

Identification of Medical Three-Dimensional Objects

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Abstract—This paper deals with identification of objects modelling organs of human body in 3D computer model of the body. For this purpose, we use two existing methods for classification of 3D objects, which are based on finding and comparing features of models of 3D objects. The experiments were done with models of bones of a human body. They showed that the methods are able to classify type of bones, e.g., vertebrae, ribs, bones of arms, but they are not able to recognize a specific bone, e.g., a specific vertebra, rib, or bone of hand or feet. Therefore, we also implemented another method, which tries to take into account layout of the bones in a specific part of the human body. This method is based on measuring a distance between 3D objects. After implementation we experimented with all these methods to find out effectivity of them in various recognition tasks.

Keywords—3D models of human body, classification of 3D objects, descriptor of 3D object

I. INTRODUCTION

Future of majority of sectors is in collaboration with information technology. Thankful technology, we can simulate some processes. For example, one of a European research project founded by the European Union's 7th Framework Program was *RASimAs* project (Regional Anaesthesia Simulator and Assistant). This project aimed at providing a simulator to train physicians in performing regional anaesthesia and an assistant to help anaesthesiologists during the procedure. For this connection of medicine and technology, 3D models of human body are needed. Several such models exist, but they have some issues, which penalize their application [1].

Within *RASimAs* project a method for rating models was proposed [2]. The method is based on quantification of intersections between the objects that a model of human body is composed of. However, it has some insufficiencies. One of the most important weaknesses of the method is that it recognizes all the intersections as errors. However, some intersections (e.g., between specific vessels and muscles) are natural, and they should not be classified as errors of the model. This implies that intersections should be divided into two groups – “wrong” intersections, which do not exist in a human body and which contributes to the error of the model of a human body, and “good” intersections, which exist in a human body and which should not be taken into account in quantification of the quality of the model. To define, which intersections are good and which are wrong, individual objects of the model have to be classified.

Classification of 3D objects requires the 3D objects to be represented in a way that captures the local and global shape characteristics of the object. This requires creating a 3D descriptor or signature that summarizes the important shape properties of the object. Unfortunately, finding a descriptor that is able to describe the important characteristics of a 3D object is not a trivial task. The descriptor should be able to capture a good balance between the global and local shape properties of the object, so as to allow flexibility in performing different tasks. The global properties of an object capture the overall shape of the object, while the local properties capture the details of the object. Each descriptor has its own strength and weakness for different queries and tasks. According to [3], there are three categories of 3D objects representation: *feature-based methods*, *graph-based methods*, and *view-based methods*.

Feature-based 3D object descriptors are most popular. They focus on geometric properties of a 3D model to define shape of an object. Some methods like Osada [4] and Ohbuchi [5] include

generating points on the surface of the model and measurement relations among them. *Graph-based* methods use the topological information of the 3D object to describe its shape. The graph that is constructed shows how different shape components are linked together. The graph representation includes model graph, Reeb graph [6] and skeleton graphs. These methods are known to be computationally expensive and sensitive to small topological changes. The most effective *view-based* shape descriptor is LightField descriptor developed by Chen [7]. The method captures objects from various angles, so we get set of 2D images.

For the purpose of recognizing objects of a human body, we implemented two feature-based methods. Namely, we implemented Osada's and Ohbuchi's method for creating descriptor. In the experiments, we focused on measuring success of the methods in recognition problem. We have done more experiments like recognition in same model, recognition in various models (Zygote and Anatomium). After getting new model we tried to classify objects. Also we tried to assign a group to an object automatically according another model. At the end, we experimented with a new method that is based on measuring a distance between objects.

II. OBJECTS RECOGNITION

In this section, we focus on methods for objects recognition that we implemented. At first, we describe existing methods like Osada and Ohbuchi including creation of descriptor and measuring difference between descriptors. The second part is dedicated to definition of our suggested method based on measuring a distance between 3D objects.

A. Osada's Descriptor

Osada's descriptor is creating as follows. Firstly, we generate points at random location on surface of the model. Then distance between every possible pair of generated points ($N(N - 1)/2$ pairs for the N generated points) is computed. The descriptor is a 1D histogram created by counting the population of the point-pair distances that fall within a certain distance interval. As it is based on the unoriented point set representation, it is insensitive to the orientation of the surface in the original model. There can be measured different properties, but we have chosen D2 shape function which measure distance between two random points on the surface. This shape function classifies objects better than the other four shape function that were studied in [4].

Generating random points respect surface area of polygonal model. So first we iterate through all polygons and compute its area and store it in an array along with cumulative area of triangles. Next, we select a triangle with the probability proportional to its area by generating a random number between 0 and the total cumulative area. To generate a point at random location on the surface of a triangle we use formula $P = (1 - \sqrt{r_1})A + \sqrt{r_1}(1 - r_2)B + \sqrt{r_1}r_2C$, where A, B, C are vertices of the triangle, and r_1, r_2 are pseudo-random numbers from interval $(0,1)$ (Figure 1).

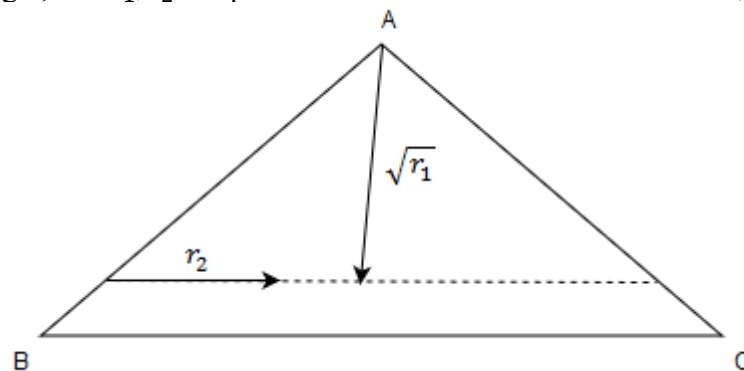


Figure 1 Random point in a triangle

A.1. Comparing Descriptors

Having constructed the shape distribution for two 3D models, we are left with task of comparing them to produce a dissimilarity measure. There are many standard ways of comparing two functions f and g representing probability distributions [4]. One of the comparing method is the *probability density function* (PDF) norm which outperformed the χ^2 statistics and Bhattacharyya distance and, in general, it is better than the *cumulative distribution function*, because peaks and valleys of PDF curves are easier to discriminate. So, the dissimilarity measure is computed by the mentioned way as follows:

- **PDF L_N :** Minkowski norm of pdf: $D(f, g) = (\sum |f - g|^N)^{\frac{1}{N}}$

Dissimilarity between two descriptors is illustrated in Figure 2, where we can see descriptor of *deltoid* (orange) and *latissimus dorsi* (blue) muscles and highlighted dissimilarity.

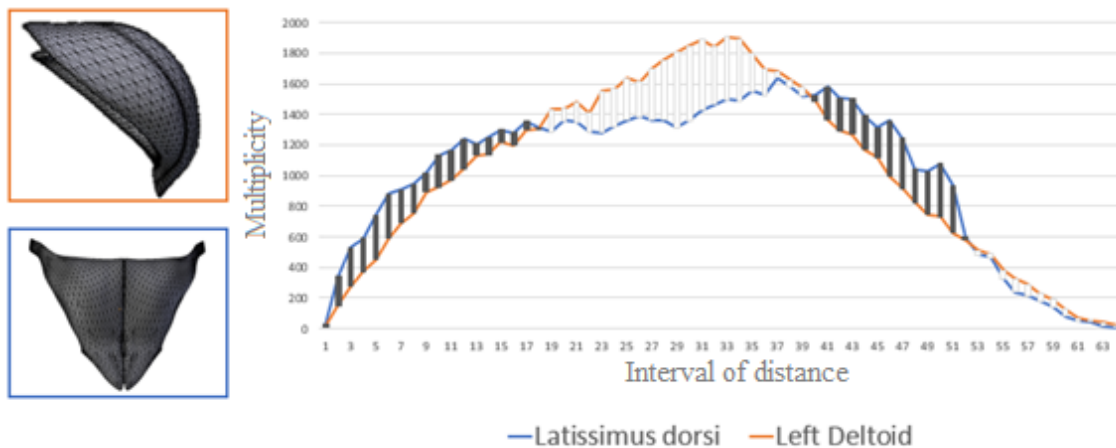


Figure 2 Difference between two descriptors

A.2. Modification of Osada's Method

We add a little modification to the original Osada's method. In this modification we generate N pairs of points on the surface of the object. Distance of each generated pair of points is included into histogram. For example, in original method we get 523,776 measured distances with 1,024 generated points. In the modification we need 1,047,552 generated vertices for the same amount of distances. The rest of the steps remains same.

B. Ohbuchi's Descriptor

Another descriptor has been proposed by Ohbuchi [5]. This descriptor is an extension of Osada's descriptor. It uses a Quasi-random number sequence by Sobol [8] for generating numbers r_1 and r_2 for obtaining a point in a triangle of the surface (Figure 1) instead of a pseudo-random number sequence used by Osada. This descriptor also takes into account the inner product of the direction vectors of the generated points.

In this case methods offer two types of descriptors. If the surface of the input model is known to be orientable, we employ *mutual Angle-Distance histogram* (AD) shape feature. If we cannot assume the surface of the models to be properly and consistently oriented, we employ *mutual Absolute-Angle Distance histogram* (AAD). The AD and the ADD shape feature are 2D histograms of distance and angles formed by pairs that are generated on surface of a given 3D object. In computing the AD or the AAD shape feature, an orientation of the point is inherited from the surface normal vectors of polygon on which the points are generated. The angle between a pair of points is represented as the inner product of the direction vectors of the points. The

difference between the AD and the ADD is that the AAD ignores the sign of the inner product. Consequently, the ADD is more robust for models having inconsistent surface orientations than the AD. The AD shape feature measures for each pair of points p_1 and p_2 the 3D Euclidean distance $d = \sqrt{(p_1 - p_2)^2}$ between the points and the inner product $a = n_1 * n_2$ of the direction vectors n_1 and n_2 of the points. Given the distance and the inner product for every pairs of the points, the AD is a joint 2D histogram of the distance d and the inner product a . ADD histogram is computed like the AD, except that the ADD ignores the sign of the inner product.

B.1. Dissimilarity Measures

Assume that $\mathbf{X} = (x_{i,j})(1 \leq i \leq I_d, 1 \leq j \leq I_a)$ and $\mathbf{Y} = (y_{i,j})(1 \leq i \leq I_d, 1 \leq j \leq I_a)$ are the descriptors for models A and B. Descriptors are in fact a 2D matrix of dimension $I_d \times I_a$, in which I_d is a number of distance intervals and I_a is a number of angular (inner product) intervals. The L_1 norm-based distance $D_{L_1}(X, Y)$ and the L_2 norm-based distance $D_{L_2}(X, Y)$ for the AD and AAD descriptors are defined as follows [5]:

$$D_{L_1}(\mathbf{X}, \mathbf{Y}) = \sum_{i=1}^{I_d} \sum_{j=1}^{I_a} |x_{i,j} - y_{i,j}|,$$

$$D_{L_2}(\mathbf{X}, \mathbf{Y}) = \sum_{i=1}^{I_d} \sqrt{\sum_{j=1}^{I_a} (x_{i,j} - y_{i,j})^2}.$$

The L_1 or L_2 distance among a pair of column vectors, each of which consists of values from angular bins at the distance bin i , is computed first. Then, a simple sum of these distance values over all the I_d intervals is computed

C. Recognition Using Distance between 3D Objects

The second approach to recognition of 3D objects uses distance between 3D objects. To evaluate the similarity of the 3D objects from two models, the general formula for calculation of the Euclidean distance was chosen, i.e.:

$$d(p, q) = d(q, p) = \sqrt{(q_1 - p_1)^2 + (q_2 - p_2)^2 + \dots + (q_n - p_n)^2} = \sqrt{\sum_{i=1}^n (q_i - p_i)^2},$$

where p and q are points in Euclidean n -dimensional space. It is necessary to determine points between which this Euclidean distance will be calculated. So, the point representing the middle point of the object's bounding box displayed as green box in Figure 3 was chosen for this task. These point's coordinates have been obtained by finding the coordinates of two opposing vertices of object's bounding box connected by diagonal and calculating the point lying in the middle of this diagonal. This point was declared as the center of the object's bounding box and therefore as the center of the 3D object. Every such point in 3D space is defined by three coordinates x, y, z , so formula for calculating the distance of two such points and thus the distance of two 3D objects in 3D space looks like this:

$$d(p_1, p_2) = \sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2 + (z_1 - z_2)^2},$$

where p_1 and p_2 are points representing the middle points of objects' bounding boxes.

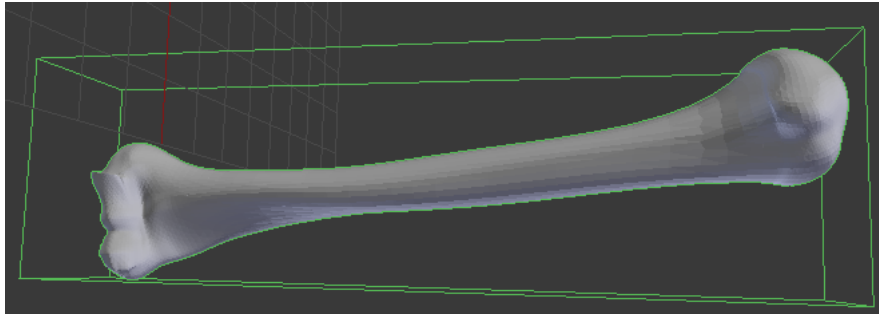


Figure 3 Bounding box of object

The distance between two objects defined by Euclidean distance was used while executing experiments. Object bounded by red box in Figure 4 was an unknown object that we want to recognize. We created capture set of objects bounded by green bounding box in Figure 4 for experimental purposes. They are chosen as random objects in each used anatomical model. In consideration to the objects in such a defined capture set, distance from the object being recognized will be calculated. Measuring distances between unknown objects and objects of this capture set was used as an alternative approach for identifying objects of a human model.

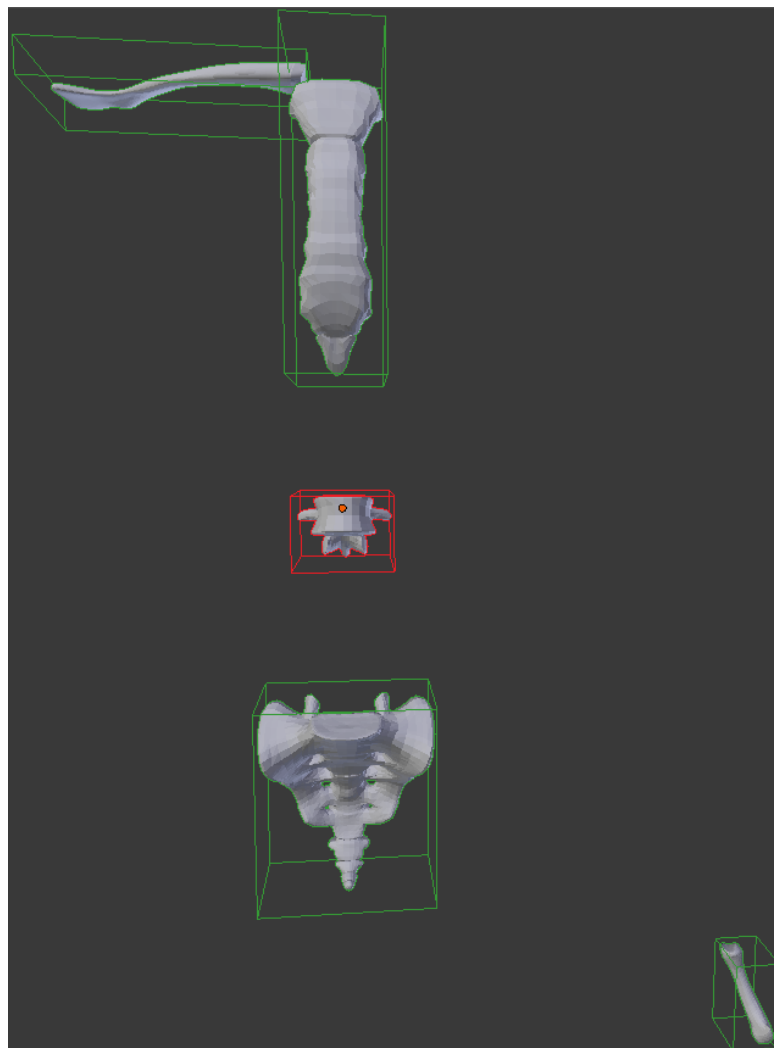


Figure 4 Objects of capture set (green) and searched object (red) with the bounding boxes

III. EXPERIMENTS

A. Recognizing 3D Objects using Descriptors

The methods described above were implemented as a Blender add-on. In this part, we performed experiments to find out performance of these methods in recognition tasks. We mostly work with two human body models, Zygote and Anatomium. Before the experiments, we tested the connection between amount of generated points and precision. In this test we found out that our modification of Osada's method produce results with better precision, so we used this modification instead of the original method in the experiments. In all the experiments we generated 2,048 random points on surface during creating Ohbuchi's descriptor because it is an appropriate trade-off of performance and time consuming. In Osada's descriptor we generate 1,178,880 pairs of vertices (equivalent of 1,536 generated point). Generating more points did not bring more advantage it just took more time to create the descriptor. Results of all the experiments are presented in Table 1 below.

Table 1 Summary of experiments

Experiment		Skeleton	Muscle
Recognizing object in same model	Osada	149 out of 149	287 out of 287
	Ohbuchi	147 out of 149	270 out of 287
Assigning a group	Osada	87 out of 102	x
	Ohbuchi	89 out of 102	x
Recognizing object in different model	Top	Osada	25 out of 103
		Ohbuchi	20 out of 103
	Top 5	Osada	58 out of 103
		Ohbuchi	60 out of 103

A.1. Recognizing Object in Same Model

The goal of the first experiment was to recognize and find an object from the first model in the second one only by using a descriptor. At the beginning, we created two same Zygote models of skeleton with left sided objects. We selected one object from the first model and try to look for an object with the most similar descriptor in the second model. If the both object matched, the output was successful. For example, if we selected the skull in the first model, we expected to recognize the skull in the second model. The results of the experiment (the first two rows in Table 1) can be concluded as follows:

- By using modified Osada's descriptor in Zygote skeleton model (dataset in Figure 6) composed of 149 objects (bones), all the objects in the second model were recognized correctly. In Zygote muscle model, which contains 287 left sided objects, 269 objects were correctly identified. Most complicated object to recognize were Rotatores muscles, where one mesh represents more muscles simultaneously, for example Long Rotatores 11 a Long Rotatores 12 were defined by objects with the same mesh. An example of rotatores muscles is in Figure 5.
- By using Ohbuchi's descriptor in the same skeleton model, we correctly recognize 147 objects out of all 149 objects. The first error is observed on vertebra disc and the second is displayed in Figure 7, where the green arrow targets on the selected object and the red arrow on the recognized object. In Zygote muscle model we correctly identified 270 objects out of 287. Most errors are caused by Rotatores muscles as well as we mentioned with Osada's descriptor.

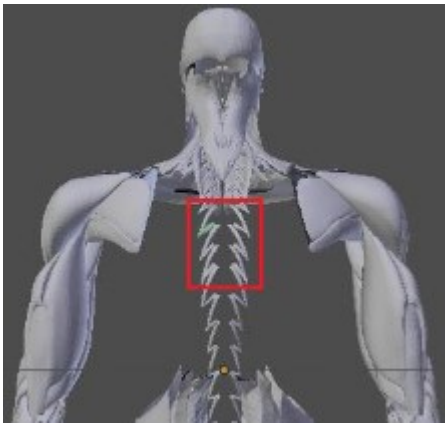


Figure 7 Rotatores muscles

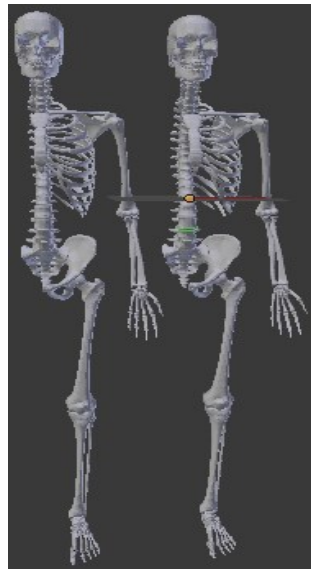


Figure 6 Used dataset

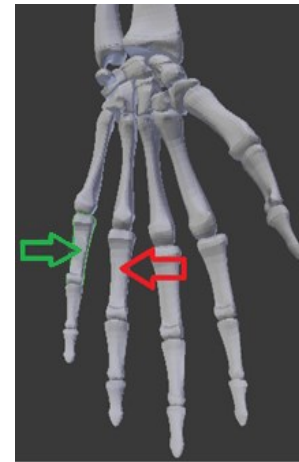


Figure 5
Problematic objects

A.2. Assigning a Group

The second set of experiments was very similar to the first one. Zygote skeletal model was manually divided into five groups (hand, vertebra disc, leg, foot and chest). The Anatomium model was divided at the same way but automatically using a descriptor. We measured how many objects were assigned properly. We obtained the following results (the middle part of Table 1):

- By using modified Osada's descriptor, we achieved that 87 objects out of 102 were assigned to correct group.
- By using Ohbuchi's descriptor, we got 89 objects with a correct group. Most risen errors were caused by bones of hands and feet.

A.3. Recognizing Object in Different Model

In the next set of experiments, we tried to recognize an object in Anatomium model based on descriptors of objects from Zygote skeleton model. So, we selected one object in Zygote model and, subsequently, we try to find this object in Anatomium model. Both models were customized to be compatible, so each of them contains 103 objects. In this case the results were following (the last four rows in Table 1):

- By using modified Osada's descriptor we correctly identified 25 out of 103 objects. In case we would accept correct object occur in top five of the most similar objects instead of the first, we got 58 positives results. The most problematic types of objects were vertebrae because of inequality between vertebrae in Anatomium and Zygote (Figure 9). Other problematic groups were Phalanges Proximalex, Phalanges Mediae a Phalanges Distales which are depicted on Figure 8.
- By using Ohbuchi's descriptor we correctly recognized 20 out of 103 objects. However, if we focus on top five most similar objects we get 60 positive results. Problematic groups of objects are same as in the already mentioned Osada's descriptor.

A.4. Classification of Objects

In this experiment we only focused on problematic objects as vertebrae and bones of hands. In the first part of the experiment, we measured the distance between Zygote objects and Anatomium objects where problem with objects differences occurred. Simultaneously, we obtained a new model [9] so we focused on average distance between pairs of distances Zygote–Anatomium and

Zygote—the new model. If recognized object, i.e., the object with the smallest average distance, matched with a selected object, we classified it as a success.

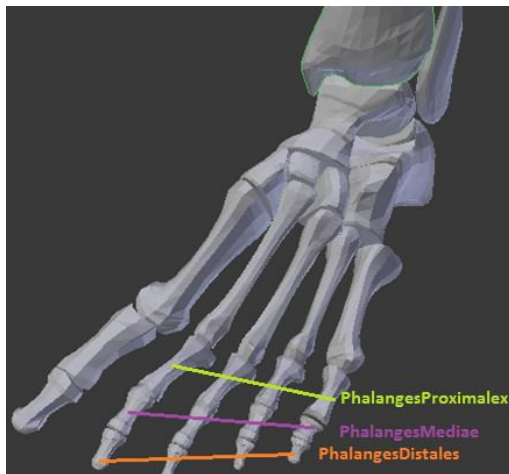


Figure 9 Phalanges Proximales, Phalanges Mediae and Phalanges Distales

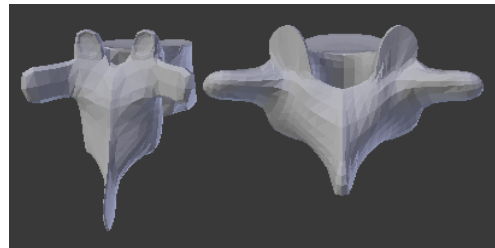


Figure 8 Anatomium ThoracicSpine8 and Zygote ThoracicSpine8

Before applying the new model, we carried out experiments on vertebra column of Zygote and Anatomium. We correctly identified 4 vertebrae out of 25 objects. When we focused on top three most similar objects we got 8 positives output. With added new model, we correctly recognized 6 vertebrae and 13 vertebrae occurred in the top three most similar objects. So, we achieved better results after adding another model. We got all these results with Ohbuchi’s descriptor. By using the modified Osada’s descriptor, we got the same output as with the previous method. But after adding the new model we correctly identified 9 vertebrae out of 25 object and also 13 vertebrae occurred in the top three most similar objects.

We repeated this experiment with the new dataset which contains bones of hand because this group was also problematic. Ohbuchi’s descriptor provided only 1 correctly recognized object out of 19 bones and 10 objects were in the top three most similar object. After adding the new model, we identified 9 object and 13 objects were among the top three most similar objects. By using modified Osada’s descriptor we recognized 3 bones out of 19 and 8 objects were in the top tree most similar objects. After adding the new model, we identified 4 objects and 11 objects were among the top three most similar objects. All these results are summarized in Table 2

Table 2 Summary of the second set of experiments

Experiment			Vertebra bones	Palm bones	
Classification objects	Without the new model	Top	Osada	4 out of 25	3 out of 19
			Ohbuchi	4 out of 25	1 out of 19
		Top 3	Osada	8 out of 25	8 out of 19
			Ohbuchi	8 out of 25	10 out of 19
	With the new model	Top	Osada	9 out of 25	4 out of 19
			Ohbuchi	6 out of 25	9 out of 19
		Top 3	Osada	13 out of 25	11 out of 19
			Ohbuchi	13 out of 25	13 out of 19

B. Identification of 3D Objects using Distance

We assume the correctness of used 3D anatomical models. So, it follows that the relative distances between each two objects should be equal. It is the reason why we decided to use

distance between objects for identification purposes. The results of individual identification methods and performed experiments are summarized in Table 3.

Table 3 Summary of experiments using distance

Experiment		Skeleton	Muscle
Recognizing object in identic model		240 out of 246	501 out of 506
Recognizing object in transformed model		240 out of 246	500 out of 506
Recognizing object in different model	Legs	4 out of 11	x
	Vertebral column	2 out of 24	x

B.1. Identification in the Identic Model

Next experiments presented the second approach by using distance between 3D objects. The identic model was created as the copy of the named model, which leave all transformations unchanged. It means both models had the same dimension and rotation. The required element during evaluation of compliance of 3D objects was a capture set of objects containing already named objects, with respect to which the distance of each 3D object is calculated. The match is evaluated when all the distances to the objects in the capture set of objects agree. The success of this recognition method is summarized in the first row of Table 3.

B.2. Identification in the Transformed Model

The same model was used as the transformed model and also as the named model, but with changed dimensions and rotation. Considering the transformation of unnamed model, the match was evaluated in case, when the ratio of objects' volume and the ratio of distance between objects agree. However, the values of ratios varied slightly, therefore the variance of the ratios values was calculated and used as an acceptable variation while the conformity assessment. The match is evaluated if the ratio of objects' volume and the ratio of objects' distance agree. The success of the objects recognition in the transformed model is displayed in the second part of Table 3.

This experiment was also based on distance calculation between objects considering the capture set of objects. However, the difference is in ordering the individual objects according to these distances. We did not consider the summation of all distances among a particular object and objects from the capture set of objects but to the individual distances among these objects. We arranged objects by these distances in ascending order. The match was evaluated when the location of the object in the arrangement matched in both the named and the unnamed model with respect to all objects from the capture object set was same.

As the different model (Anatomium) was used for experimentation and its object were not known and named, it was not possible to evaluate the accuracy of the recognized objects. Therefore, the experiment was performed only on the group of leg bones and vertebral bones. The success of the objects recognition in the different model is summed up in the last part of the Table 3.

IV. CONCLUSION

We focused on two existing methods and used it for identification of 3D medical objects. We also proposed the method where the distance between 3D objects is used. After implementation of them, we experimented with these methods. We were interested in success of object

recognition in a same model and in various models (Zygote and Anatomium). Subsequently, we got new model where we also tried to classify objects.

We found out that it is needed to generate 2,048 random points on surface during creating Ohbuchi's descriptor because it is an appropriate trade-off of performance and time consuming. In Osada's descriptor we generated 1,178,880 pairs of vertices (equivalent of 1536 generated point). Instead of origin Osada's method we used modified version which generally produce better results than Ohbuchi's one although creating Ohbuchi's one took 50% less time. In the first experiment where we tried to identify objects according a same model we achieved the best results. In the next experiment we tried to automatically assign groups to Anatomium model. Despite of two models we successfully assigned a group to majority of objects. In the third experiment we tried to recognize an object in Anatomium using Zygote objects. In this experiment we got the worst results because Anatomium and Zygote skeletal model are little different, e.g. vertebrae (Figure 9). To improve this output, we added the new model and try to repeat experiments on problematic objects. With this step we reached slightly improvement.

The second approach based on distance between 3D object showed that using distance between 3D objects for object identification purposes is not very successful in case of different models. However, there is some potential for improving the method.

All mentioned approaches have their shortcomings, such as the accuracy of the calculations caused by the accepted variance at compliance assessing. However, if we combined all these methods together, maybe, it could be possible to create a robust approach for identification of objects (organs) in one (unnamed) model based on another (named) model. We plan to solve this problem in our next research. We also plan to combine these methods with other types of methods, such as graph-based or view-based methods.

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