# BONE MODEL MORPHING FOR ENHANCED SURGICAL VISUALIZATION

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## ABSTRACT

We propose a novel method for reconstructing a complete 3D model of a given anatomy from minimal information. This reconstruction provides an appropriate intra-operative 3D visualization without the need for a pre or intra-operative imaging. Our method £ts a statistical deformable model to sparse 3D data consisting of digitized landmarks and bone surface points. The method also allows the incorporation of non-spatial data such as patient height and weight. The statistical model is constructed using Principal Component Analysis (PCA) from a set of training objects. Our morphing method then computes a Mahalanobis distance weighted least square £t of the model by solving a linear equation system. First experimental promising results with model generated from 14 femoral head are presented.

## 1. INTRODUCTION

Three dimensional (3D) models of the patient are routinely used to provide image guidance and enhanced visualization to a surgeon to assist in navigation and planning. These models are usually extracted from 3D imagery like CT or MRI. To avoid the high radiation dose and costs associated with such scans, image free approaches have been researched extensively and are becoming popular especially in orthopedic surgery. In a non-image based approach, building a 3D model that is speci£c to the patient anatomy is quite challenging. This is usually done by building a deformable model and adapting it to the patient anatomy.

Statistical models of shape have been researched as a powerful tool to build deformable 3D models. The basic idea in model building is to establish from a training set the pattern of legal variations of shape. The model is adapted to the patient anatomy using digitized landmarks and bone surface points obtained during surgery. The main problem here is to extrapolate this extremely sparse three-dimensional set of points to obtain a complete surface representation. The

extrapolation procedure also called bone morphing is done via a statistical principal component analysis (PCA) based shape model. Fleute et al £t the morphed model surface to sparse intra-operative data via jointly optimizing morphing and pose [1]. Chan et al [5] optimize morphing and pose separately using an iterative closest point (ICP) method. In our prior work [6] we proposed to iteratively remove shape information coded by digitized points from the PCA model. The extrapolated surface is then computed as the most probable surface in the shape space given the data. Unlike earlier approaches, this approach was also able to include non-spatial data, such as patient height and weight. It is only applicable though for a small set of known points.

We propose a novel morphing method considering the problem as a linear equation system, solving for the shape parameters that best describe the unknown shape. We propose to have additional terms in the objective function that minimize Mahalanobis shape distance. In this paper we demonstrate proof of principle of our method using a femoral head model generated from 14 CT datasets and evaluated using leave-one-out experiments (Jackknife procedure).

## 2. METHOD

### 2.1. Model Construction

The basic idea of building a statistical model based on principal component analysis is to establish, from a training set, the pattern of legal variations in the shapes for a given class of images. The point distribution model (PDM) proposed in the seminal work by Cootes [2] is a deformable model built from the statistical analysis of a population of objects.

A key step in this model building involves establishing a dense correspondence between shape boundaries over a reasonably large set of training images. Our previous comparison study [4] of some of the popular correspondence establishing methods revealed that for modeling purposes the best of the correspondence method was Minimum Description Length (MDL) [3]. Correspondence was initialized with a semi-automatic landmark driven method and then optimized based on the MDL criterion.
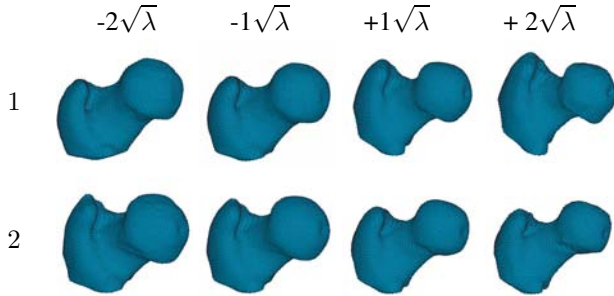
We construct a deformable statistical shape model based

| $-2\sqrt{\lambda}$ | $-1\sqrt{\lambda}$ | $+1\sqrt{\lambda}$ | $+2\sqrt{\lambda}$ |

**Fig. 1**. The £rst two eigen modes of variation of our model. The shape instances were generated by evaluating $\bar{x} + \omega\sqrt{\lambda_k}u_k$ with $\omega \in \{-2, .., 2\}$

on the corresponding point positions. Each member of the training population is described by individual vectors $\bar{x}_i$ containing all 3D point coordinates. The aim of building this model is to use several training datasets to compute the principal components of shape variation. Principal Component Analysis (PCA) is used to describe the different modes of variations with a small number of parameters. For the computation of PCA, the mean vector $\bar{x}$ and the covariance matrix $D$ are computed from the set of object vectors(1). The sorted eigenvalues $\lambda_i$ and corresponding eigenvectors $p_i$ of the covariance matrix are the principal directions spanning a shape space with $\bar{x}$ representing its origin. Objects $x_j$ in that shape space can be described as linear combination with weights $b_j$ calculated by projecting the difference vectors $x_i - \bar{x}$ into the eigenspace.(3)

$$D = \frac{1}{n-1}\sum_1^n (x_i - \bar{x}) \cdot (x_i - \bar{x})^T \quad (1)$$

$$P = \{p_i\}; \; D \cdot p_i = \lambda_i p_i; \quad (2)$$

$$b_j = D^T(x_j - \bar{x}); \; x_j = \bar{x} + P \cdot b_j \quad (3)$$

Figure 1 shows the variability captured by the £rst two modes of variation of our model varied by $\pm 2$ standard deviation.

## 2.2. Morphing

Bone Morphing is the process of recovering the patient speci£c 3D shape of the anatomy from the few available digitized landmarks and surface points. Our approach uses the statistical based shape model built earlier to infer the anatomical information in a robust way. This is achieved by minimizing the residual errors between the reconstructed model and the cloud of random points, and provides the best statistical shape that corresponds to the patient.

Earlier bone morphing methods were based on £tting procedures in Euclidean space and have the disadvantage

that these are often computationally expensive and only a small set of shape variations can be considered. The morphed model also does not represent the most probable shape given the input data but rather a constrained £t. Our novel morphing method operates directly in the PCA shape space incorporating the full set of possible variations. The method consists of two steps

- Initially a small point-set of anatomical landmarks with known correspondence to the model is digitized. This is used to register the patient anatomy to the model. This also provides an initial estimation of the 3D shape with only a few digitized points.

- To improve the prediction additional points can be interactively incorporated via closest distance correspondence. A color coded feedback is given to the surgeon which shows regions where the prediction is accurate and regions where the prediction could be improved. This assists the surgeon in deciding the location where to digitize extra points.

The morphing computation is based on formulating the problem as a linear equation system and then solving for the shape parameters that best describe the unknown shape. An additional term in the objective function minimizes the Mahalanobis shape distance. The objective function that we minimize is de£ned as follows

$$f = \gamma * \sum_{k,j=1}^{N} \|\vec{Y_k} - (\vec{X_j} + \sum_{i=1}^{m}\alpha_i\vec{p_i}(j))\|^2 + \sum_{i=1}^{m}\frac{\alpha_i^2}{\lambda_i^2} \quad (4)$$

with $N$ the number of points that are digitized, $\vec{Y_k}$ is the kth digitized point, $\vec{X_j}$ is the point in the mean model that is closest to $\vec{Y_k}$, $\vec{p_i}(j)$ is the $j_{th}$ tuple of the $i_{th}$ shape basis vector, $\lambda_i$ the $i_{th}$ eigen value and $\alpha_i's$ are the $m$ shape parameters that describe the shape. The £rst term of the function minimizes the distance between the predicted shape and the set of digitized points. This is similar to the Euclidean distance term used by Fleute [1] . The second term controls the probability of the predicted shape. This term ensures that the predicted shape has minimal Mahalanobis shape distance. The factor $\gamma$ is a parameter that weights the two terms of the function. The optimal value of lambda is dependant on the application and was for our tests empirically determined to be between 1E-5 and 1E-6.

To determine the shape parameters $\alpha_i$ that best describe the unknown shape, the function $f$ is differentiated with respect to the shape parameters and equated to zero. This results in a linear system of $m$ unknowns, which is solved with standard linear equations system solvers using QR decomposition.
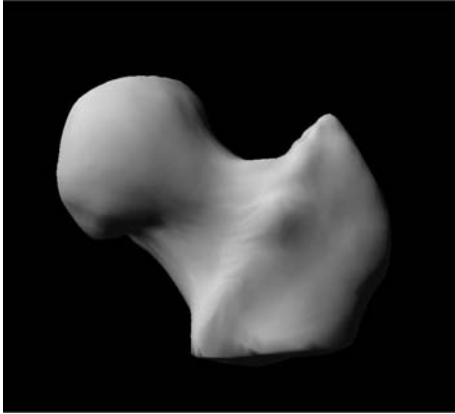
**Fig. 2**. A typical femoral head of the population that was used in the leave-one-out test.
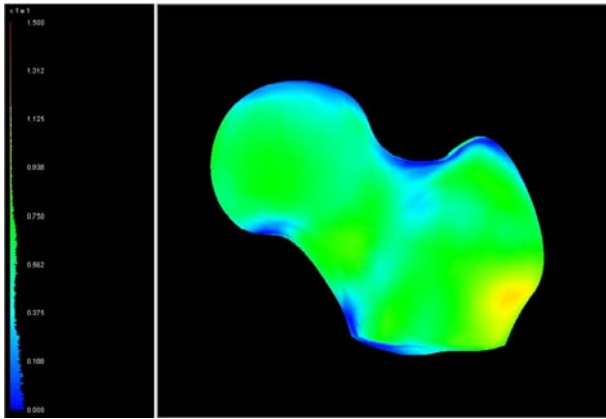


**Fig. 3**. The average shape of the population with color coded distance map to the actual shape in Fig 2. The mean error is 3.37 mm and the median is 2.65 mm
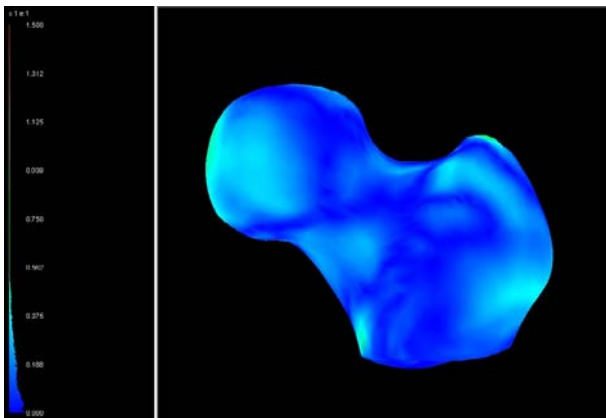


**Fig. 4**. The shape based on only 6 digitized points with color coded distance map to the actual shape in Fig. 2. The mean error is 1.50 mm and the median error is 1.25 mm
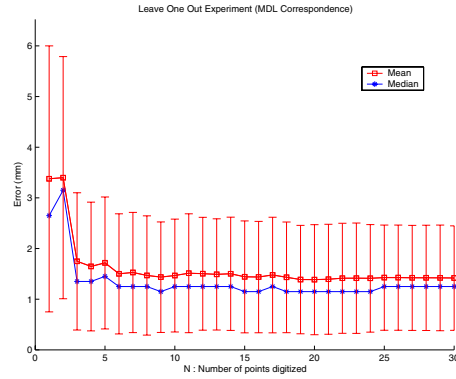


**Fig. 5**. A typical leave-one-out case experiment with MDL correspondence. The mean and the median of the error is plotted against the number of digitized points

## 3. RESULTS

In this paper we demonstrate proof of principle of our method using the femoral head structure. 14 CT scans of the femoral head were segmented and a sequence of correspondence establishing methods was employed to compute the optimal PCA model [4].

A series of leave-one-out experiments was carried out to evaluate the new method. Three anatomical landmarks, the femoral notch and the upper and the lower trochanter are used as the £rst set of digitized points. This simulates the surgical scenario where we need to initially register the model to the patient anatomy. The remaining points are added uniformly across the spherical parameterization so that they occupy different locations on the bone surface.

We studied two different correspondence methods for incorporating additional points into the estimation scheme. The £rst was to use the implicit correspondence implied by MDL. This was feasible because the MDL correspondence is known from the modeling step. In this scenario a very good estimate with mean error of 1.5mm was obtained with as few as 6 digitized points (Figure 4). Figure 5 shows the error plot for one typical case for the leave-one-out case, with the error plotted against the number of digitized points. Figure 6 shows the cumulative statistics of all leave-one-out experiments using the MDL correspondence.

The second correspondence scheme does not use the implicit correspondence. This is the realistic case, as no correspondence would be available in a real scenario. In this case the correspondence was established via closest distance. The errors are therefore magni£ed due to mis-correspondences and hence more points would be needed to be digitized to get a good estimation. Figure 7 shows the cumulative statistics from all the different leave-one-out experiments using closest point correspondence.
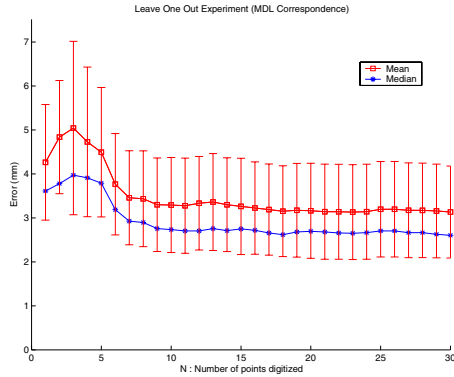
**Fig. 6**. Statistics cumulated from the different leave-one-out experiments with MDL correspondence. The average of the mean error and the average of the median is plotted against the number of digitized points



**Fig. 7**. Statistics cumulated from the different leave-one-out experiments with closest point correspondence. The average of the mean error and the average of the median is plotted against the number of digitized point

## 4. DISCUSSION

In this paper we have demonstrated a novel technique to predict the three dimensional model of a given anatomy using statistical shape models. Our scheme is novel in that it operates directly in the PCA shape space and incorporates the full set of possible variations. It is also fully interactive, as additional bone surface points can be incorporated in real-time. The added advantage of this scheme compared to our earlier approach is that it can interactively incorporate a large set of bone surface points.

A visual (color-coded) feedback to highlight regions of high and poor accuracy assists the surgeon to choose regions to digitize additional points. The expected accuracy of the current model can be visualized at any stage of the procedure. The computation time is mainly independent of the number of points intra-operatively digitized, and largely depends on the number of members in the population.

The relation between shape and parameters such as sex, height, weight, pathology is an interesting area of research. The formulation and implementation of our bone morphing is such that we can include these other patient parameters into the estimation procedure. Alternatively we can also predict the parameters based on the shape using the morphing method. In our future work we plan to study the importance and the predictive power of these parameters.

The gamma parameter plays a vital role in balancing the predictive error term and the probability term. We empirically £xed its value to adapt to the case when small number of points are digitized. We believe that this parameter could be relaxed to get a much better estimate as more points are digitized. In our future work we plan to study the relationship between number of members in the population, number of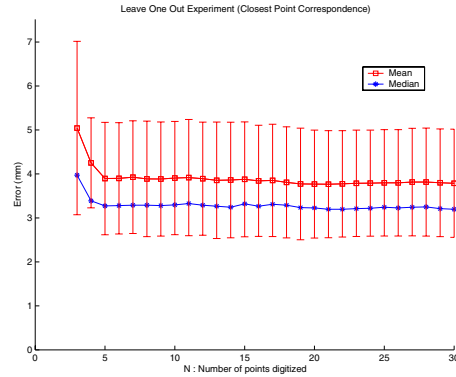 digitized points and gamma. Also as part of our future work we plan to build an application incorporating segmented bone contours from ultrasound and ¤uoroscopic images into our morphing scheme.

## 5. REFERENCES

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