Automatic 3D point matching of segmented images using shape-contexts

J. Carballido-Gamio[1], K-Y. Lee[1], S. Majumdar[1]

[1]Musculo-skeletal and Quantitative Imaging Research Group, Department of Radiology, University of California, San Francisco, San Francisco, California, United States

Introduction

Point matching between two shapes is a common problem in medical image processing techniques such as registration. The purpose of this work is to present and validate a 3D automatic point matching technique applied to medical imaging. The technique utilizes 3D descriptors called *shape-contexts* that characterize the shape of each point based on the distribution of points around them [1]. Corresponding points on similar shapes will have similar *shape-contexts*. In comparison to other point matching techniques, the technique presented in this work does not require equal number of points for the shapes to be compared or segments with high curvature. *Shape-contexts* are invariant to translation, and they can be also invariant to scaling and rotation. The validation was performed for intra and inter-subject shape matching based on landmark tracking on segmented MR images of tibias. Rigid body registration of the corresponding images based on the point matching is also demonstrated.

$$\chi^2(h_i, h_j) = \frac{1}{2}\sum_{k=1}^{K} \frac{(h_i(k) - h_j(k))^2}{h_i(k) + h_j(k)} \qquad (1)$$

Methods

Seven tibias were manually segmented from sagittal MR images of the knee of parallel kinematics and osteoarthritis on-going projects at our institution. The segmentation was performed based on Bezier splines and the control points were saved and used to represent the bone shapes (~682 points per tibia). For each point in all shapes we computed a histogram representing the point distribution of the relative remaining points. The bins were uniform in a 3D log-polar space (r, θ [0, 2π] and φ[0, π]) to make the descriptors more sensitive to nearby points than to those far away. An example of a bin in a 3D *shape-context* is shown in red in Fig. 1a together with an image representation of the corresponding *shape-context* with a total of 1183 bins (r = 7, θ = 13, φ = 13). Fig. 1b shows a cross-section of the structure of a 3D *shape-context* in blue. All *shape-contexts* were scale invariant by normalizing the radial distances by the mean distance of all the pair-wise distances in the shape [1]. In order to match two shapes, their corresponding *shape-contexts* were compared to each other based on the χ^2 test statistic (1), a simple and effective measure of histogram similarity. The output of this statistic could be considered as the cost of matching the points of the *shape-contexts* under evaluation. Once all the pair-wise costs were computed, the optimal point matching was solved using the Hungarian method [2], which minimizes the total cost of this assignment and satisfies the criterion of 1-to-1 matching.

For intra-subject validation all tibias were matched to themselves. The initial matching was direct and then followed by perturbations of scale, orientation, and location of the shapes to be matched. The perturbations in orientation were either rotations in the three axes, or a rotation simulating knee flexion (*z-axis*, Fig. 1c). The latter situation is most common at our institution since all scans are performed with a knee holder to prevent motion. Since *shape-contexts* are not rotational invariant when computed using an absolute frame, further processing had to be completed. The solution suggested in [1] to satisfy this criterion in 2D was to find the tangent vector at each point and use it as the positive *x*-axis to compute the *shape-contexts*. Our approach was to find the mid-slices of the segmented images and compute rotational invariant *shape-contexts* to perform 2D point matching followed by the computation of a rotation matrix to align these 2D slices in 3D. The rotation matrix was calculated using the closed form solution presented in [3] and applied to the whole shape to have an initial rough alignment of the two shapes before 3D *shape-context* computation (Fig. 1c). The main assumptions here were that both shapes were similar at their mid-slices (common for tibias), and that the *shape-contexts* were insensitive to small perturbations [1]. Then rigid body registration using the point matching to compute the scaling, rotation, and translation factors as suggested in [3] was accomplished for qualitative validation. Quantitative validation was performed based on landmark tracking.

For inter-subject validation all subjects were matched to the same target and all matching was direct with no perturbations in scale or orientation. However, an initial rough alignment was also applied following the procedure described above. Since no *a-priori* knowledge was available about the exact matching of shapes coming from different subjects, the only way to validate the results was based on visual tracking of landmarks and visual assessment of rigid body registration results.

Results

When either no perturbations were applied, or only scaling, translation, and rotation simulating knee flexion were applied for intra subject validation, then the point matching was perfect. When rotations in the remaining axes were applied the performance was still robust as it can be seen in Fig. 1d, which is a scatter plot of the point matching results. The blue line in Fig. 1d represents perfect matching, and the red points represent deviations from it. However, after a second iteration with no initial alignment based on the mid-slices, the point-matching either was perfect or misclassified 2 points at most. All points were correctly classified after a 3rd iteration. These additional iterations were much faster than the 1st assignment.

Visual assessment of landmark tracking and rigid body registration results also showed good performance for the inter-subject matching, and further validation is in progress based on work similar to that proposed in [4].

Discussion and conclusions

In this work we have presented and validated a 3D point matching technique that allows automatic landmark identification and matching on segmented images. The point matching technique presented in this work is invariant to translation, and can be invariant to scale and rotation. We have also shown for medical imaging applications an alternative way to make the descriptors less sensitive to rotations. This alternative is useful when clean 3D normals cannot be computed, and only requires an initial rough alignment taking the mid-slices as references for the 3D shape orientations, followed by additional iterations of point matching and registration. Quantitative and qualitative results demonstrated the excellent performance and robustness of the technique.
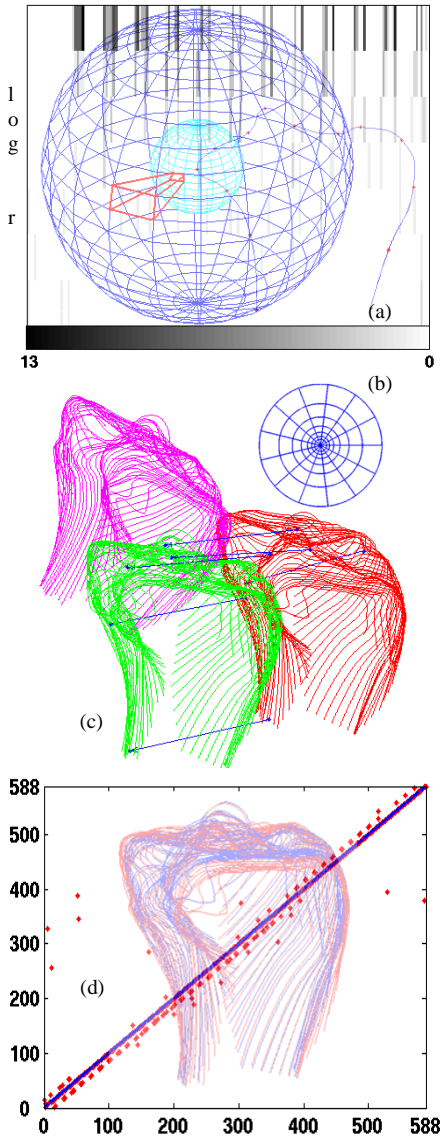
Fig. 1. (a) 3D *shape-context*. (b) Cross-section of a 3D *shape-context*. (c) Intra-subject point matching. Target shape (green); target shape after rotation (10º *x*, 10º *y*, 20º *z*), scaling (0.9), and translation (-9 *x*, 14 *y*, -23 *z*; magenta); target shape after initial rough alignment (red); some point correspondences (blue arrows). (d) Point correspondences and registration results of (c).

References [1] S. J. Belongie, *et. al.*, "Shape matching and object recognition using shape contexts." *IEEE Trans. PAMI*, 24, 4, 509-522, 2002. [2] Niclas Borlin, Dept. of Computing Science, Ume University, Sweden. [3] B. K. P. Horn, *et. al.*, "Closed form solution of absolute orientation using orthonormal matrices," *J Opt Soc A*, 5, 7, 1127–1135, 1988. [4] I. D. Grachev, *et. al.* "A method for assessing the accuracy of intersubject registration of the human brain using anatomic landmarks." *Neuroimage* 9, 250-268 (1999).