Shape model-based point set registration with local density weighting applied to the incomplete femur

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by

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A thesis submitted in partial fulfillment for the degree of Master of Science

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Preface

During my masters program of Biomedical Engineering I attended the Medical Visualization course, given by Anna Vilanova. The final lectures consisted of a series of short presentations given by guest speakers. One of them was done by Peter Krekel, founder of the startup company Clinical Graphics. He demonstrated a product that his company was working on: a patient specific PDF report that included an interactive 3d visualization of the hip. The visualization was aimed to show femoroacetabular impingement: colliding parts on the femur and the acetabulum that hinder movement.

I was so impressed by the presentation that I decided to do an assignment at the company. I initially worked on interpolation of radial MRI slices. This was later followed by an internship that focused on the validation of state-of-the-art registration algorithms on registration problems with sparse data. We came to the conclusion that the current algorithms were not quite satisfactory in terms of performance and ease of use.

In extension to the internship, I started this master research project in June 2017, in which I continued to work on the registration problem of partial data. The findings of the research are included in this paper. During the project I was supervised by Korijn van Golen at Clinical Graphics and Lucas van Vliet at the TU Delft. In retrospect I can conclude that the feedback I received from them played a significant role in the end result of this research.

Tim Moerkerken Delft, February 2017

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Abstract

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Pre-operative planning aids clinicians by providing insight into patient-specific problems before surgery is performed. For treatment of femoroacetabular impingement (FAI), a range of motion (ROM) simulation is used, based on collision detection on segmented CT or MRI-data. Imaging data of the femur is often incomplete, due to the fact that radiologists want to minimize radiation dose and scanning time. The lack of data negatively influences the range of motion simulation. In this research we present a statistical shape model (SSM) based point set registration method that is able to accurately register to incomplete femur data. It is based on an iterative schema that minimizes the squared distance between the target data and the modes of variation in the SSM. We introduce a weighting vector that is derived from point density in the target data to force each point to equally contribute to the final solution. This greatly improved registration performance in the distal femur region. Furthermore, we introduced an iteratively increasing amount of modes of variation in the solving approach. This lead to faster convergence while achieving more accurate registration. The implemented method outperforms current state-of-the-art registration algorithms.

Keywords: non-rigid registration, statistical shape models, partial data, femur

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1 Introduction

Femoroacetabular impingement (FAI) is a condition where the range of motion in the hip joint is limited due to abnormal contact between the proximal femur and the acetabulum. This often leads to hip pain, joint stiffness and progressive damage to the cartilage. A variety of causes for FAI have been described, such as excessive sporting activities and post-traumatic or congenital deformities. Treatment can be done with arthroscopic surgery. The surgeon corrects the FAI by trimming the acetabular rim or femoral head. Radiological identification of FAI can be a challenging task, especially when coping with small deformities. Digital motion simulation on 3D radiological image data can be used to accurately simulate the range of motion (ROM) in the hip joint [1]. Such a simulation provides the surgeon with highly detailed information about blocking protrusions on the bone, which can aid in a more satisfactory outcome of the procedure [2].

ROM simulation is performed on a point set representation of the surface of the bone. The set of points is acquired by performing manual segmentation on CT or MRI image data [3]. However, real world image volumes frequently consist of missing parts, to reduce absorbed radiation dose (CT) or minimize scan times and costs (MRI). This often means that essential anatomical landmark points for ROM calculation are not included in scanned images. The challenge is to retrieve missing parts of the bone, as shown in Figure 1.1, and thereby performing better motion simulation.



FIGURE 1.1: The registration problem of the partial femur. On the left the data points retrieved from manual point selection on a CT scan. On the right the reconstructed shape that we want to obtain. Note that commonly only very little imaging data of the distal femur is available.

A solution to this problem is to register an annotated bone atlas to the sparse data that is available. Point set registration can be divided into rigid and non-rigid registration. Rigid registration strictly performs scaling, rotation and translation to the atlas. Rigid registration is the simplest form of registration and is widely studied [4]. Non-rigid registration allows more complex deformations to the atlas and is therefore more suitable for clinical purposes. Existing non-rigid methods are based on likelihood maximization of a probability density field [5] or are based on statistical deformable models [6–8].

This report presents a novel Statistical Shape Model (SSM) based registration method that is able to robustly register a complete bone model to a sparse and incomplete set of points. The registration method exploits Principal Component Analysis (PCA) to obtain all the significant modes of variation that are apparent in a training set. It then performs a regularization step, which is a least squares solving process to find a linear combination of modes of variations (MOV) that minimizes the distance to the points in the target set.

The algorithm presented in this paper is (1) able to register to heavily truncated datasets by using a cluster based weighting method that forces each distinguishable cluster in the target data to have an equal contribution to the final solution. This allows the registration algorithm to fit an entire femur bone to just a subset, for example the proximal femur and distal femur. Furthermore, the algorithm uses (2) an alternation between ICP and SSM regularization to optimize point correspondence for each iteration, which greatly improves the convergence process. Lastly, the algorithm uses (3) an increasing amount of modes of variations as the iterations go by, starting with the most significant MOV and ending with the least significant one. This prevents the algorithm from over-fitting on higher order MOV.

This article is structured as follows: Chapter 2 describes previous work that has been done in this research area. Chapter 3 describes the theory behind the registration method and includes a step-by-step overview of the algorithm. Chapter 4 contains a description of the performed evaluation experiments (Chapter 4.1) and the corresponding results (Chapter 4.2). Chapter 5 consists of conclusions and recommendations for future work.

2 Related work

In this chapter we discuss the work that has been done in the field of point set registration and its use in anatomical reconstruction of sparse data for preoperative hip planning. We discuss femoroacetabular impingement and its difficulties in classification. Furthermore we cover point set registration and the applications of statistical shape models.

2.1 Femoroacetabular impingement

Femoroacetabular impingement (FAI) is a medical condition where the femur and the acetabulum collide during ordinary movement. The collision is caused by anomalously protruding bone in the hip joint region. FAI can be subdivided into two categories, as shown in Figure 2.1.

The first one is known as cam impingement and is caused by an abnormal femoral head [9]. The increased radius of the femoral head's sphere causes shear forces during rotation in the acetabular socket. The second type of impingement is called pincer impingement and is caused by an over coverage by the acetabular rim [10]. During movement, the rim can have blocking interaction with the femoral neck or head.



FIGURE 2.1: The two types of femoroacetabular impingement (Source: Parvizi, 2007 [10]). Pincer impingement at (a) and cam impingement at (b).

2.1.1 Classification

Classification of the cam type of FAI utilizes concativity measurements, also known as alpha angle measurements [11, 12]. For the classification of the pincer FAI type, acetabular coverage measurements are performed. This is an angle that quantifies how much of the femoral head is covered by the acetabular rim. Both types of classification do not reflect the dynamic interaction between the joint components. Morphological parameters that describe the relative positioning and movement between the femur and the acetabulum also play a role in FAI. These parameters are the femoral version, the acetabular version and the femoral neck-shaft angle and have shown to significantly improve characterization of FAI [13].

2.1.2 Femoral version

Current radiographic imaging protocols only yield limited data around the knee region [14–16]. Of the aforementioned morphological parameters, only the femoral version suffers from the lack of knee data. The femoral version is the angle between the posterior condylar line (PCL) and the femoral neck line when projected along the femoral shaft. Berger et al. [17] define the PCL as a line tangent to the two most extending points (lateral and medial condyles) at the posterior side of the distal femur. After performing a study on 193 knees, Talbot and Bartlett [18] found the PCL to be extremely variable in comparison to other anatomical features. Victor and van Doninck, however, demonstrated low inter- and intra-observer variability in the registration of condyles on CT scans of the complete knee [19].

2.2 Point set registration

Registration is a method to transform an object in such a way that it aligns with another target object. If the objects are images, the registration method is called intensity based registration. If the objects are point clouds, we speak of point set registration. In order to generate 3D bone models, CT and MR images of the hip are commonly segmented by means of thresholding [20, 21] or manual point selection. Since segmented data is available in our case, only point based registration approaches will be investigated in this section.

2.2.1 Rigid registration

One of the most well known registration approaches is ICP, introduced by Besl et al [4]. The ICP algorithm uses a nearest-neighbor match between two point sets to find point correspondence. Then an optimal rigid transformation is determined by minimizing the squared distance between the moving and the target shape. The method introduced by Besl used a quaternion transformation matrix to transform the moving shape. This operation was only restricted to translation and rotation. Later the quaternion matrix was replaced by a transformation matrix extracted from a singular value decomposition (SVD) on the covariance matrix of the corresponding point sets, which also allowed the estimation of scale [22].

This method is might not be suitable for clinical purposes that demand high accuracy, since the method lacks flexibility in the moving shape to cover large variability between patients.

2.2.2 Mixture models

Myronenko and Song [5] introduced a non-rigid registration algorithm where one point set is represented by Gaussian mixture model (GMM) centroids. The point set is then iteratively adjusted to maximize the GMM posterior probability with respect to the other dataset. Optimally, the two point sets are aligned. Core of CPD is that the GMM are forced to move coherently. The noise in the dataset is modelled by a uniform distribution with parameter ω . This parameter, however, greatly affects the registration result. Wang proposed a method for finding the optimal value for ω [23], which appeared to be a time consuming task.

Ma et al added local neighborhood structure information to GMM centroids [24]. A local feature descriptor is computed for each point in both point sets. Then a minimal cost algorithm is used to match the local features of both shapes. That information is then incorporated in a posterior probability. The algorithm performed better than CPD on very noisy datasets, but showed comparable performance on clean datasets. It also introduces a costly $O(N^3)$ complexity operation to the instruction set.

Gerogiannis et al replaced the GMM by a Student's-t mixture model [25]. This approach was limited to rigid registration. Zhou and Zheng later introduced a Student's-t mixture model based non-rigid point set registration algorithm [26]. This type of mixture model has a heavier tail than a Gaussian distribution and is therefore more robust against noise. This was evident from performance comparisons with CPD. The Student's-t mixture model outperformed CPD for low signal to noise datasets. Again, when the data was free of noise, only marginal differences were found.

The downside of these algorithms is that they all require parameter tuning in order for them to work. This process can be tedious and requires theoretical knowledge about the underlying algorithm. Furthermore, these mixture model based registration algorithms only work well when the data has unit variance. This might force the user to downscale its data, which can lead to a change in initial alignment.

2.2.3 Statistical shape models

Cootes et al. introduced a technique to build a statistical shape model (SSM) out of flexible objects by performing a principal component analysis (PCA) to a set of point wise corresponding shapes [27]. The SSM is a description of the modes of variation that are present in the set of objects that were used for training the model. Each shape from the training set can be reconstructed by adding a specific superposition of modes of variation to the mean shape of the training set. Section 3.2 explains the theory behind shape models in more detail. New shapes can be generated by combining arbitrary modes of variation

Including this technique in a registration method means that a-priori knowledge is required in the form of training data. Point correspondence between training shapes is necessary to build the SSM. Lorenz and Krahnstöver obtained point correspondence in the training data by projecting vertices of a template mesh to the surface of segmented training data [28]. There are several registration methods that successfully use a trained SSM in a registration approach.

Fleute and Lavallée showed one of the earliest examples of the combination of SSM and registration [6]. They modelled the knee joint for the use in anterior cruciate ligament reconstructive surgery using 11 dry femurs. The model was then fitted to a sparse set of intra-operatively acquired points, by solving for a combination of modes of variation that minimize the point-to-point distance between the moving and target shape.

Benameur et al. used segmented contours rather than points, for the shape model based reconstruction of the scoliotic verterbrae from two conventional radiographic views [29]. Lamecker proposed a similar method for the registration of pelvic bones in x-ray data [30]. As opposed to Benameur, Lamecker uses silhouettes of the shapes as a similarity measure. The silhouettes are extracted by projecting the data on the planes of the orthogonal coordinate system. The usage of silhouettes instead contours improved the robustness of the registration, since many contours in a typical registration task have no well-defined corresponding counterpart.

Rajamani [7] proposed a similar registration approach as Fleute and Lavallée. The method operates directly in the PCA shape space, rather than the Euclidean space. This results in the addition of scale as an additional statistical parameter. Furthermore, the method includes outlier rejection based on a Gaussian kernel, which improves results

on noisy data. It can, however, have an averse effect for registration tasks that consist of incomplete shapes. Validation of the algorithm showed accurate reconstruction after a leave-one-out experiment on 14 proximal femurs.

Wu [8] introduced a two-phase registration method for the femur, where local SSM refinement is added to GMM based non-rigid registration by incorporating surface information into the registration process. The method requires that both surface information of the target and moving model is available. To improve computational efficiency, surface interpolation is used to reduce the complexity of the model.

The discussed statistical shape model based registration methods provide possible approaches to reconstruct the incomplete femur. The advantage of this registration type is that it is not reliant on manual input for crucial parameters and that it is capable of performing clever deformations based on previously seen data. The majority of the discussed algorithms had accurate performance on sparsely sampled subsets of bones, but lacked tests on heavily truncated data, that is, data with large gaps and inhomogeneities in cluster densities.

3 Methods

This section starts with an overview of the data that was used in this research. Then the theory of the introduced registration method is described.

3.1 Data description

Our database consists of 275 segmented CT scans of a complete femur with 21,096 vertices and 42,188 triangles. The segmentation was performed by a clinical expert using the software Mimics by Materialise. The vertices were placed in such a way that the shapes had a vertex to vertex correspondence. We decimated the amount of vertices to 10,000 to reduce calculation times. These datasets are used for training and validation.

3.2 Training the SSM

Historically a registration algorithm consists of a moving shape that is to be transformed to best match the target shape (often called static shape). In our case the moving shape is a statistical shape model that is built by performing PCA on a training set. The training set should consist of point clouds that have a vertex correspondence and resemble the same object. It is important that the clouds are well aligned, which can be done using the generalized Procrustes algorithm [31]. A 3-dimensional point set with k amount of vertices, as part of a training set **X** with m samples, can be defined as

$$\mathbf{x} = \begin{pmatrix} x_0 & y_0 & z_0 \\ \vdots & \vdots & \vdots \\ x_k & y_k & z_k \end{pmatrix},$$
(3.1)

with $\mathbf{x} \in \mathbf{X}$ and $\mathbf{X} = \begin{pmatrix} \mathbf{x}_0 & \mathbf{x}_1 & \dots & \mathbf{x}_m \end{pmatrix}$. Note that we use zero-based indexing in the entirety of this report. In general, a training set \mathbf{X} is of shape $m \times k \times d$, with d = 3 for the 3-dimensional case. Now the mean shape of the training set is

$$\bar{\mathbf{x}} = \frac{1}{m} \sum_{i=0}^{m} \mathbf{x}_i,\tag{3.2}$$

which is with the requirement that all the point clouds in the training set are well aligned. Now a covariance matrix is calculated for each dimension:

$$\mathbf{C} = \frac{1}{m-1} (\mathbf{X} - \bar{\mathbf{x}})^T (\mathbf{X} - \bar{\mathbf{x}}), \qquad (3.3)$$

which has a shape of $k \times k \times d$ and is symmetric. The eigenvalues of **C** can be found by solving for λ in $|\mathbf{C} - \lambda I| = 0$. The eigenvalues will be positive due to symmetry. Then, for each λ_i a corresponding eigenvector can be found by solving:

$$(\mathbf{C} - \lambda_i)\mathbf{v}_i = \mathbf{0}.\tag{3.4}$$

In this context, an eigenvector describes how each vertex behaves with respect to the corresponding vertex in the mean for a certain mode of variation. Each eigenvector represents a unique variation and its corresponding eigenvalue expresses how pronounced that mode of variation is in the training set, which is visualized in Figure 3.1. By ordering the eigenvalues from high to low, the modes of variation are ordered in terms of significance. Now every shape in the training set can be represented by the mean shape of the training set plus a linear combination of modes of variation:

$$\mathbf{x}_{\mathbf{i}} = \bar{\mathbf{x}} + \mathbf{c} \mathbf{V},\tag{3.5}$$

with $\mathbf{V} = \begin{pmatrix} \mathbf{v}_0 & \mathbf{v}_1 & \dots & \mathbf{v}_t \end{pmatrix}$ the eigenvector matrix and \mathbf{c} a *t*-dimensional coefficient vector with shape parameters. Important is to note that $t \leq m$, due to the fact that \mathbf{V} is directly derived from \mathbf{X} .

3.3 Rigid alignment

After training an SSM, the mean shape $\bar{\mathbf{x}}$ is used to align the shape model with the target points \mathbf{y} that has j elements. This is done by using the ICP algorithm, where $\bar{\mathbf{x}}$ is considered to be the moving shape. This algorithm requires point correspondence in both point sets. Since this information is often not available in real life data, the closest distance is used as an estimation. For each point on the target shape a closest point on the moving shape is found, which is the corresponding moving point set \mathbf{x}^* with j elements. For the first step of the algorithm \mathbf{x}^* is a subset of $\bar{\mathbf{x}}$. Now a rigid transformation T is computed that minimizes the squared distance between both corresponding point sets:

$$\mathbf{d}^2 = ||\mathbf{y} - T(\mathbf{x}^*)||^2, \tag{3.6}$$



FIGURE 3.1: Illustration of the effect of the first three individual modes of variations with respect to the mean, as in Equation 3.5. The first mode clearly describes the size of the bone, the second bone explains the tilt angle of the femur head and the last mode portrays the width of the femur.

The optimal transformation T, which is restricted to scaling, translation and rotation, is extracted from a single value decomposition on the cross-covariance matrix of \mathbf{y} and \mathbf{x}^* , which is intensively explained by Besl [4].

3.4 Finding shape parameters

Now the corresponding moving point set is rigidly aligned with the target data. The error can be further reduced by adding a certain linear combination of modes of variation to the residual. Only the vertices in the modes of variation that have correspondence to the target set will be used, that is $\mathbf{V}^* \subset \mathbf{V}$. The new error becomes:

$$\mathbf{d}^2 = ||\mathbf{y} - T(\mathbf{x}^* + \mathbf{c}\mathbf{V}^*)||^2.$$
(3.7)

Best registration performance is achieved when the error is minimized. Optimal values for the shape parameters \mathbf{c} can be computed by performing a least-squares solve on the residual:

$$\arg\min_{\mathbf{c}} ||\mathbf{y} - T(\mathbf{x}^{\star} + \mathbf{c}\mathbf{V}^{\star})||^2, \quad lb \le c_i \in \mathbf{c} \le ub,$$
(3.8)

with $lb, ub \in \mathbb{R}^n$ and lb < ub. Each sub-element $c_i \in \mathbf{c}$ represents how many standard deviations that mode of variation deviates from the mean. This minimization problem is bound-constrained to prevent highly unlikely shape parameters from occurring and is solved by using a conjugate gradient method for large-scale bound-constrained minimization problems, introduced by Branch et al. [32].

3.5 Weighting

The shape parameters \mathbf{c} from Equation 3.8 are derived under the assumption that every point in the target shape is equally important. This approach, however, will lead to registration inaccuracies for truncated shapes. Points from sparse target sets, especially ones obtained from segmentation on medical images, are not always equally sampled. Dense clusters will overrule sparse clusters, since they have more terms that will contribute to the squared distance error that is to be minimized. We introduce a weighting vector, to correct for this behavior. Now the minimization problem becomes:

$$\underset{\mathbf{c}}{\operatorname{arg\,min}} \left(\mathbf{w} \odot \left| \left| \mathbf{y} - T(\mathbf{x}^{\star} + \mathbf{c} \mathbf{V}^{\star}) \right| \right|^{2} \right), \tag{3.9}$$

with \mathbf{w} the weighting vector and \odot an element-wise multiplication, to control the contribution of each point in the solution for \mathbf{c} .

Our definition for \mathbf{w} is based point isolation. Points that are a member of a dense cluster, need to individually have lesser weight than those of isolated points. Point isolation is determined by evaluating Gaussian mixture models on every point in the target set, which results in a Gaussian distribution field:

$$p(\mathbf{s}) = |2\pi \mathbf{\Sigma}|^{-\frac{1}{2}} e^{-\frac{1}{2}(\mathbf{s}-\mathbf{y})^T \mathbf{\Sigma}^{-1}(\mathbf{s}-\mathbf{y})}, \qquad (3.10)$$

where $\mathbf{s} \in \mathbb{R}^d$ and Σ a d-dimensional diagonal matrix with scale parameter σ on the diagonals. The parameter σ controls for the kernel size in all dimensions. Now we distinguish clusters in the data, by finding the modes in the created Gaussian distribution field. The influence of the scale parameter on the clustering is shown in Figure 3.2.

The method implemented in this paper uses gradient and Hessian operators on the distribution field ($\nabla p(\mathbf{s})$ and $\nabla \nabla^T p(\mathbf{s})$) and performs quadratic maximization to find the most common modes, which is explained by Miguel [33]. A point in the target set belongs to the cluster that it is geometrically the closest to. Each cluster has a density ρ , which is equal to the amount of points in that cluster. Now the weighting vector is



FIGURE 3.2: A unit-less example of the influence of the scale parameter σ on the clustering process. On the left the scale parameter is small enough to distinguish two clusters of points. On the right the scale parameter is so large that both clusters correspond to the same mode in the density field.

equal to:

$$\mathbf{w} = \begin{pmatrix} \frac{1}{\rho_0} & \frac{1}{\rho_1} & \dots & \frac{1}{\rho_j} \end{pmatrix}, \tag{3.11}$$

where each element is equal to the inverse of the density of the cluster that the point belongs to.

3.6 Iterative solving approach

Now the results of the previous sections can be used to reconstruct a complete shape:

$$\mathbf{x} = T(\bar{\mathbf{x}} + \mathbf{c}\mathbf{V}). \tag{3.12}$$

Recall that T and \mathbf{c} were obtained by using an estimation for the point correspondence between the moving and the target shape. This initial point correspondence was not necessarily optimal. Therefore the newly created complete shape can be used to update the estimation for point correspondence. This is an iterative schema and the result of one iteration can be defined as:

$$\mathbf{x}_n = T_n(\bar{\mathbf{x}} + \mathbf{c}_n \mathbf{V}),\tag{3.13}$$

with T_n the transformation that minimizes Equation 3.6 and \mathbf{c}_n the coefficients that fulfill Equation 3.9 for the points $\mathbf{x}^* \subset \mathbf{x}_n$ that now are closest to target shape \mathbf{y} . The convergence will be explained in the next subsection.

3.7 Restrictions on modes of variation

Since the modes of variations are ordered (from high variance to low variance in the training data), it is evident that the modes with more variance will have a greater influence on the global fit than the modes with low variance. It is not desirable that the modes with the smallest variance will force the moving shape in a local minimum during the first iterations. The least significant modes, however, can help the registration process to fit the finer details in the target shape. This is why we iteratively increase the amount of modes of variations. Since this solution uses less components, it should result in quicker calculation times. Now the result of one iteration looks like:

$$\mathbf{x}_n = T_n(\bar{\mathbf{x}} + \mathbf{c}_n \mathbf{V}_n), \tag{3.14}$$

with $\mathbf{V}_n = {\{\mathbf{v}_i\}_{i=0}^n, \mathbf{V}_n \subset \mathbf{V} \text{ and } n \text{ the iteration number. The solutions for } T_n \text{ and } \mathbf{c}_n$ are found by minimizing:

$$\underset{T_n}{\operatorname{arg\,min}} \left(||\mathbf{y} - T_n(\mathbf{x}^{\star})||^2 \right) \tag{3.15}$$

and

$$\underset{\mathbf{c}_{n}}{\operatorname{arg\,min}}\left(\mathbf{w}\odot\left|\left|\mathbf{y}-T_{n}(\mathbf{x}^{\star}+\mathbf{c}_{n}\mathbf{V}_{n}^{\star})\right|\right|^{2}\right),\tag{3.16}$$

with $\mathbf{x}^* \subset \mathbf{x}_{n-1}$ the corresponding points from the previous result to the target shape \mathbf{y} and $\mathbf{V}_n^* = {\mathbf{v}_i^*}_{i=0}^n$, with $\mathbf{v}_i^* \subset \mathbf{v}_i$, the subset of eigenvectors that have corresponding elements to \mathbf{y} . The registration process is completed when all modes of variation are used, that is when n = t.

3.8 Algorithm

In this section the findings of the previous sections are combined in an overview:

Ī	Algorithm 1: ICP-SSM registration schema							
ī	nput data : Training set X of shape $m \times k \times d$							
	Target set y of shape $j \times d$							
Į	parameters: Kernel size σ							
	Minimization bounds lb and ub							
C	butput : Registered shape $k \times d$							
begin								
Train SSM	· Calculate training set mean $\bar{\mathbf{x}}$ using Equation 3.2							
	· Calculate modes of variation $\mathbf{V} = {\{\mathbf{v}_i\}_{i=0}^t}$ of shape $t \times k \times d$ using Equation 3.4							
Calculate weights	· Compute Gaussian density field $p(\mathbf{s})$ with Equation 3.10							
	· Derive modes from $p(\mathbf{s})$ using a gradient-quadratic search on the Hessian [33]							
	\cdot Compute weight vector w as in Equation 3.11							
Initialize	$\mathbf{x}_0 = ar{\mathbf{x}}$							
	for $n = 0$ to t do							
ICP	· Compute the corresponding point set \mathbf{x}^{\star}							
	$\cdot \mathbf{x}^{\star}$ are the points in \mathbf{x}_n that are closest to \mathbf{y}							
	· \mathbf{x}^{\star} is of shape $j \times d$ and has an element wise correspondence with \mathbf{y}							
	\cdot Find the rigid transformation T_n that minimizes the squared distance between							
	\mathbf{x}^{\star} and \mathbf{y} Equation 3.15							
	\cdot Update \mathbf{V}^* according to found point correspondence							
Shape parameters	· Find the shape parameters \mathbf{c}_n with Equation 3.16 using $\mathbf{V}^*_{\mathbf{n}} \subset \mathbf{V}^*$							
Reconstruction	$ \qquad \qquad$							

4 Results

The aim of this research was to perform better registration on highly truncated point sets, to facilitate more accurate motion simulations during preoperative planning for hip arthroscopy. This chapter assesses the presented registration method by exhibiting a variety of experiments on sparsely segmented femur data.

4.1 Setup

All experiments in the next section are performed in five-fold cross-validation (4 folds training, 1 fold validation) on the database that is described in section 3.1. The shapes in the validation fold are manipulated in such a way that they correspond to real life cases, as explained in Appendix A. The training set represents \mathbf{X} from algorithm 1 and each shape in the validation fold represents \mathbf{y} . To quantitatively assess the registration performance we introduce two metrics:

- Mean distance (point to surface): this is the distance for each vertex from the target set to the closest point on the surface of the registered shape. These values are then averaged to get the mean distance. We solely focus on the femoral head sphere and knee regions, since they are the most vital parts for range of motion simulation.
- Femoral version error: the femoral version is an anatomical metric that is defined as the angular difference between the femoral neck axis and the transcondylar axis, as visualized in Figure 4.1. The vertices necessary for the calculation of these axes are encoded in the trained model, and can be easily recovered after registration. The femoral version is a descriptor for the pose and is a key ingredient in the determination of femoroacetabular impingement. The metric we use is the difference between the femoral version of the registered shape and that of the ground truth.

These metrics will be used to investigate the following topics:

- The influence of the weighting vector, as discussed in section 3.5.
- The influence of restrictions on the modes of variation, as discussed in section 3.7.



FIGURE 4.1: The femoral version is the angle between the transcondylar axis and the femoral neck axis. This view is the projection along the femoral shaft axis.

• The performance compared to the commonly used iterative closest point algorithm (ICP) and the current state of the art non-rigid registration algorithm: coherent point drift (CPD).

4.2 Evaluation

This subsection is an evaluation of the proposed registration algorithm, from now on referred to as ICP-SSM. The evaluation is done as explained in the previous subsection. The coming subsections contain general statistics of the cross-validation on 275 samples. For individual results, see Appendix B.

4.2.1 Influence of weight vector

In this subsection we assess the influence of the weight vector, as explained in section 3.5, on the registration performance. A kernel size $\sigma = 50$ mm was used in the weight algorithm. This value was found to be reliable for this specific use case, as will be explained in this section. In Figure 4.2 we see how the kernel size σ influences the numerical values of the weights. If the kernel size is too small, the proximal femur and the knee slice can not be separated. Starting from $\sigma = 8$ mm a clear distinction between both clusters becomes apparent.

This is in accordance with Figure 4.3, which shows the relation between the kernel size and the femoral version error. From $\sigma = 8$ mm and higher the error reduces. On the other hand, we can hypothesize that if a kernel size is used in the order of magnitude of the distance between the proximal femur and the knee, the performance will drop. This is because both areas will be classified as one cluster, as we saw from Figure 3.2. At $\sigma = 32$ mm the error seems stabilized, which means that our used value of 50 mm is justified.



FIGURE 4.2: Numerical values of the weights for different values of the kernel size σ . Both the kernel size and the values on the y-axis are in millimeters.

We test ICP-SSM against ICP-SSM without the weighting vector. Figure 4.4 shows a visualization of the performance in terms of mean distance. To see how these distance errors affect the pose estimation, a femoral version error comparison is shown in Figure 4.5. In Table 4.1 the numerical outcomes can be found.

For the unweighted method we see a knee error that is almost twice as large as the sphere error. This is to be expected, since the knee has a small number of data points compared to the sphere. When the weights are added, we are able to achieve knee errors that are comparable to the sphere error. The accuracy on the sphere is slightly lower than before. We can see that the addition of weights resulted in a decrease in the femoral version error.



FIGURE 4.3: Absolute femoral version error for ICP-SSM with respect to the kernel size σ in the weighting calculation. The mean error (-) starts to decrease at $\sigma = 4$. At $\sigma = 32$ the error difference is converged. In light blue the standard deviation of the error (\blacksquare).

4.2.2 Influence of variable modes of variation

Now we will look at the influence of the increasing modes of variation as discussed in section 3.7. Figure 4.4 shows the performance in terms of mean distance. We test ICP-SSM with weights and fixed components against ICP-SSM with weights and an increasing amount of components. Fixed components means that each iteration uses the maximum amount of modes of variations (components) in the least-squares solving approach. A slight improvement can be observed for the knee accuracy. The effects on the femoral version can be seen in Figure 4.5. Again, we see a slight reduction in the error. Furthermore, the spread of the errors also reduced. By using an increasing amount of components we also achieve faster calculation times. From 4.62 sec to 1.71 sec per task, for the same amount of iterations.

Method	Mean distance (mm)		Mean femoral version error $(^\circ)$	
	Knee	Sphere	Signed	Absolute
ICP-SSM unweighted ICP-SSM fixed components ICP-SSM	$\begin{array}{l} 1.15 \ (\pm \ 0.46) \\ 0.60 \ (\pm \ 0.17) \\ 0.54 \ (\pm \ 0.15) \end{array}$	$\begin{array}{l} 0.45 \ (\pm \ 0.11) \\ 0.49 \ (\pm \ 0.11) \\ 0.48 \ (\pm \ 0.12) \end{array}$	$\begin{array}{l} 0.57 \ (\pm \ 4.72) \\ 0.95 \ (\pm \ 4.68) \\ 0.57 \ (\pm \ 3.61) \end{array}$	$\begin{array}{l} 3.76 \ (\pm \ 2.92) \\ 3.72 \ (\pm \ 3.00) \\ 2.82 \ (\pm \ 2.32) \end{array}$

TABLE 4.1: An error comparison between different variations of ICP-SSM.



FIGURE 4.4: Mean distance between target points and registration result. The visualization is a violin box plot, where the width represents the distribution and the dashed lines represent the quartiles. ICP-SSM without limitations has the lowest knee error.

4.2.3 Comparison to other algorithms

In this subsection we test ICP-SSM against ICP (rigid) and CPD (non-rigid). The mean of the trained SSM was used as the moving shape for both ICP and CPD. In Figure 4.6 we see the mean distance comparison between all the algorithms. In order for CPD to show consistent performance for these kind of registration tasks, the rigidity parameter had to be increased significantly. That is why CPD and ICP show comparable results. ICP-SSM showed more accurate results with less spread.

The performance comparison for the femoral version is shown in Figure 4.7. Since ICP is a rigid registration method, the resulting pose of the bone should be constant for every task. This is confirmed by the mean femoral version of 16.26° ($\pm 0.67^{\circ}$), that shows only minor deviations between tasks. Numerical results for the femoral version error are shown in Table 4.2. The mean of the femoral version error is not a meaningful metric,



FIGURE 4.5: Femoral version error between different variations of ICP-SSM. It shows the difference between the femoral version of the registered mesh and the ground truth. Since this is the signed angle error, the mean values of the error lie around zero. It is apparent that the width of the distribution of ICP-SSM without limitations (rightmost) is larger around zero than for the two other implementations. Also, the quartile lines are closer to zero. This means that the ICP-SSM implementation is more consistent in achieving femoral version errors that are close to zero.

since the error values are signed and the distributions will be centered around zero. The standard deviation is more informative, since it is a measure for consistency. ICP-SSM with weighting shows a smaller standard deviation in the signed femoral version error than the other two algorithms. That means that ICP-SSM is able to achieve errors close to zero with more consistency. This is also clear in the absolute femoral version errors. With a mean of 2.82° ICP-SSM outperforms ICP (mean of 6.73°) and CPD (mean of 6.67) significantly. Error values up to 5° are often clinically tolerated for the femoral version. With a standard deviation of 2.32° ICP-SSM is bellow this threshold for 83% of the cases.



FIGURE 4.6: Mean distance between target points and registration result. We compare ICP-SSM with weighting to ICP and CPD.

Method	Mean distance (mm)		Mean femoral version error $(^\circ)$		Timing (s)
	Knee	Sphere	Signed	Absolute	Per task
ICP	$1.86~(\pm 0.85)$	$1.28~(\pm~0.60)$	$0.45~(\pm~8.58)$	$6.73~(\pm~5.34)$	0.36
CPD	$1.77~(\pm 0.74)$	$1.52~(\pm~0.94)$	$0.01~(\pm~8.48)$	$6.67~(\pm~5.23)$	20.6
ICP-SSM	$0.54~(\pm~0.15)$	$0.48~(\pm~0.12)$	$0.57~(\pm~3.61)$	$2.82~(\pm~2.32)$	1.71

TABLE 4.2: An error comparison between ICP-SSM and two popular registration methods.



FIGURE 4.7: Femoral version error, which is the between the femoral version of the registered mesh and the ground truth. A comparison between two frequently used algorithms and ICP-SSM. We can see that angle errors around zero are more common for ICP-SSM. Furthermore, the spread in the data is a lot smaller.

5 Discussion & conclusion

In this work a statistical shape model based registration method is introduced for point set registration, called the Iterative Closest Point Statistical Shape Model algorithm (ICP-SSM). It can robustly register three-dimensional bone segments with a large amount of missing data. We iteratively solve for a linear combination of modes of variation, obtained from training data, that minimize the squared distance to the target points. The solving step for the modes of variation requires a good estimation of point correspondence between the target point set and the model. That is why we incorporated a rigid registration step to each iteration of the algorithm. By performing a five-fold cross-validation on 275 sparsely segmented entire femur bones, we have shown that the algorithm is able to register realistic patient data with high accuracy.

Another contribution is the introduction of a density based weighting vector, to maintain high accuracy for under-sampled clusters in the target data. Clusters in the target data are derived from a probability density field that is generated by evaluating Gaussian kernels at each data point. Each cluster corresponds to a local maximum in the density field. The weighting correction for each point is defined as the inverse of the density of the cluster that it belongs to. We found that the best registration results were obtained once the kernel size was large enough to distinguish the two primary clusters in the data. By performing registration accuracy measurements for a large amount of kernel sizes, we found that a kernel size within 32 and 64 mm performed the best for this specific case.

A comparison between a weighted and unweighted implementation of the algorithm indeed showed large improvements for the knee accuracy (distal femur), which, in our target data, is an area with high sparsity of points. The accuracy on the femoral head sphere, however, marginally decreased. This is a trade-off that is inherent to the weighting vector, since it changes relative importance of the target points. A comparison between the femoral version of the registered result and the ground truth showed a reduction in the standard deviation of the error, from a standard deviation of 4.72° to a standard deviation of 3.61° .

Finally, we added a restriction on the modes of variation. Rather than using all available modes of variation in the least-squares solve process, solely the most significant mode of variation is used in the first iteration. Every following iteration adds another, less significant, mode and the algorithm aborts when all available modes are used. This addition showed improvements in the estimation of the pose. The standard deviation in the femoral version error went down from 4.68° to 3.61° . Another advantage of this method is that it does not require arbitrary stopping criteria. Furthermore, we saw a speed increase of almost a factor of 3.

We have tested the algorithm against ICP (rigid) and CPD (non-rigid). ICP-SSM outperforms the other algorithms in terms of distance accuracy and pose estimation. CPD had large difficulties with a target set of this sparsity. The rigidity parameter had to be increased, in order to not classify isolated points as outliers. This is why CPD and ICP show similar performance.

The mean absolute femoral version error obtained using ICP-SSM was found to be 2.82° with a standard deviation of 2.32° . Generally an error within 5° is found to be clinically acceptable for the estimation of the femoral version. In 17% of the cases our method yields an error that is larger than the accepted threshold. This means that if one is going to use ICP-SSM for this specific use-case, manual inspection is necessary if the subject is a pathological edge case.

We offer a framework that is applicable to any kind of bone structure. Yet, our validation was only performed on the femur. That is why future work should include validation for more types of bones. Our used kernel size of 50 mm in the weight determination was case specific and requires further attention for other registration problems. A method to calculate the optimal kernel size beforehand would be a useful extension to the current implementation of the algorithm. Our method was developed for a use case where target data is hand picked and does most likely not contain outliers. For future research it would be interesting to test the robustness of the algorithm on noisy data.

A | Manipulated shape

To create the manipulated shape (Fig. A.1c), only those points from Fig. A.1b are used that are inside the conventional scanning regions (Fig. A.1a). The selection strategy is done automatically and selects roughly 250 points per femur, which is similar to what a human scan processor would place during a segmentation task. Points with high curvature are prioritized in the process, as shown in Fig. A.2.



FIGURE A.1: (a) Typical scan regions highlighted in green. (b) Complete femur from the database. (c) Manipulated shape after automatic point selection.



FIGURE A.2: This is a slice of the distal femur with the automatically sampled points. Only points with high curvature are selected.

B Individual results

In this section more detailed results are shown. In Fig. B.1 it is clear that CPD lacks the flexibility to fit the Trochanter Minor (x: 40, y: 140). Decreasing the rigidity, and thus making the moving shape more flexible, will lead to very poor performance in the knee (not visible in this figure) or even a collapse of the moving shape into the densest cluster of the target shape. ICP-SSM does not have this rigidity problem, since the allowed point movement is derived from real world data.



FIGURE B.1: Registration results of CPD, ICP-SSM without weights, and ICP-SSM for an arbitrary subject from the validation set (\times) . The colormap represents the distance to the ground truth.

From Fig. B.1 and Fig. B.2 we can see that ICP-SSM without weights has difficulties with fitting the knee, as explained in Sec. 3.5. We can see that the unweighted version of ICP-SSM has difficulties with registration on the knee. The addition of weighting clearly shows improvements in that area.



FIGURE B.2: Registration results of CPD, ICP-SSM without weights, and ICP-SSM for an arbitrary subject from the validation set (\times). The colormap represents the distance to the ground truth.

C Reference registration algorithms

In the results section our algorithm is compared to ICP and CPD. The theory behind ICP is already briefly covered in section 3.3. We will now briefly discuss the theory behind CPD.

Let \mathbf{x} be the dataset with the static shape and \mathbf{y} be the dataset with the moving shape. If we create Gaussian kernels around each individual point in dataset \mathbf{x} , we can calculate the contribution for every point in \mathbf{y} with respect to those kernels. The individual contributions are then weighted by the sum of all the contributions, to form the posterior density matrix. In general this looks like:

$$\mathbf{P} = \frac{w_m^{(k)} f\left(\mathbf{x}_n; \mathbf{y}_m^{(k)}\right)}{\sum_{m=1}^M w_m^{(k)} f\left(\mathbf{x}_n; \mathbf{y}_m^{(k)}\right)},\tag{C.1}$$

where $f(\mathbf{x_n}; \mathbf{y_m^{(i)}})$ is the used kernel and w_m is a weight factor for $\mathbf{y_m}$. The index k stands for the iteration of the algorithm. Important is to note that this algorithm requires normalization, so that the shapes have zero mean and unit variance.

To make sure that the moving shape will move coherently, a gram matrix is stored:

$$\mathbf{G} = \exp\left(-\frac{1}{2\beta^2} \|\mathbf{y}_i - \mathbf{y}_j\|^2\right) \tag{C.2}$$

Now the posterior densities can be used to calculate a transformation matrix $\mathbf{W}^{(k)}$ by solving:

$$\mathbf{W} = \left(diag(\mathbf{P}1)\mathbf{G} + \lambda(\sigma^2)^{(k)}\mathbf{I}\right)^{-1} \left(\mathbf{P}\mathbf{X} - diag(\mathbf{P}1)\mathbf{Y}^{(k)}\right),$$
(C.3)

with 1 a column vector of ones and $diag(\cdot)$ the diagonal matrix that is formed from its arguments. Both λ and β in Equation C.2 control the smoothness of the transformation.

Finally the moving shape can be updated:

$$\mathbf{Y}^{(k+1)} = \mathbf{Y}^{(k)} + \mathbf{G}\mathbf{W}^{(k)} \tag{C.4}$$

This process repeats until a certain criterion is fulfilled. This can be when a maximum iteration count is reached or when the change between iterations is too small. Such an optimization approach is also known as the EM-algorithm.

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