Anatomical landmarks position estimation in incomplete 3D humerus models

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***Abstract*—A general method for estimating the anatomical landmarks location on incomplete 3D bone model was proposed in order to use standardized anatomical frame conventions. An estimate of the location of missing anatomical landmarks was obtained by matching the incomplete bone model under analysis to a template of a complete bone model on which anatomical landmarks have been previously identified. The methodology was tested on three humeri. Results have shown that while the method provided reliable results when the models of the bone portion and of the complete bone belonged to the same subject, errors highly increased (up to 19 deg) when bone meshes, relative to different subjects, were used.**

***Keywords*—Anatomical frame definition, humerus, bone meshes.**

I. INTRODUCTION

Joint kinematics can be determined in a repeatable and clinical meaningful manner, by using standardized anatomical frame (AF) definitions. The International Society of Biomechanics (ISB) [1] has proposed a standardization recommendation for the definition of the AFs of the upper extremities based on the use of selected anatomical landmarks (ALs).

Standard magnetic resonance imaging (MRI) is a powerful tool in those clinical applications where the joint motion can be analyzed in quasi-static conditions [2] and small displacements need to be detected. However, due to its limited field of view, often, only portions of the 3D model of the analyzed bones can be reconstructed, while complete bone models are needed to use ISB recommendations.

This problem could be overcome by obtaining the missing ALs by matching the MRI-based portion of the subject-specific 3D bone model (SBP), to a template of a complete bone model (TBC) on which the relevant ALs have been previously identified. Established algorithms exist for surface matching, popular ones being based on the Iterative Closest Point (ICP) algorithm [3] for which an initial guess of the transformation between the bone meshes is required. The reliability of the abovementioned registration exercise would depend on the size of SBP and the similarity level between SBP and TBC morphologies. In this preliminary study, the feasibility and the assessment of the level of accuracy and repeatability of the procedure for the ALs estimate when applied to the proximal portion of the human humerus, was evaluated. To this purpose, two experimental scenarios which can be encountered in the clinical practice were simulated. First, the ALs estimate procedure was tested to different SBPs characterized by different extents (expressed as percentage of the humerus length) using as TBC the bone applied to SBP and TBC belonging to different subjects.

II. MATERIAL AND METHOD

A. Data sets

Three left humeri were scanned and the 3D corresponding mesh models reconstructed ($TBC_{1,2,3}$). For each bone model, the following ALs were identified by an expert: lateral and medial epicondyle (LE, ME), greater and lesser tubercle (GT, LT) and the geometrical center of the humerus head (GH). GH was identified by fitting a sphere to the humeral head. From each TBC, three SBP were generated by isolating different proximal portions identified as percentage of the complete humerus length (14%, 16%, 20%) ($SBP_{1,2,3}^{14\%,16\%,20\%}$). These values were chosen to simulate different sizes of the MRI acquisition volume.

B. Procedure for the estimation of the ALs on the SBP

In order to estimate the position vectors of both LE and ME, in the same system of reference used to describe the SBP point set, the next steps are followed:

1) *Registration of first approximation* - Three anatomical landmarks GT, LT, and GH were manually identified by an operator on the SBP (Fig. 1a). Using the three pairs of

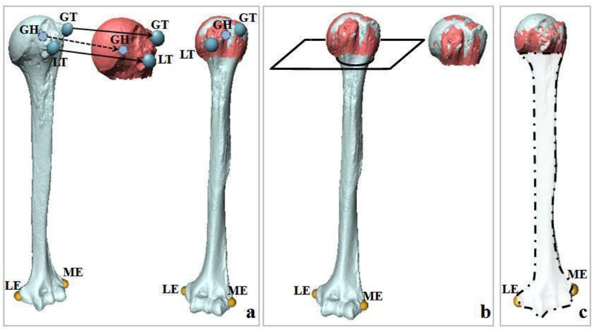

Fig. 1. Registration procedure. TBC (gray) to SPB (red) registration of first approximation (a). TBC iso-shaping (b). Final registration (c).

corresponding points, TBC and SBP were uniformly scaled, registered and the meshes expressed in a common reference frame.

2) *TBC iso-shaping* - A TBC iso-shape was automatically created by isolating a portion from the whole TBC using a separation plane coinciding with the most distal slice plane of the SBP (Fig. 1b).

3) *Final registration* - ICP algorithm was then employed to refine the registration between SBP and the iso-shaped TBC portion once the centers of mass were made to coincide. The model of the same subject. Secondly, the same procedure was position vectors of both LE and ME, identified on the TBC, were then expressed in the same system of reference of the SBP point set (Fig. 1c).

C. Application 1: SBP and TBC of the same subject

Each $SBP_{1,2,3}^{14\%,16\%,20\%}$ was matched to the corresponding *TBC* (Table I). For $SPB_1^{16\%}$, the ALs estimate procedure was performed three times by the same operator to verify the method sensitivity to the registration of first approximation.

TABLE I
EXPERIMENTAL SCENARIOS

	TBC_1	TBC_2	TBC_3
$SPB_1^{14\%}$	x	x	x
$SPB_1^{16\%}$	**xxx**	x	x
$SPB_1^{20\%}$	x	x	x
$SPB_2^{14\%}$	x	x	x
$SPB_2^{16\%}$	**xxx**	x	x
$SPB_2^{20\%}$	x	x	x
$SPB_3^{14\%}$	x	x	x
$SPB_3^{16\%}$	x	x	x
$SPB_3^{20\%}$	x	x	x

Different combinations of SBP and TBC tested. In light gray and dark gray are reported Application 1 and Application 2, respectively. The symbol **xxx** is referred to the combination which was tested three times.

D. Application2: SBP and TBC of different subjects

Each $SBP_{1,2,3}^{14\%,16\%,20\%}$ was matched with the two TBC belonging to different subjects (Table I). For $SPB_2^{16\%}$, the ALs estimate procedure was repeated three times by the same operator, using as template TBC_1.

Data analysis

Since the SBPs were generated from the corresponding TBC, the true positions of both LE and ME for each SBP were known and used as ground truth for evaluating the magnitude of the errors associated to the ALs estimation procedure. Humerus AFs were defined from both the estimated and the true LE and ME positions and their relative orientation (α, β, γ) was computed using the Euler angles representation suggested by Grood and Suntay (1983) [4].

III. Results

When SBP and TBC belonged to the same subject, the errors associated to the AFs definition were negligible for all different SBP extents analyzed (14%, 16%, 20%) and were lower than 0.1 deg for all angles (α, β, γ). Errors on the AF identification, due to variability with which GT, LT, GH were manually identified during the registration of first approximation, ranged, over the three repetitions, between 0.1-0.4 deg, 0.0-0.1 deg and 0.0-0.2 deg for α, β and γ, respectively. On the contrary, when the TBC and the SBP belonged to different subjects, the errors in the AF definition increased for all angular components and ranged, over the different TBC-SBP combinations (Table I), from 0.2-1.9 deg for α, 2.7-19.0 deg for β, 0.3-4.3 deg for γ. By estimating the ALs for different registrations of first approximation ($SPB_2^{16\%}$-TBC_1), AFs estimation errors varied, over the three repetitions, from 0.5-0.9 deg for α, 13.5-16.3 deg for β, 1.1-1.8 deg for γ.

IV. Conclusion

A general method for the estimate of the position of missing ALs on incomplete 3D bone model was presented. The methodology was applied and preliminarily tested on 3D bone models relative to the proximal portion of the human humerus. Preliminary results have shown that this method can be successfully employed when the portion of the 3D model of the bone, SBP, and the template, TBC, refer to the same subject. Under this condition, even with a limited portion of the SBP of the humerus (14% of the humerus length) it is possible to accurately estimate the position of the missing ALs. Moreover, the manual identification of the ALs, necessary for the registration of first approximation, and the TBC iso-shaping procedure did not appear to be critical. On the contrary, the performance of the method was unsatisfying when tested on SBPs and TBCs of different subjects. In this case, errors associated to the AF identification were up to 2 deg, 19 deg and 4 deg for α, β and γ, respectively. The large variability observed for the tested SBP-TBC combinations confirmed that the accuracy of the method is heavily affected by the degree of similarity between the morphology of the SBP and that of the template selected for the matching. The largest errors found for β can be explained by the high level of symmetry of the proximal portion about the humerus long axis and the variability characterizing the angle of humeral torsion [5]. The validity of present study is limited by the low number of samples analyzed. However, our preliminary results may suggest the critical role played by morphological variability. This issue might be faced using appropriate statistical models [6] or by selecting from large databases the template most morphologically similar to the portion of the 3D model of the bone. The applicability and the evaluation of this approach to different type of bones, such as the scapula, calls for further and specific analysis.

Acknowledgement

This work was partially supported by Sardegna DISTRICT (P.O.R. Sardegna 2000-2006 Misura 3.13).

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