REGISTRATION PROCESS FOR REAL-TIME EVALUTION IN BIOMEDICAL APPLICATION

T. Vancouillie[1], J. Victor[2], P. De Baets[3], M.A. verstraete[2] and S. Herregodts[2]

[1] Ghent University, Belgium
[2] Ghent University, Department of Physical Medicine and Orthopaedic Surgery, Belgium
[3] Ghent University, Laboratory Soete, Belgium

Abstract: The study of knee kinematics is used to analyse joint disorders, design of prosthetic devices, impact of surgical treatments and in general the study of the locomotion. In order to allow researchers to immediately visualise and interpret the influence of certain changes during tests and between different test setups, a testing procedure that allows on-line evaluation of knee kinematics, based on the principles of computer assisted navigation surgery, is established. A major challenge for this evaluation method is to identify the position of the bone relative to the attached markers prior to testing. In order to deal with this challenge a registration process is introduced. The theoretical derivation and optimisation of this registration process is derived and afterwards applied to a practical testing environment.

Keywords: Knee joint; Real-time evaluation; Registration

1   INTRODUCTION

Computer assisted navigation is a tool that helps the surgeon with real-time information regarding the position of surgical instruments and implants in relation to the skeleton during surgery. Computer assisted navigation can either be active, in combination with the use of surgical robots, or passive, where the surgeon stays in control. With passive navigation, the computer software aids the surgeon in positioning the instruments and implants relative to the patient's anatomy [1].

The concept of computer assisted navigation is often compared to GPS systems that are used in cars. These systems give feedback by constantly displaying the car's location on a digital map. In computer assisted navigation this kind of feedback is given by displaying the locations of the surgical instruments relative to the patient [2, 3].

Figure 1. Computer assisted navigation in knee arthroplasty [4]

It is essential that the patient's anatomy and surgical instruments are tracked in the three dimensional space, so that the interaction between both can be visualised on a computer platform. The tracking is made possible by attaching marker sets to both, which can be localised by a tracking system. For instance, these tracking systems can consist of optical cameras that emit infrared light that is reflected by the retroreflective surfaces of the spherical markers. The reflected beam is then detected by the sensors of the cameras. This allows to estimate the marker positions in the three dimensional space [5]. Obviously only the marker motions can be tracked, this means that the movement of the markers thus represent the movement of the object to which they are attached. The software therefore has to know the position of the object relative the markers [2].

With respect to the bones, two general methods are used to find the relative position of the bone compared to the attached markers. A CT based computer navigation system uses a pre-operative CT scan of the patient, which is used to create 3D reconstructions of the bones. A pointing device, visible by tracking its attached markers, is used to digitise predetermined anatomical reference points on the patient's anatomy.

Afterwards, the 3D reconstruction is matched to the patient's anatomy, i.e. registration [1, 2, 3, 6]. In clinical literature, it has been shown that the use of pre-operatively CT scans in computer navigation system offers opportunities to enhance surgical precision in total knee arthroplasty [7, 8]. Alternatively image free computer navigation system can be used. In that case, a database of CT scans instead of a CT scan of the patient is used. The digitised predetermined anatomical reference points, which corresponds to the patient's anatomy, is now used to fit on a virtual bone. This is done by positioning and deforming a statistical bone model developed from a database of CT scans [1, 2, 3, 6].

2   REGISTRATION PROCEDURE

In the pre-testing phase a computed tomographic (CT) scan is made of the fresh frozen lower limb specimen. Sequentially, this is used for a 3D reconstruction of the femur and tibia, generated by Mimics® (version 18.0, Materialise NV, Leuven, Belgium). The 3D reconstruction is saved as a STL file, which is a triangular representation of the 3D surface geometry [9]. When the lower limb is subjected to a test, markers are attached to both bones.

The goal of the registration procedure is identifying the position of the 3D reconstructions relative to the attached marker set. If this relative positioning is known for a certain bone it is possible to know where the bone is positioned in the three dimensional space, just by tracking the markers attached to it.

Registration is defined as the geometrical transformation that aligns point clouds in two frames of reference, so that the associated attributes with those point clouds can be viewed and analysed jointly [3]. One point cloud is already obtained, namely the vertices of the 3D reconstruction of the patient's femur or tibia.

The second point cloud is obtained by digitising the patient's anatomy, i.e. femur and tibia, in real-time, by the use of a pointing device. Digitisation of for instance the femur is done by moving the pointing device's tip over the femur surface while tracking both markers of the pointing device and attached marker set, i.e. scanning. Next, software calculates the spatial position of the point of contact between pointing device tip and femur surface. The final result is a digital image consisting of contact points which are spatially positioned relative to the marker set attached to the femur, i.e. fixed markers.
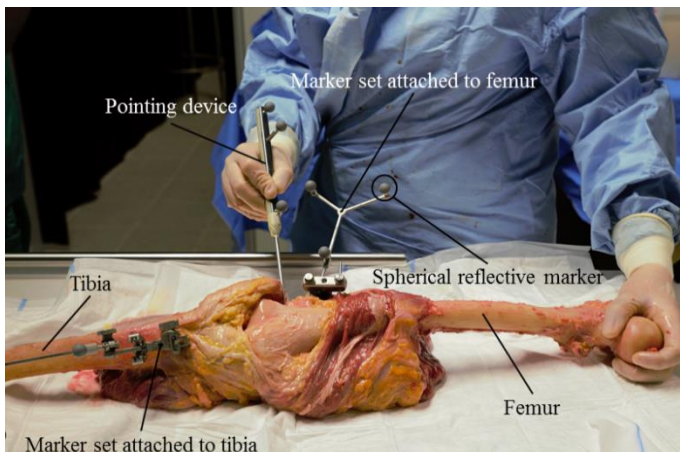

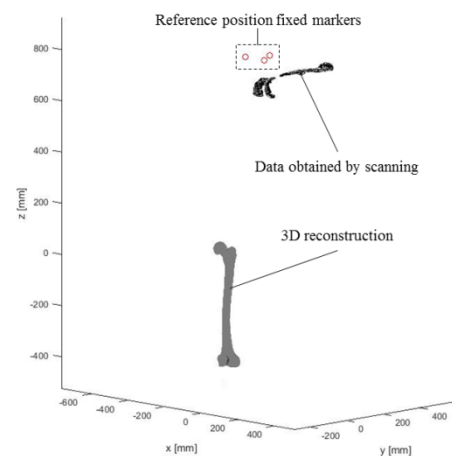Figure 2. Registration of the femur using a pointing device

Figure 3. 3D reconstruction and the data obtained by scanning before matching

Eventually, a matching algorithm is applied that calculates the transformation matrix that fits the 3D reconstruction of the femur in the digitised femur, which is positioned relative to the fixed markers. This registration process is also repeated for the tibia.

3   MATCHING

Matching is used here to calculate the transformation matrix that fits one point cloud in another one. The previous derived point clouds that are used will from now on be called *model* ($M \in R^{3 \times n_M}$), i.e. 3D reconstruction of the bone, and called *data* ($D \in R^{3 \times n_D}$), i.e. the digitised patient's anatomy resulting from scanning.

3.1   Iterative closest point algorithm
The iterative closest point algorithm is designed to efficiently register two point clouds, a data and a model point cloud [10]. The algorithm will pull the data points step by step closer to the model points and shall eventually stop when stopping conditions are reached [11].

The ICP algorithm relies on the least squares error to derive the transformation matrix to match two point clouds, model $M = [m_i] \in R^{3 \times n_M}$ and data $D = [d_i] \in R^{3 \times n_D}$. First, the algorithm calculates the point correspondences $M_c = [m_{c,i}] \in R^{3 \times n_D}$ by the use of the k-d tree nearest neighbour search algorithm. The model point m_i that is geometrically closest to data point d_i is taken as the corresponding point $m_{c,i}$. Sequentially, the algorithm uses singular value decomposition to find the optimal rotation $R \in R^{3 \times 3}$ and the translation $t \in R^{3 \times 1}$, which minimize the cost function $E(R, t)$ in Eq. 1 [10, 17].

$$E(R,t) = \sum_{i=1}^{n_D} \left[m_{c,i} - (R \cdot d_i + t) \right]^2 \tag{1}$$

Because of the step by step convergence, the algorithm achieves its final transformation by executing an iterative process as displayed in Figure 4.
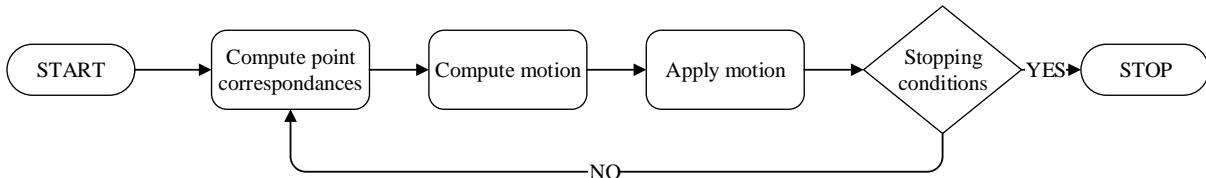

Figure 4. Flowchart of the iterative closest point algorithm

3.2 Hybrid algorithms

The ICP algorithm pulls the data points step by step closer to the model points, which minimises the cost function, iteratively. However, ICP will converge monotonically to the nearest local minimum. Without proper pre-alignment, the algorithm rarely finds the absolute minimum due to the high chance of getting stuck in a local minima. This shows the need for a robust hybrid algorithm, that allows finding the absolute minimum [10-12].

Figure 5 illustrates an example of the local minimum problem. If the ICP algorithm is applied to the data point set with a starting position (black dot) different from the indicated yellow region, the algorithm will converge to the nearest minimum which is a local minimum, resulting in a mismatch. A hybrid algorithm should therefore be designed in that way that it tries to find a starting position that will lead to the absolute minimum, in Figure 5 this corresponds to a starting position in the yellow region.
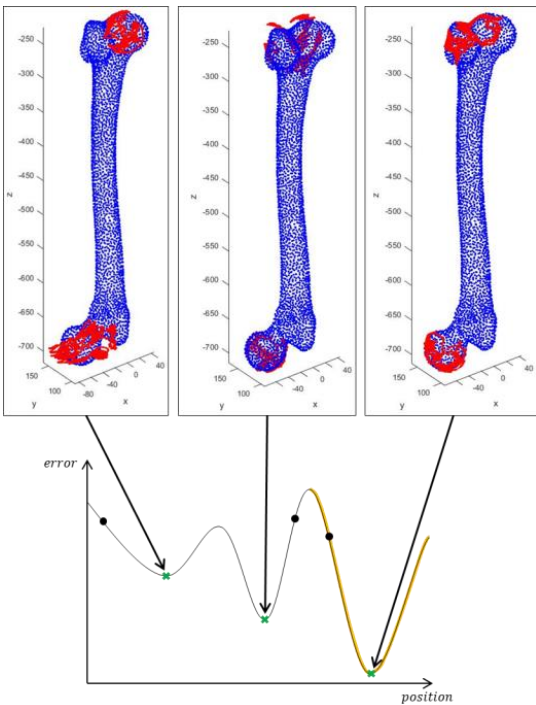

Figure 5. Example local minimum problem with matched data point set (red) and 3D reconstruction vertices (blue)
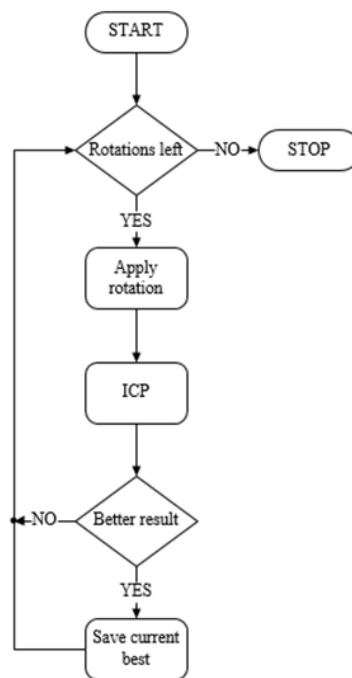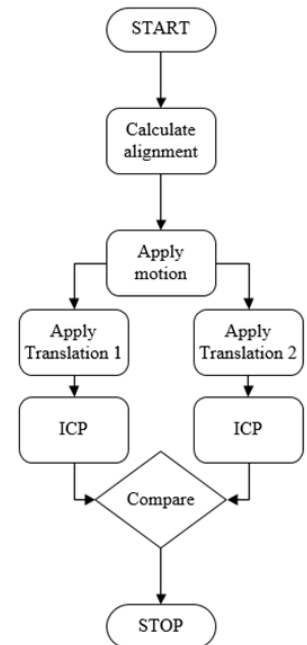
Figure 6. Flowchart RICP

Figure 7. Flowchart IAICP

First, a hybrid algorithm will generate a start position for the data point set. Sequentially, this generated start position is used as input for the ICP algorithm. As last, the hybrid algorithm checks if the output of the

ICP algorithm is better than the current lowest obtained minimum. This process is repeated till pre-determined stopping conditions are attained.

However, a problem arises with hybrid algorithms. In order to find a starting position that converges to the absolute minimum, they often have to calculate a high amount of different starting positions. Originally the complete point sets were used for that, so that immediately an accurate estimation was obtained. Using these complete point sets with hybrid algorithms gave extremely high calculation times with a standard computer. The idea came along to work with two kind of point sets, low detailed (reduced) and high detailed (complete), by adjusting the amount of points in a point set.

3.2.1 Rotational Iterative Closest Point (RICP)

The basic idea of RICP is that the ICP algorithm is applied to several different starting positions of the data point set. These positions are provided by rotating the original data point set around every axis using roll, pitch and yaw angles as parameters. Sequentially changing one parameter stepwise by a fixed angle will lead to n^3 possible starting positions, with n a natural number given by $n = 360/\text{step angle}$.

The best match is found by the starting position that gives the smallest root mean square deviation when applying the ICP algorithm. It is rather obvious that RICP does not guarantee that the resulting match is the absolute minimum. To increase the probability of finding the absolute minimum, the step angle has to be chosen very small. But choosing a small step angle will tremendously increase the amount of possible starting positions and along the corresponding calculation time.

It was noticed that the calculation time decreased significantly when data point set and model point set were positioned close to each other. This brings the idea of computing the centroids of the point sets and applying a translation on them so that the origin and centroids are aligned. In order to increase variability in the algorithm, an offset compared to the origin can be adjusted for the data point set.

3.2.2 Initial Aligning Iterative Closest Point (IAICP)

In the IAICP algorithm the starting position for the ICP algorithm is based on pre-aligning the data point set compared to the model point set by calculating one proper start position [11]. The pre-alignment is achieved by means of three anatomical reference points (model), virtual identified on the 3D reconstruction as suggested in the PhD-study of Professor Jan Victor [18], and three indicated points (data), identified by the surgeon during the registration process [19]. The latter points have to be indicated in the suggested regions given in Table 1 a and b, for femur and tibia respectively. The regions need to be chosen in a way that the indicated points are close to the corresponding anatomical reference points. Providing that the point correspondences are known, the pre-alignment is calculated by least squares minimization using singular value decomposition as in the ICP algorithm.

Table 1. Anatomical reference points and the corresponding regions where an indicated point should be appointed for (a) femur and (b) tibia

(a)

Anatomical ref. point	Indication region
Femoral Head Center	Head
Femoral Medial Condyle Center	Medial Epicondyle
Femoral Lateral Condyle Center	Lateral Epicondyle

(b)

Anatomical ref. point	Indication region
Tibial Ankle Center	Ankle
Tibial Medial Condyle Center	Medial Tibial Plateau
Tibial Lateral Condyle Center	Lateral Tibial Plateau

However, it seemed that reaching a local minimum is still possible up to now. This is solved by using two start positions, originated by applying a translation of five centimetres to the pre-aligned starting position perpendicular to the plane formed by the three anatomical reference points.

4 PRACTICAL TEST

The practical test involves the registration procedure subjected to three fresh frozen knee specimen, consisting out a femur and a tibia.

4.1 Set up

First, the 3D reconstructions of the bones are made and the corresponding anatomical reference points are determined. The obtained 3D reconstructions are remeshed to a mesh size of 0.5, 5 and 10mm.

Sequentially, the specimen are removed of soft tissue and certain muscles. Afterwards, markers are mounted onto the bones. The cleaned regions, where no cartilage is present, are scanned with a pointing device. The obtained scan data is reduced to a minimum spacing of 5 and 10mm. Finally, the 3D construction and corresponding scan data is matched by the use of optimised hybrid algorithms which were discussed earlier on.

The goal is to analyse efficiency and calculation time of each method applied to a real situation. Further on the error distribution, defined as the distance between the data points and the corresponding closest model points, is evaluated for the lowest obtained minimum.

4.2 Results

The resulting absolute minima obtained from matching are shown in Figure 8, it displays the 3D reconstruction together with the matched data. The spatial error distribution is represented in the form of a heat map. The maximum of the heat map, per plot, is chosen as the maximum resulting distance between the points of the 3D reconstruction and the 90% closest data points.

To validate that the obtained absolute minimum reflects the optimum positioning, the spatial error distribution is analysed. This is done by checking if the spatial error distribution is a homogeneous distribution. Especially by validating the position of the bone compared to the data in posterior-anterior, medial-lateral and proximal-distal direction. From the graphs it is concluded that the perceived error distribution is a preferred solution. This is due to the use of a control tool designed to check if the error is homogeneous distributed over the bone, and in this way validate the match.

The statistical variables obtained from the computed error are listed in Table 2.The average values in Table 2 will be used as guideline values when applying the registration process. It is thus concluded that a preferred match is attained if a mean value and a standard deviation is found which is lower than the guideline values. It is important to keep in mind that by forming this conclusion, two assumptions are used. The first assumption is that the data obtained by the pointing device is identical to the patient's anatomy. However in reality this is not the case, the pointing device is subjected to noise from the motion capturing system. The second assumption is that the 3D reconstruction is not subjected to any accuracy influences when constructed, this is of course in reality not the case.

Table 2. Overview of the error in the form of a statistical variable for every specimen

Statistical variable	Specimen 1		Specimen 2		Specimen 3		Average	
	Femur	Tibia	Femur	Tibia	Femur	Tibia	Femur	Tibia
Mean [mm]	0.70	0.45	0.35	0.66	0.64	0.39	0.56	0.50
Standard deviation [mm]	0.52	0.39	0.23	0.45	0.39	0.20	0.38	0.35
Median [mm]	0.55	0.36	0.29	0.54	0.55	0.34	0.46	0.41

An overview of which method has resulted in the absolute minimum is listed in Table 3. If a method resulted in the absolute minimum, this is indicated by a cross. Else it has got stuck in a local minimum, indicated by an empty field. The efficiency is calculated for every method. A distinction is made between the match efficiency of femur and tibia. This is because a difference is noticed between femur and tibia matching efficiency. This difference is due to the difference in shape of registered points of femur and tibia. The femur has a more asymmetrical shape, due to the femoral head, so there is less chance of getting stuck in a local minimum. This mismatch can be avoided by using the IAICP algorithm, the pre-alignment seems to work perfectly.

Table 3. Overview of which method results in the absolute minimum (cross) and the eventual efficiency

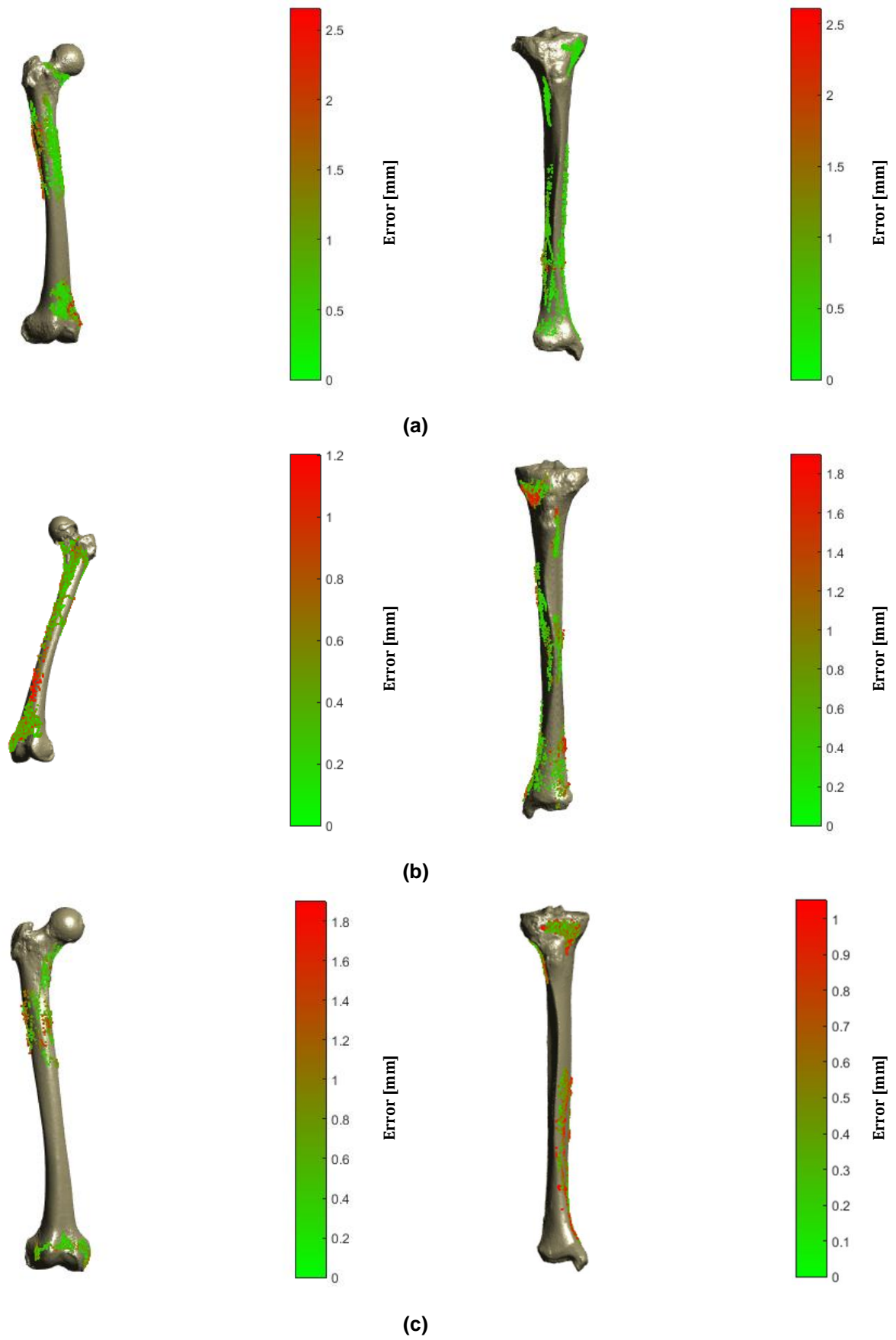| Method	Step angle [°]	Offset [mm]	Specimen 1		Specimen 2		Specimen 3		Efficiency [%]		
			Femur	Tibia	Femur	Tibia	Femur	Tibia	Femur	Tibia	Both
IAICP	N/A	N/A	×	×	×	×	×	×	100	100	100
RICP	90	0	×		×		×		100	0	50
	30	0	×		×		×	×	100	33	67
		250	×		×	×	×	×	100	67	83

Figure 8. Error distribution obtained for femur left and tibia right for (a) specimen 1, (b) specimen 2 and (c) specimen 3

Based on match efficiency, the IAICP is by far the best method, followed by the RICP algorithm, with step angle 30° and offset 250mm. With this step angle, the algorithm calculates 1728 different starting positions. The step angle here is thus sufficient small enough to get a fast and accurate estimate. In order to gain higher efficiency, the step angle could be lowered, but this would tremendously increase the calculation time. The 250mm offset also increases the chance of finding the absolute minimum compared to 0mm offset. This is due to the presence of a distinct translation movement during matching when there is a sufficient offset.

Regarding calculation time, listed in Table 4, there are no big differences noticed within the same method. Although RICP 30° both with and without offset have the same amount of starting positions, a big difference in calculation time is noticeable. This is due to the offset, where a larger distance between data and model point sets is present. This will take more time to converge, as already explained.

Table 4. Overview of the calculation time of each method

Method	Step angle [°]	Offset [mm]	Calculation time [sec]		
			Femur	Tibia	Average
IAICP	N/A	N/A	27.56	31.52	29.54
RICP	90	0	12.78	13.76	13.27
	30	0	34.90	29.53	32.21
		250	52.70	47.90	50.30

Based on both optimal efficiency and calculation time, it seems that the best method is by far the IAICP algorithm. The best alternative is the RICP algorithm with step angle 30° and offset 250mm. This algorithm should thus be used as an alternative when no anatomical reference points or indicated points are available.

5   CONCLUSIONS

The registration process introduced here is based on matching two point clouds. An algorithm widely used for this, is the iterative closest point algorithm. Implementing this algorithm in the registration process revealed a local minimum problem. To overcome this issue, hybrid algorithms were developed. These hybrid algorithms calculate a pre-alignment transformation matrix with reduced point sets. Thereafter, the pre-aligned complete point sets are used as input for the iterative closest point algorithm, if the hybrid algorithm calculated a proper pre-alignment this converges to the absolute minimum

The practical experiment showed that the initial aligning iterative closest point algorithm is by far the best algorithm. This is due to the pretty accurate pre-alignment based on indicated points and anatomical reference points. However, such points are not always available, in that case the rotational iterative closest point algorithm with a step angle of 30° and an offset of 250mm is the best alternative. This algorithm calculates 1728 different starting positions, by rotating around every axis at an offset to the origin of 250mm.

6   NOMENCLATURE

3D   Three Dimensional

IAICP   Initial Aligning Iterative Closest Point

ICP   Iterative Closest Point

mm   millimetre

RICP   Rotational Iterative Closest Point

sec   seconds

7   ACKNOWLEDGEMENTS

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