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Three-Dimensional Morphometric Analysis of the Distal Femur: A Validity Method for Allograft Selection Using a Virtual Bone Bank

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Abstract

Tumor excision is the primary treatment of aggressive or recurrent benign bone tumors and malignant bone sarcomas. This requires a surgical resection with the potential for large residual osseous defects that could be reconstructed using fresh frozen allografts. Virtual bone banks enable the creation of databases allowing a 3D pre-surgery evaluation of such allgorafts, based on segmentation of DICOM-CT images. This study demonstrates the usefulness of patient specific 3D models for an accurate host–donor allograft match. We describe one way to select the best match according to size and shape. The results suggest that a robust and realiable technique has been established. Since it is difficult to plan an allograft on a distal femur deformed by the tumor, we propose to plan the surgery on the contralateral side. Our results support this limb symmetry hypothesis. The use of this measurement protocol enables accurate selection of allografts from a contralateral healthy femur 3D CT model achieving the best match possible considering the geometry of available allograft candidate femur specimens.

Keywords:
Bone transplantation, Bone bank, Computer-aided surgery

Introduction

Tumor excision with wide surgical margins is the primary treatment of aggressive or recurrent benign bone tumors and malignant bone sarcomas [1]. This requires a surgical resection, with the potential for large residual osseous defects that could be reconstructed using fresh frozen allografts [2].

As diagnostic and therapeutic techniques improve, patients with musculoskeletal sarcomas should expect increased survivals, decreased complications and side effects, and an improved quality of life. That is why functional longevity of the reconstruction becomes a major concern, especially in young and physically active patients. Emphasis has been placed on biologic reconstructive alternatives due to concerns involving the durability of prosthetic materials, and the increasing survivorship of patients with sarcomas. Poor anatomical matching of both size and shape between the host and the donor can significantly alter joint kinematics and load distribution, leading to articular fractures or joint degeneration [1,2]. Determination of the distal femur size and shape is critical to obtain an appropriate allograft. In addition to this, it is difficult to plan an allograft on a distal femur deformed by the tumor.

The objective of this study was to develop a protocol to search and select of the best match (distal femoral allograft) from a virtual bone bank system, and to verify its intra- and inter-observer reliability. The feasibility of such protocol is based on our hypothesis, which states that the symmetry of the contralateral distal femur will provide the best match in preoperative planning allograft selection.

Materials and Methods

A total of thirty-three fresh-frozen whole femora were selected from the bone bank for this IRB-approved study, 15 right and 18 left (age range: 16-58 y.o., 35.9 ± 12.0 y.o.; 22 males and 11 females) were used in this study. 3D reconstructions of all specimens were created from CT images (Figure 1). The following distal femur morphometric parameters were measured with specialized 3D software (Mimics, Materialise, Belgium) on a plane perpendicular to the long axis of the bone: 1. Transepicondylar axis (A): the distance between the most medial point in the medial epicondyle and the most lateral point in the lateral epicondyle. 2. Medial condyle distance (B), determined as the distance between the most anterior and most posterior points, respectively, in the anterior-posterior direction. 3. Lastly, the length of the lateral condyle (C) determined with the same method used for the medial condyle (Figure 2).

Intra- and inter-observer reliability of this protocol was assessed measuring 33 and 20 femora, respectively, and was evaluated using an intra-class correlation coefficient.

Size symmetry was evaluated using R square coefficient between right and left A-B-C measures from the same donor in 10 cases (Figure 2).

Shape symmetry of the distal femur was evaluated also in the 10 cases by comparing a left femur model and a mirror image model of a right femur in each pair (Figure 3).

Point-cloud models were created from the surface polygon mesh model by using vertex points of the polygon (Figure 4). The 3D left femur model and the 3D right mirror femur model were registered by using a volume merge method [3].

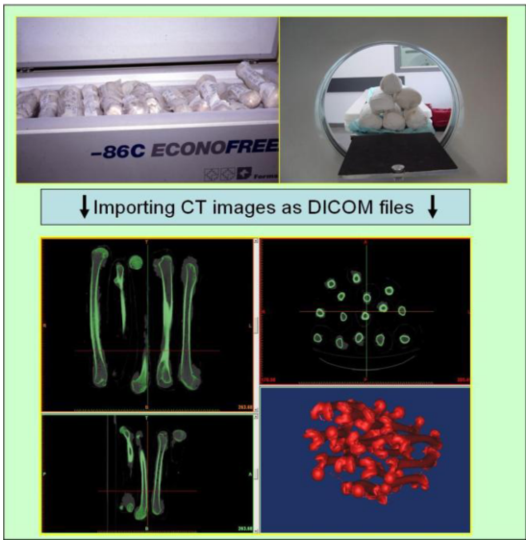

Figure 1 -Images from the CT scanner are imported and reconstructed as 3D objects with Mimics software

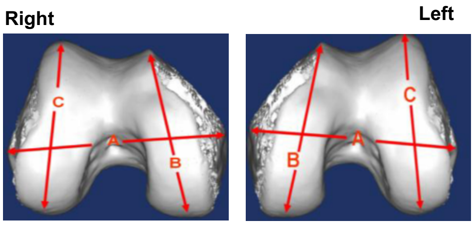

Figure 2 - Distal view: A-B-C size analysis parameters between right and left sides. A: Transepicondylar axis, B: Medial condyle distance and C: length of the lateral condyle.

The volume merge method was created with custom software program in Microsoft Visual C++.NET 2003 with Microsoft Foundation Class programming environment (Microsoft Corp, Redmond, WA). In the volume merge method, the right mirror femur (the moving femur) was virtually rotated and translated towards the left femur (the stationary target). These rotations and translations of the femur were conducted in 0.1° and 0.1 mm increments, respectively, until the moving femur merged with the stationary target. The degree of volume merging was maximized in real-time through rotation or translation of the moving femur using the following algorithm. A voxel with a dimension of 1.0 x 1.0 x 1.0 mm was created for each point of the stationary target. The number of points of the moving femur that fell within the voxel of the stationary target was determined and the percentage of volume merge was defined by a ratio of the number of the voxels including the moving femur points to the total number of the voxels on the stationary target [3]. The accuracy of the volume merge method was evaluated using a phantom with 8 precision ceramic balls (19 mm in diameter). The phantom was placed on a high precision 4-degree of freedom table. The phantom was scanned at 5 translated positions in x-direction with 0.1 mm increment up to 0.5 mm and at 10 translated positions in z-direction with 0.1 mm increment up to 1.0 mm. It was also scanned at 10 rotated positions about x-axis with 0.1° increment up to 1.0° and at 5 rotated positions about z-axis with 0.1° increment up to 5°. A total of 30 scans were analyzed using the volume merge method and system accuracy was determined using translations and rotations. The values were compared with the known translation and rotation values and errors in these calculations were evaluated. Mean absolute translation error was less than 0.1mm in x-direction and z-direction. Mean absolute rotation error was less than 0.2º about x-axis and z-axis. The translation in x-axis and rotation about z-axis correspond to transformation in axial-plane and the translation in z-axis and rotation about x-axis correspond to transformation in the sagittal plane [3].

Following the registration of the left and the right mirror distal femora, a closest distance algorithm was used to evaluate 3D shape matching between the left femur and the right mirror femur [4,5]. Distances between one point in the point-cloud model of the left femur and all points in the right mirror femur were calculated in 3D space. The closest distance at the point in the left femur was defined as the least distance among all distances. This procedure was repeated for all points in the left femur and mean closest distance from all measured closest distances of the closest distances was determined for each pair of the distal femur (Figure 5 and Figure 6).

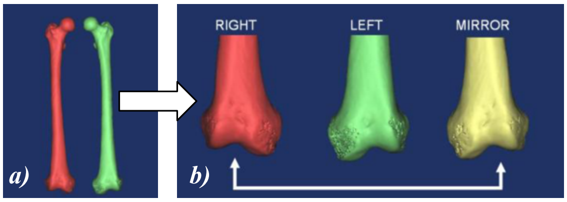

Figure 3 - Volume Merge Method. a) Pairs of femurs from the same donor, b) mirror image.

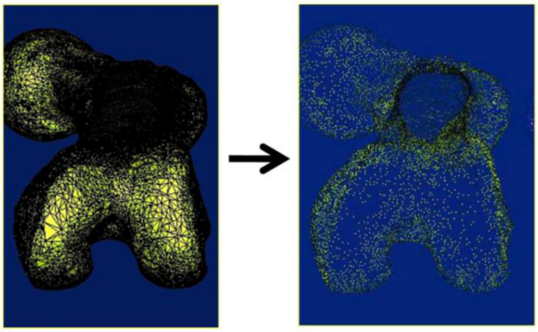

Figure 4 - 3D bone reconstruction exported as a point- clouds model.

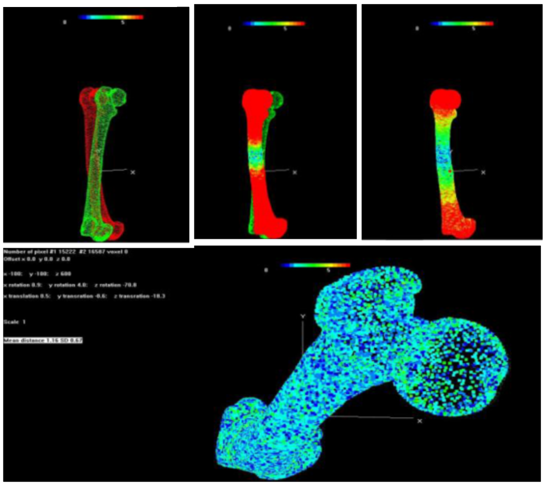

Figure 5 – Using the point – cloud model, a pairs of femurs from the same donor overlapped using our custom software able to recognize mean closest-point distances.

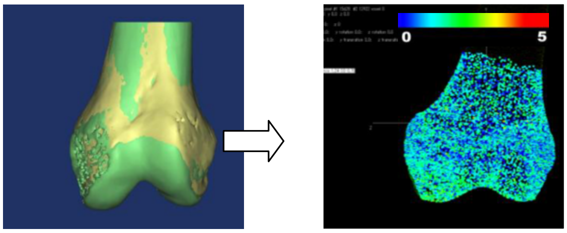

Figure 6 - Volume Merge Method, a) overlapping distal femurs and b) Volume merge superposition. Color scale: 0 to 5 mm: Dark blue indicates closest proximity (best match) between two superimposed point clouds.

Results

Protocol metrics: A single operator was tested for intraobserver repeatability while using the above-mentioned A-B-C protocol twice on thirty-three distal femoral allografts, obtaining an intraclass correlation coefficient of 0.99 in almost all measures (Table 1). Interobserver consistency of two separate observers was quantified when they measured the A-B-C parameters of twenty distal femoral allografts leading to an intraclass correlation coefficient of 0.99 in all measures (Table 2). R square coefficient between right and left side was 0.99 in the ten pairs evaluated (Figure 2).

Shape compliance: Evaluation of the overlapped original and mirror point-cloud models with the custom C++ program found that the average closest distance between points was 0.89±0.07 mm. (Figure 7). This result is within the CT slice thickness of 0.5 mm and CT resolution of 0.625 mm/pixel.

Table 1 - Intraobserver analysis using A-B-C protocol.

Distance	Femurs	n	Intraclass correlation	95% CI	
				Lower Bound	Upper Bound
Transepicondylar	Right	15	0.997	0.991	0.999
	Left	18	0.999	0.998	1.000
Medial Condyle	Right	15	0.963	0.869	0.988
	Left	18	0.997	0.991	0.999
Lateral Condyle	Right	15	0.995	0.873	0.985
	Left	18	0.998	0.996	0.999

Table 2 - Interobserver analysis using A-B-C protocol

Distance	Femurs	n	Intraclass correlation	95% CI	
				Lower Bound	Upper Bound
Transepicondylar	Right	10	0.999	0.996	1.000
	Left	10	0.999	0.995	1.000
Medial Condyle	Right	10	0.996	0.982	0.999
	Left	10	0.997	0.968	0.999
Lateral Condyle	Right	10	0.997	0.986	0.999
	Left	10	0.997	0.990	0.999

No.	Mean	SD
1	0.91	0.57
2	0.84	0.56
3	0.97	0.62
4	0.80	0.55
5	0.87	0.58
6	0.89	0.58
7	0.79	0.54
8	1.03	0.61
9	0.93	0.58
10	0.89	0.56

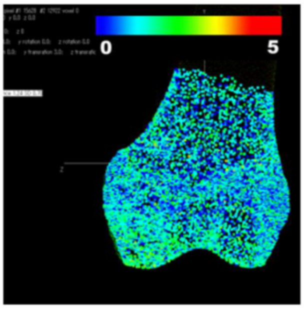

Figure 7 - Shape Compliance: mean of distal femur differences in millimeters.

Discussion

The selection of the bank allografts has been closely related to the progress of the current visualization method. During the first decades traditional X-rays were used, assuming a transplantation selection error that reached the centimeter scale. Then donor-recipient two dimensional measurement protocols were established in CT scan images that narrowed down the bias to the millimeter scale.

More accurate data and a more precise donor-recipient selection can be achieved using various complementary techniques such as the multislice CT scan–digital representation of subject-specific models and CAD (computer aided design), software, moving a step closer to the creation of a virtual interactive musculoskeletal system (V.I.M.S.) [6].

The volume merge technique used in the current study for the registration of between the left and the right mirror femora has been used for kinematic analyses of lumbar spine, cervical spine, ankle joint, and and shoulder joint [3,7,8]. This technique also allows registration of the organ taken by different imaging modalities [7].

In the closest distance analysis, only the magnitude of the distance vector was evaluated and not its direction. Therefore, the distance was not evaluated in the normal direction to the surface of the femur and the distance may be overestimated. Especially, when the closest distance is small, overestimation is expected to be larger. However, this amount of overestimation does not exceed the spatial resolution. Calculation of the distance between a point to the polygon surfaces may improve shape matching evaluation. However, the random orientation of each individual polygon mesh element may vary significantly on the complex and irregular bone surface. Future studies will be required to establish better algorithms to evaluate bone surface geometry matching. Nonetheless, due to large macroscopic differences in size and geometry expected in a clinical setting, the magnitude of the error associated with the current method would be negligible for practical purposes and ready to be used with a virtual bone bank system (Fig. 8). Additionally, another limitation of this study is the small amount of samples.

Conclusion

This work demonstrates the usefulness of three-dimensional models when searching for the best similar host–donor allograft match and proves our symmetry hypothesis. The results suggest that a robust, reliable and most importantly, repeatable technique, has been established.

On the other hand, the results stemming from the use of this measurement protocol enable accurate selection of allografts from a contralateral healthy femur CT achieving the best match possible considering the geometry of available allograft candidate femur specimens (Figure 8). This newly developed method is a good example of translational research that can be readily applied to the patient with minimal effort.

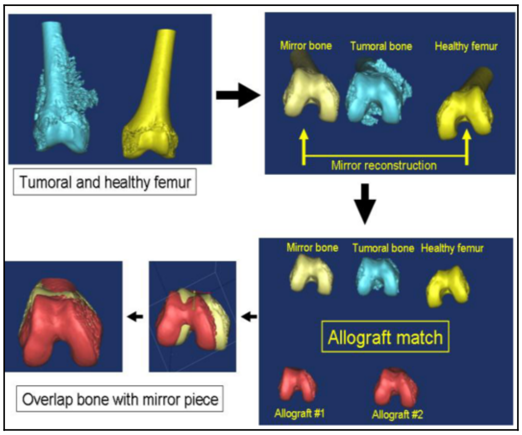

Figure 8 – Searching and selecting the best match in a Virtual Bone Bank System.

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