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Scaling Methods of the Pelvis without Distortion for the Analysis of Bone Defects

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Abstract: For the development of new types of hip implants for acetabulum revision, it is beneficial to analyse the acetabular defects of the indication group in advance. In order to be able to specially compare the bone defects with each other, a normalisation and accompanying scaling of the pelvis is necessary. Uniform scaling is required so that the bone structures are not distorted.

In the following study, three scaling methods based on the minimal bounding box and sphere principle are compared with a method using 14 landmarks on the pelvis. The landmark method is applied to determine the true scaling factor. For the comparison of the different methods, 40 female pelvic models with an acetabular defect are analysed.

In the comparison of the scaling methods, the method using minimal bounding spheres shows the least deviation from the landmark method (mean difference 3.30 ± 2.17 %). Due to the fact that no preprocessing (definition of the landmarks) is required and the fast implementation of the algorithm, the minimal bounding sphere is to be preferred to the landmark method for a fast size estimation.

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Florian Hinterwimmer, Institute for AI and Informatics in Medicine, Technical University of Munich, Munich, Germany Christian Fritz, Michael F. Zäh, Institute for Machine Tools and Industrial Management, School of Engineering and Design, Technical University of Munich, Garching near Munich, Germany **Keywords:** Pelvis, Landmarks, Size Comparison, Scaling, Minimal Bounding Box, Minimal Bounding Sphere.

1 Introduction

Bone defects in the acetabulum are currently categorised according to the Paprosky classification [6]. However, this type of categorisation hardly allows any conclusions to be drawn about the subsequent implant geometry [4]. With the help of detailed bone defect analyses in the area of the acetabulum [3], the previous classification methods can be further developed and thus provide better information about the implant geometry to be used. In order to compare bone defects and their extent, it is beneficial to scale and normalise the bone structures on one defined reference geometry.

The use of landmarks on the pelvis allows an accurate description of the pelvic geometry and size, which can be used for subsequent analysis of bone defects in the pelvis, especially in the acetabulum. However, this method also requires timeconsuming pre-processing to determine the landmarks. In the following study, three other scaling methods based on the principle of the minimal bounding box and sphere are presented and compared with regard to their deviations from the landmark scaling method as an alternative method.

2 Methods

3D scaling of an object without distortion can be done with the same factor in all three directions. Scaling in all three spatial directions with different factors would ultimately lead to a distortion of the anatomical structures. Three methods are presented below that allow scaling without distortions.

2.1 Pelvis Database

To compare the different scaling methods, 40 female patient pelves were used. For the planning of the implant revision, the complete pelvis of the patients was scanned by computer tomography (CT). Due to the upcoming revision, some of the pelves were severely deformed (Paprosky classification of the acetabular bone defects: IIa: 1, IIb: 7, IIc: 2, IIIa: 18, IIIb: 10,

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unknown: 2). The CT scans were then segmented using the inhouse segmentation software of AQ Solutions GmbH (Hürth, Germany). These segmented models were also utilised for the development of the individual implants that were later inserted. For the analysis in this study, only the defective hemipelves were used.

As a reference pelvis for the deformed models, a mean pelvis structure consisting of several healthy pelves from previous studies was used [2, 8]. The mean pelvis structure was based on 523 CT-scanned pelves (female: 208, male: 315) segmented by medical experts. Afterwards the mean pelvis shape was calculated using the point correspondence information of each point on the pelvis [8]. This pelvis shape corresponds to 100 % in the size comparison.

All triangulated surface meshes of the defective pelves were loaded into Matlab 2020b (MathWorks Inc.; Natick, Massachusetts, USA) and the scaling methods were implemented accordingly.

The landmark points of the pelves were uniformly defined by a medically educated person. The hip centre reconstructed for implant planning is taken as the acetabular centre. Two further landmarks could not be identified directly at the pelvis.

To determine the centre of the foramen obturatum (13), four points were selected on the edge of the foramen obturatum. The four points span the major and minor axes of an approximated ellipse. The two points, where the two skew lines are closest to each other, were detected and the midpoint of the connecting line of the two points represents the orientation point for the foramen obturatum.

The landmark representing the point of curvature of the ilium (14) was determined using the landmarks asis and psis. The maximum distant point perpendicular to the connection asis and psis at the crista ilaca (free cranial edge of the ilium) corresponds to the landmark curve ilium.

2.2 Scaling Reference: Landmarks

The landmark method is defined as the true pelvis size ratio compared to the reference pelvis and applied as ground truth for the scaling methods minimal bounding box and sphere.

For the landmark method, 14 landmarks are defined on the pelvis describing the geometry of the pelvis (Fig. 1). The connecting lines and distances between the landmark points are determined (total: 91 connecting combinations). The distances are normalised to the corresponding distance of the mean pelvis shape and the mean size value is calculated to all distances. This corresponds to the size ratio to the reference pelvis and enables a one-factor scaling of the pelvis.

The following 14 anatomical landmarks were selected on the pelvis to describe the pelvis size ratio (Fig. 1):

- 1. anterior superior iliac spine (asis)
- 2. tuberculum pubicum (*tp*)
- 3. posterior superior iliac spine (*psis*)
- 4. posterior inferior iliac spine (*piis*)
- 5. spina ischiadica (si)
- 6. acetabulum centre (acentre)
- 7. anterior inferior iliac spine (aiis)
- 8. incisura ischiadica major (*iim*)
- 9. incisura ischiadica minor (*iimin*)
- 10. symphysis pubica proximal (spp)
- 11. symphysis pubica distal (*spd*)
- 12. tuber ischiadicum (ti)
- 13. centre of foramen obturatum (fo)
- 14. curve ilium (ci)



Fig. 1: Mean pelvis shape of 523 pelves with the 14 defined landmarks for the size comparison.

2.3 Scaling: Minimal Bounding Box

Two different methods were applied in Matlab for the scaling method minimal bounding box with right angles. In both functions the triangulated mesh is considered as a pure point cloud and first a convex hull is generated around the point cloud.

The iterative procedure according to [5] converges for a bounding box where one side of the box matches one face of the convex hull and the volume is minimal (abbr. Box Hull) (Fig. 2). The calculation is based only on heuristics, but the author indicates that he was able to determine the minimal bounding box in a large number of tests.

According to [7], the second method utilises the singular value decomposition (SVD) of the points on the convex hull to obtain the axes of the minimal bounding box (abbr. Box SVD). In both methods, the diagonal was used as a parameter for the size comparison to the reference pelvis. The diagonal of the room is calculated over all three edge lengths and thus contains the information of all three dimensions.



Fig. 2: Pelvis with acetabulum defect (Paprosky IIIa) and a minimal bounding box for scaling (Box Hull).

2.4 Scaling: Minimal Bounding Sphere

The minimal bounding sphere (abbr. Sphere) is based on the algorithm of [9], which implemented Welzl's algorithm [12]. In this algorithm, the triangulated mesh is also considered as a point cloud (Fig. 3). A sphere can be defined by four points on its bounding surface. Welzl's algorithm divides the set of points into two sets, one set whose points are contained in the sphere and one set whose points are on the bounding sphere. The method works recursively and allocates all points inside the sphere at the beginning. In each iteration, an attempt is made to remove a point from the enclosed set of points and recursively the minimum bounding sphere of this reduced set is determined. Depending on the position of the removed point, it is reassigned to the two sets. This procedure is repeated until there are no more contained points or there are four boundary points. The iteration ends and a minimal boundary sphere is calculated based on the boundary points.



Fig. 3: Pelvis with acetabulum defect (Paprosky IIIa) and a minimal bounding sphere.

Tab. 1: Mean difference and standard deviation (S.D.) of the Box Hull, Box SVD and Sphere methods compared to the scaling reference (landmark method).

Size Difference	Box Hull	Box SVD	Sphere
Mean Difference	3.64 %	4.89 %	3.30 %
S.D.	2.37 %	2.96 %	2.17 %

3 Results

The size ratio of all 40 female pelves normalised to the reference pelvis (mean pelvis shape) is calculated using all three scaling methods (Box Hull, Box SVD, Sphere). The calculated size factor using landmark method is applied to validate the three other approaches. The table 1 and the graph in Fig. 4 show the average deviation of the respective method compared to the size comparison of the landmark method.



Fig. 4: Mean difference (bar) and standard deviation (errorbar) of the scaling methods used compared to the scaling reference (landmark method).

4 Discussion and Conclusion

For the analysis of bone defects such as acetabular defects, it is important that when scaling the individual pelvic geometries, these are not distorted. Individual scaling in all three directions of space implies a distortion of the geometries and could therefore lead to a falsification of the bone defects and their shape. An analysis of the bone defects is helpful for the development of new implants, such as the comparison of acetabular defects for hip implants for better classification.

In this paper, several scaling methods without distortion for the hemi-pelvis were presented. The scaling method using defined landmarks and their distances from each other is the most accurate method and works even with severely deformed bone geometries. However, this method is very time-consuming because the landmarks for each individual pelvis have to be defined in data preprocessing. Automated methods using artificial intelligence already exist for determining the landmarks on the pelvis. However, these are trained on healthy pelvic geometries and do not work with strongly deformed bone geometries [1]. The minimal bounding box is a commonly method for determining the size of objects in 2D and 3D. With a mean difference of 3.64 \pm 2.37 %, the Box Hull method can also be used to estimate the pelvis geometry. Furthermore, the minimal bounding box also allows individual scaling in all spatial directions with distortion. Due to the round shape of the ilium and the ischium, in the case of a hemi-pelvis, the method using a minimal bounding sphere is also suitable. This approach shows the least deviation scaling with landmarks (mean difference of 3.30 \pm 2.17 %) and can be used as a simple and quick estimation of pelvis size. Even when using highly deformed pelves it could be shown that the scaling methods are well suited for a quick estimation. For all four scaling methods, the pelves do not need to be aligned with each other and no common coordinate system is necessary.

Only female pelvic geometries were used for the comparison of the scaling methods. Separately, the comparison with male pelves must also be considered. However, two thirds of hip operations are performed on women [10].

The bounding box and sphere approach uses only the 3D point clouds for the calculation instead of the triangulated meshes with the connectivity information. Because of this, it is necessary to use a mesh with sufficient point resolution (mean number of points of the pelves: 273,870). A mesh with a uniform edge length of 0.5 mm was created in advance for all pelves.

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