: FROM RESEARCH TO INDUSTRY

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Background: Radiation therapy has become an indispensable tool in the fight against cancer. About 50% of all cancer patients receive radiation therapy as part of their treatment, contributing to the success that survival rates of cancer patients have doubled since the 1970s. The aim of radiotherapy is to induce the death of tumor cells with ionizing radiation. With the advent of computer aided planning, it has become possible to optimize the radiation treatment in a way that delivers an optimal radiation dose to the target volume, while at the same time minimizing the radiation exposure to healthy neighboring tissue. This necessitates the segmentation of not only the target organ affected by cancer, but of a large number of “organs at risk”. In clinical practice, this segmentation is still mostly performed manually. This presents an interesting scenario for the translation of statistical shape models from the research environment to industry and clinical practice. So far, there has been a large gap between the success statistical shape models in research and their actual use in clinical practice. Some important reasons for this gap are: (1) Most of the time, the physician/user actively chooses manual segmentation, because it is often the most accurate, reliable, and understandable segmentation method, especially if only a single organ is segmented. (2) The shape and appearance of diseased organs (e.g. cancer) may differ drastically from the healthy organs used to train the model. (3) It is often difficult to acquire enough example data and segmentation to build a sufficient shape model. For the radiotherapy target organ, these problems are still very much present, and we believe that manual segmentation will prevail, here. For the essentially healthy “organs at risk”, however, this is not the case: (1) Hardly any user prefers to tediously hand-segment a large number of healthy organs. (2) Healthy organs can be well represented by the shape model. (3) The large amount of previous treatment plans provide generous training data for shape models. Thus, from a researcher’s perspective, radiotherapy treatment planning presents a great opportunity to translate an exciting and powerful technique into everyday clinical practice. From a healthcare point-of-view, shape models can help make radiotherapy planning more quick, robust, and reliable, thus ultimately making treatment available to more patients throughout the world.

Aims: Establishing statistical shape model based segmentation in clinical radiotherapy planning at Varian Medical Systems (VMS), a leading manufacturer of radiotherapy devices and software.

Methods and Data: We included a statistical shape model-based segmentation method based on the open source toolkits statistomo [1] and elastix [2] into VMS’ proprietary .Net segmentation software, which posed a few implementation challenges. Due to the strict government regulation of the medical device industry, we will need to evaluate if a complete reimplementation is preferable to obtaining regulatory approval for the use of open source toolkits. We applied our method to segment the larynx (a), which is considered an “organ at risk” for head and neck radiotherapy. The initial study was performed with 20 data sets. 10 of these had to be discarded from the training set because of inconsistent ground truth segmentations. These were later used as test examples. The validation training examples were registered with elastix in order to build a statistomo deformation model using the registration results. Segmentation was then performed by registering the model’s mean CT intensity image (b) to the input image, constraining the registration to instances of the shape model. The segmentation results (c) are promising and provide a basis for future evaluation.


Figures: (a) Larynx in Varian’s software (blue), (b) Mean image, (c) Segmented larynx.
Background: For the computer simulation research, shape and property data are needed. Also test results on exercise are needed to verify the simulation model. We constructed spine library include images, shape models and movement properties.

Aims: To introduce our spine library and applications.

Methods: One part of our library was constructed from cadavers. The library included X-ray, CT images, L-spine BMD and shape models. The CT scan was taken with plastic ball for size calibration. Some samples were performed to test the flexion-extension, lateral bending, and torsion. The other part was constructed from patients. It included CT images and shape models (head and upper cervical). The shape models were reconstructed by 3D modeling software (Mimics Ver.16, Materialise, Belgium) after size calibration.

Results: We had about 100 sets of spine CT and models from cadavers with property data. And the number of head & upper cervical samples were minimum 20 for each age and sex.

Conclusions: This spine library is being used for researches in the fields of applied anatomy and biomechanical simulation.

Acknowledgements: The reconstruction of head & upper cervical shape models and relative research was supported by National Research Foundation (NRF-2013R1A1A1009600).

Figures: contents of whole spine library (left); head & upper cervical library (right); (a) whole spine CT, (b) whole spine X-ray, (c) 3D shape model, (d) BMD of L-spine, (e) anthropometry data, (f) moment-range of motion curve, (g) head & neck model, (h) anthropometry data, (i) upper cervical models.
Shape Challenge
Abstracts
Background: A critical aspect of statistical shape modeling [1] is the data preprocessing, including segmentation, meshing and the establishment of anatomical correspondences between the training samples. The software Amira already proposes various automated and interactive tools for image segmentation and meshing. The correspondence establishment step can be performed using non-rigid registration, but is currently not implemented in this software.

We propose a method for automatic non-rigid registration of meshes, based on a variant of the Iterative Closest Point (ICP) algorithm [2], and show how to use it practically for learning a statistical shape model from a set of segmented datasets.

Non mesh rigid-registration - As an ICP variant, our method maintains the main characteristics of the algorithm. Pairs of corresponding points are estimated by associating vertices from the source mesh to the closest point on the target surface (not necessarily a vertex, but any point on a triangle). Then, a deformation model (either Bookstein thin-plate-splines [3], or Radial Basis Function (RBF) [4]) is fitted to these sets of points (or a subset), and applied to the reference. The process is iterated until convergence.

Statistical Shape Model Learning - In order to learn a statistical shape model from the segmented liver datasets provided by the Challenge organizers [5], we start by meshing each dataset into a triangulated surface, and roughly aligning them rigidly. A simple translation matching the center of mass of all samples is considered sufficient for this initial alignment, as the images were apparently acquired in similar conditions with respect to patient positioning.

For statistical model learning, we use a Principal Component Analysis model, implemented in the Statismo library [6], retaining 90% of the variance. The training samples are obtained by deforming a reference mesh onto each original mesh.

The ICP mesh matching is performed as follows:
- at each iteration, correspondences are computed for 500 vertices of the reference randomly and uniformly distributed over the surface,
- an L2-norm RBF deformation model is employed, with a smoothing factor manually fixed for the whole experiment,
- 200 ICP iterations are performed.

The reference mesh is initially selected randomly among the higher resolution datasets, decimated to 5000 triangles, and remeshed using Lloyd relaxation. This reference is then iteratively replaced by the mean model obtained at the previous iteration. Three such iterations were performed to reach the submitted model.

Discussion: A simple approach a proposed for generating a statistical shape model is proposed, based on non-rigid registration of meshes inspired from the ICP algorithm. Besides the raw performances of the algorithm, which will be better analyzed in view of the other submissions to the Challenge, a number of drawbacks and possible improvements can be highlighted.

The estimation of correspondences based on a random subset as performed here greatly improves the computational time, but make the metric random, limiting the possibility to enforce a robust convergence criterion. A possible improvement could be to compute a distance map from the target model, and use it to estimate a global distance metric piloting the convergence. Correspondence estimation could also be speeded-up by computing the source point for each pixel of the distance map.

Furthermore, as all ICP methods, the proposed algorithm may get stuck in a local minimum. Adding interactivity, e.g. by manually defining some correspondences, could help in those cases. In this case, it would be necessary to weight the contribution of automatic (unreliable) and user-defined (more reliable) pairs of landmarks. Accounting for salient shape features such as high curvature areas could be another path for improving the automatic estimation of correspondences.

Acknowledgements: FEI

Deformable Liver-Model using Gaussian Process Registration

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Background: Statistical shape models (SSM) are evolving since their introduction by Cootes et al. [1]. The central problem of building an SSM is to establish correspondence between the shape descriptions of different objects. Lüthi et al. [2] presented a method for non-rigid registration using Gaussian processes with the idea to model deformations with a Gaussian process \( \mathcal{GP}(\mu, k) \) with the mean function \( \mu \) as the reference shape and a covariance function \( k \) (also known as a kernel). By computing a low-rank approximation of \( k \) a parametric model can be approximated so that each deformation can be written as

\[
\mathcal{M}(\alpha)(x) = \mu(x) + \sum \alpha_i \lambda_i \phi_i(x)
\]

with \( \alpha_i \) as the deformation parameters, \( \lambda_i \) as the eigenvalues and \( \phi_i \) as the eigenvectors of the approximation. Many different kernels to model the deformation fields have been proposed in literature. R. Opfer [3] proposed a refinable B-spline kernel which allows describing model deformations on multiple scale-levels. In contrast to one single-scale kernel, multiple levels of deformation scales can model coarse deformations as well as finer structures of the target shape. Another important aspect is the ability to consult expert knowledge by including landmarks. Lüthi et al. [4] described a method to use landmark points as additional information by integrating them in the deformation prior.

Aims: To build a statistical shape model of liver shapes using Gaussian process registration with landmarks. In respect to the challenge rules the shape model should be compact, generalize well and also be specific to its class of objects.

Methods: In a first step a polygonal mesh was extracted from all the 59 binary images of different livers and aligned their center to the origin. The quality varies over the examples of the dataset. Some have only coarse resolution or do not even represent the full liver shape like the example on Fig (a). To build the reference, Poisson surface reconstruction [5] has been used to re-mesh and smooth one of the example shapes, which was chosen as the reference shape (Fig (b)). In a second step a low-rank approximated B-spline model has been built with 1000 degrees of freedom from which a random sample is illustrated on Fig (c). The B-spline kernel was built with 6 different scale levels from coarse to fine deformations. For most of the examples which represent a full liver shape landmarks were chosen and included in the deformation prior. Using this deformation model the reference was registered to the polygonal meshes of the dataset. In a last step, the registered shapes were used to build a statistical shape model. To increase the generality of the resulting model a low-frequency Gaussian kernel was combined with the statistical shape model.

Conclusions: Only examples which represent a complete liver shape were taken into account for the model building. A model building process that would allow including partial shape information could improve the quality of an SSM even with a low quality dataset.

References:

Figures: (a) Reference shape and (b) Random sample from B-spline model (c) Bad example from dataset
A Hybrid Registration Scheme for Constructing a Statistical Shape Model of the Liver

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Background: Statistical shape analysis is an important tool for understanding anatomical structures from medical images. Statistical models give efficient parameterization of the shape variations found in a collection of sample models of a given population. For example, the Segmentation of the Liver Competition 2007 (SLIVER07) provides a platform for testing and comparing different approaches [1]. Interestingly, among all the approaches, the SSM-based method was found to have the best performance [2]. Thus, it is important to develop an efficient method for constructing SSM of the liver.

Aims: In total, 59 liver segmentations are given by the challenge organizer but not all of them are appropriate for model building due to the fact that some of them do not contain a complete liver segmentation. Ultimately, we have selected 33 out of the 59 segmentations. The aim of this study is then to develop an efficient method to align all the 33 segmentations in order to construct a SSM of the liver.

Methods: Although each one of the selected 33 samples contains a complete liver model, the segmentation quality is different from data to data. Thus, we have intentionally selected one of the training data with good segmentation quality as the reference object and all other 32 segmentations as the floating objects. A hybrid registration scheme, which combines an Expectation Conditional Maximization (ECM)-based point set registration [3, 4] with an intensity-based diffeomorphic registration algorithm [5], was then developed to automatically find the correspondences between vertices on the surface mesh of the reference object to the associated vertices on the surface mesh of each floating object.

The goodness of the correspondences was then evaluated by calculation following four measures: (1) average mean distance between the surface meshes before and after correspondence establishment; (2) model compactness; (3) model generalization; and (4) model specificity. The last three quantities are measured directly on the resultant SSM using the definitions introduced in [6]

Results: The average mean distance between the surface meshes before and after correspondence establishment was 0.13 mm. Figure (a) shows the first three eigenmodes of the liver SSM and Figure (b) shows the three measures, i.e., model compactness, model generalization, and model specificity, of the constructed SSM of the liver. Our compactness study showed that about 95% total amount of variations of the SSM were explained by the first 19 eigenmodes.

Conclusions: A hybrid registration scheme was developed and validated on the challenge data for constructing a SSM of the liver.

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Figures: (a) First three eigenmodes of the SSM, and (b) from left to right: model compactness, model generalization and model specificity.
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Finally, we would like to thank all participants for attending our 1st SHAPE congress. We look forward to seeing you all at the next event.