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|---|---|---|
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| | Prefix | |
| | Suffix | |
| | Division | |
| | Organization | Polish-Japanese Academy of Information Technology |
| | Address | Koszykowa 86, 02-008, Warszawa, Poland |
| | Email | |
| Author | Family Name | **Wereszczyński** |
| | Particle | |
| | Given Name | **Kamil** |
| | Prefix | |
| | Suffix | |
| | Division | |
| | Organization | Polish-Japanese Academy of Information Technology |
| | Address | Koszykowa 86, 02-008, Warszawa, Poland |
| | Division | Institute of Informatics |
| | Organization | Silesian University of Technology |
| | Address | Akademicka 16, 44-100, Gliwice, Poland |
| | Email | |
| Corresponding Author | Family Name | **Kulbacki** |
| | Particle | |
| | Given Name | **Marek** |
| | Prefix | |
| | Suffix | |
| | Division | |
| | Organization | Polish-Japanese Academy of Information Technology |
| | Address | Koszykowa 86, 02-008, Warszawa, Poland |
| | Email | mk@pja.edu.pl |
| Author | Family Name | **Bąk** |
| | Particle | |
| | Given Name | **Artur** |
| | Prefix | |
| | Suffix | |

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|---|---|---|
| | Division | |
| | Organization | Polish-Japanese Academy of Information Technology |
| | Address | Koszykowa 86, 02-008, Warszawa, Poland |
| | Email | |
| Author | Family Name | **Wojciechowska** |
| | Particle | |
| | Given Name | **Marzena** |
| | Prefix | |
| | Suffix | |
| | Division | |
| | Organization | Polish-Japanese Academy of Information Technology |
| | Address | Koszykowa 86, 02-008, Warszawa, Poland |
| | Email | |

Abstract

Parts of a joint anatomy, such as bones or the joint center can be robustly identified in an ultrasound image with the help of an articulated or structural model. Such a model is a structure of parts that represent the bones and skin as polygonal chains and the join as a point, where the parts remain within specified geometric relations. The parts are identified by registration or a match of a structural description derived from the ultrasound image with the articulated model. To account for anatomical differences between the subjects, a library of joint models must be constructed, each model representing a class of joints, where all models together cover the range of possible anatomies. A new method of unsupervised learning is proposed for constructing the library of joint models by clustering structural descriptions computed from image annotations. The clustering method uses an inter-model distance measure defined as a minimum of the objective function that measures a discrepancy between structural descriptions. The objective function is minimized through a search for a best match between two structural descriptions. The method presentation is illustrated with the results of its application to ultrasound images of finger joints.

# Learning Articulated Models of Joint Anatomy from Utrasound Images

Jakub Segen[1], Kamil Wereszczyński[1,2], Marek Kulbacki[1](✉), Artur Bąk[1], and Marzena Wojciechowska[1]

[1] Polish-Japanese Academy of Information Technology, Koszykowa 86, 02-008 Warszawa, Poland
mk@pja.edu.pl

[2] Institute of Informatics, Silesian University of Technology, Akademicka 16, 44-100 Gliwice, Poland

**Abstract.** Parts of a joint anatomy, such as bones or the joint center can be robustly identified in an ultrasound image with the help of an articulated or structural model. Such a model is a structure of parts that represent the bones and skin as polygonal chains and the join as a point, where the parts remain within specified geometric relations. The parts are identified by registration or a match of a structural description derived from the ultrasound image with the articulated model. To account for anatomical differences between the subjects, a library of joint models must be constructed, each model representing a class of joints, where all models together cover the range of possible anatomies. A new method of unsupervised learning is proposed for constructing the library of joint models by clustering structural descriptions computed from image annotations. The clustering method uses an inter-model distance measure defined as a minimum of the objective function that measures a discrepancy between structural descriptions. The objective function is minimized through a search for a best match between two structural descriptions. The method presentation is illustrated with the results of its application to ultrasound images of finger joints.

## 1 Introduction

One of many medical applications of ultrasound imaging is focused on detection, assessment and monitoring of synovitis, an inflammation of synovial membrane often associated with rheumatoid arthritis [1,2]. While the examination and analysis of ultrasound images directed towards synovitis assessment is currently performed manually by specialists, there is a need for automating this process to decrease its cost and to reduce the discrepancy in human scoring. A project named Medusa [3], conducted in Poland and Norway has as its objective construction of a synovitis estimator, that will process unannotated, and unlabeled ultrasound images of joints, to assess for each the presence and a degree of synovitis. The first stage of such processing is the identification of anatomical elements in the image, namely the skin, bones and the joint, by comparing an


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ultrasound image of a joint with structural descriptions of articulated models that are stored in a dataset called the Class Model Library (CML). As a result of the comparison a model is selected which gives the best registration score, or the best match. Using the best matching model, the skin, bones and joint in the target image can be identified according to the mapping provided by the result of the match operation. The matching between models from CML and the ultrasound image is computed using the recently proposed method for image registration using structural descriptions [4]. An example of a structural description, overlaid on an ultrasound image as yellow polygonal chains, is shown in Fig. 1. The focus of this paper is the construction of the CML library. A new method of unsupervised learning, based on clustering structural descriptions, uses as a distance measure for the clustering the minimum of the objective function that results from the method of registration of structural descriptions described in [4]. While the authors don't know of any work which is closely related to the proposed learning method, the approach to modeling, recognition and learning by parts in computer vision, represented by [5–8] is similar in spirit.

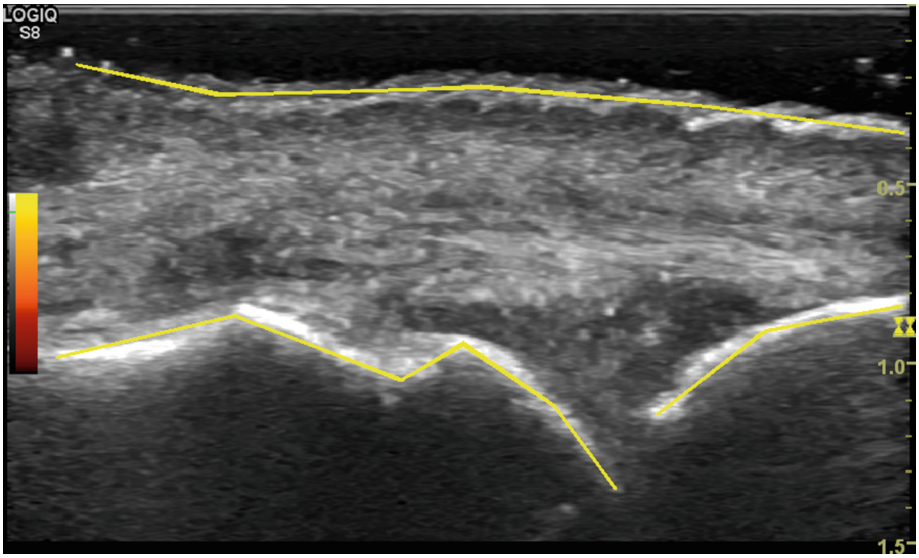


**Fig. 1.** The yellow polygonal chains that mark the skin and the bones form a structural description of the ultrasound image (Color figure online)

The CML is built during the learning phase, using as training data the annotations from a training set of ultrasound images of joints. The learning phase is done once, after the acquisition and annotation of ultrasound training images are completed. The registration method that compares the annotated images expects a structural description where the skin and bone parts are represented as a polygonal chain (piecewise linear curve), that is a chain of connected line segments. However, the skin and bone elements in the annotated ultrasound images

are drawn using smooth curves. To obtain a structural description form required by the registration method, the annotation curves need to be approximated with polygonal chains, or linearized. The curve linearization method is described in Sects. 2 and 3 describes the learning method for constructing a CML.

## 2 Curve Linearization

The linearizing approximation of a smooth curve is done through a simple recursion, based on Douglas-Peuker algorithm [9]. In the first step a curve to be linearized is compared to a line drawn from the curve's first point to the last, and a point of the curve that is farthest from the line is found. If its distance is smaller than a threshold value, the line is the approximation result, otherwise the curve is divided at the farthest point, and the same operation is applied to each of the two segments, terminating when none of the curve segments needs to be divided. This process is illustrated in Figs. 2 and 3 shows the examples of linearization results for four images.

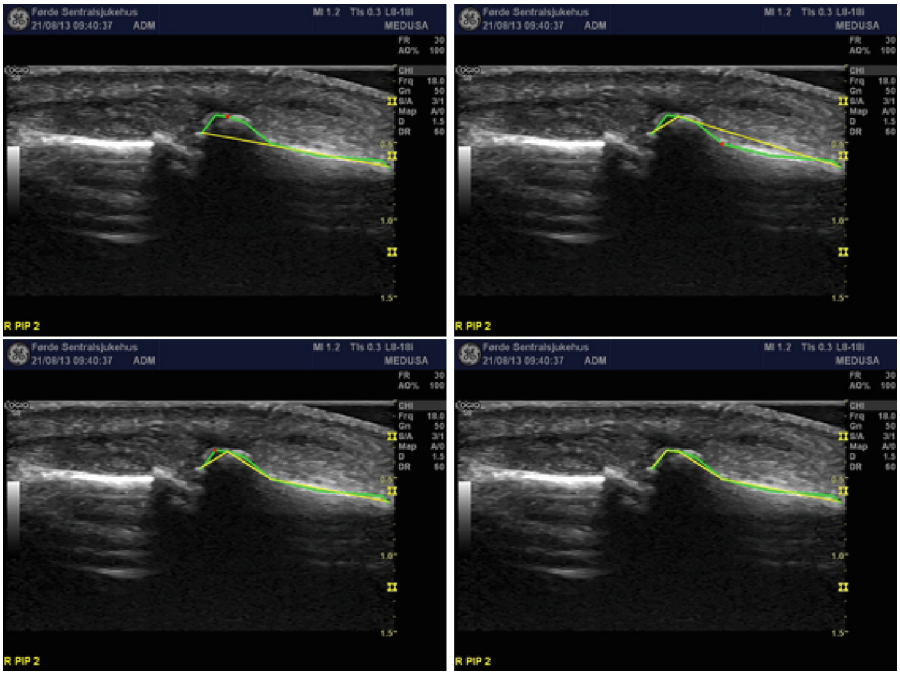


**Fig. 2.** Linearization: steps 1,2,3,4

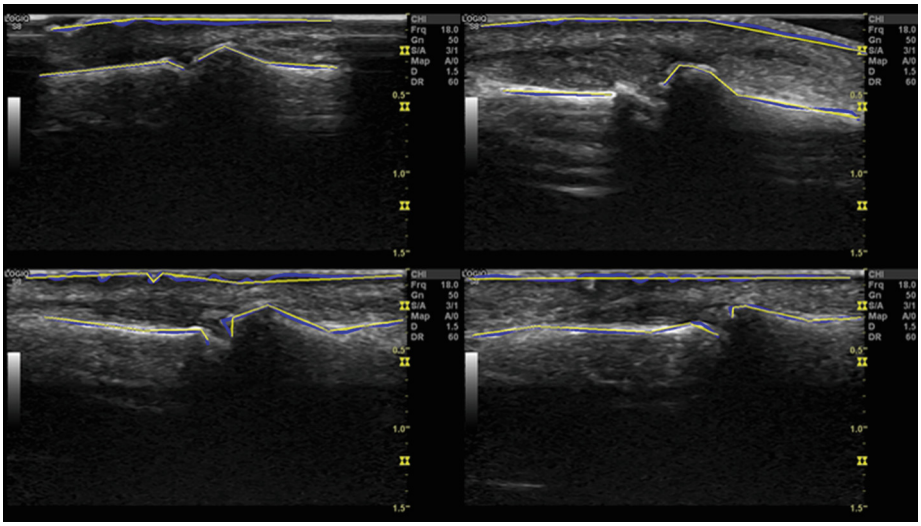

**Fig. 3.** Examples of linearization of annotation curves. Original curve - blue, polygonal chain - yellow (Color figure online)

## 3 Learning Class Models

The method for registering structural descriptions, described in [1] uses an objective function (cost) to guide a search for a best correspondence between two structural descriptions, $X$ the target and $R$ the reference, represented as sets of planar features. This search allows the reference $R$ to be transformed by a rigid, planar transformation $T$, and it aims at finding a mapping $Map$ that maps nodes of $X$ to the nodes of $R$, and a transformation $T$, that to minimize the cost value:

$$Q(X, R, T, Map) = \sum_{i=1}^{n} d^2(X_i, T(R_{Map(i)})) + mC_R \tag{1}$$

where $n$ and $m$ are the numbers of nodes in the target and the reference structures, respectively, $C_R$ is a regularization coefficient and $d^2(x, r)$ is the squared distance between the nodes $x$ and $r$. The node distance $d^2$ is computed from the sum of a vector $v_p$ that projects a midpoint of $r$ onto $x$ and a vector $V_s$, which is the minimal translation of the center of $r$ in parallel to $x$, that makes the length of the intersection of x with a projection $r_p$, of $r$ onto the line extending $x$, equal to the minimum length of $r_p$ and $x$, as it was described in [1].

$$d^2(x, r) = (v_p + v_s)^t (v_p + v_s) \tag{2}$$

The minimal cost value achieved in the process of registration of two feature sets, $X$ and $R$, is given in [1], in Eq. (2):

$$Q^{Opt}(X, R) = Min_{Map,T} Q(X, R, T, Map) \tag{3}$$

The value $Q^{Opt}(X, R)$ is used here as a squared distance measure between the sets $X$ and $R$, that is

$$d^2(X, R) = Q^{Opt}(X, R) = Min_{Map,T} Q(X, R, T, Map) \tag{4}$$

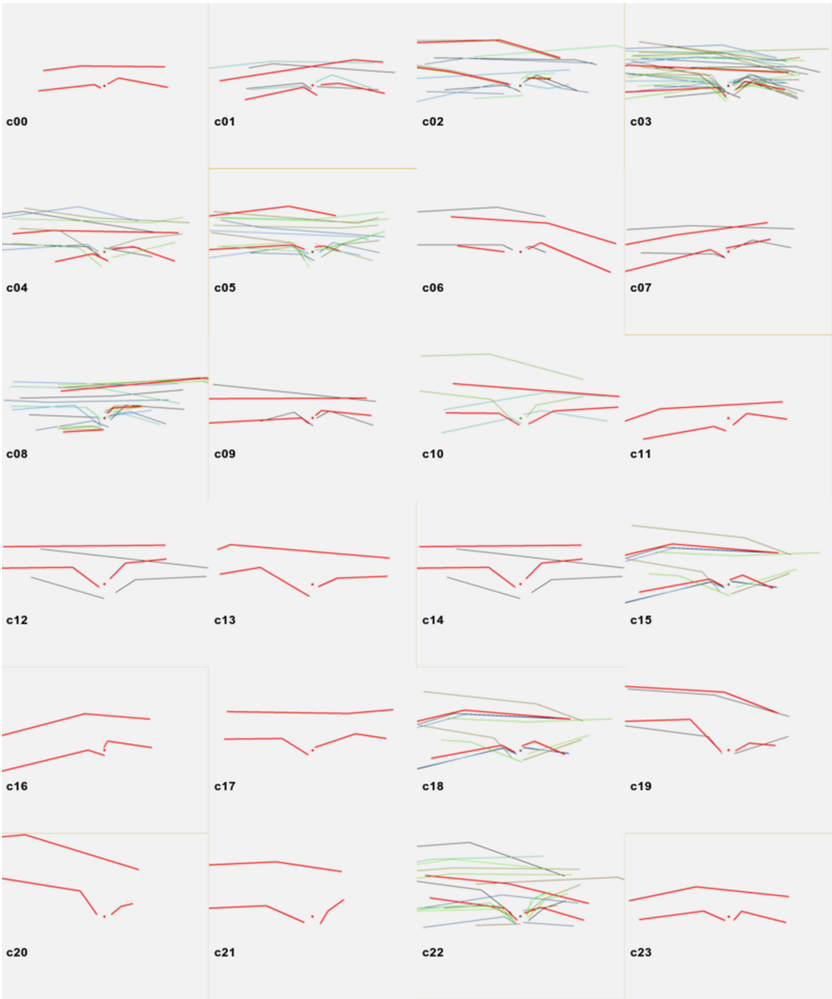


**Fig. 4.** Example of structural description clustering. Cluster centers are drawn in red (Color figure online).

The proposed method for learning class models, uses this distance measure for comparing and clustering structural descriptions obtained from annotated training images. A cluster of structural descriptions is a set $C = C(1), C(2), ...C(k)$

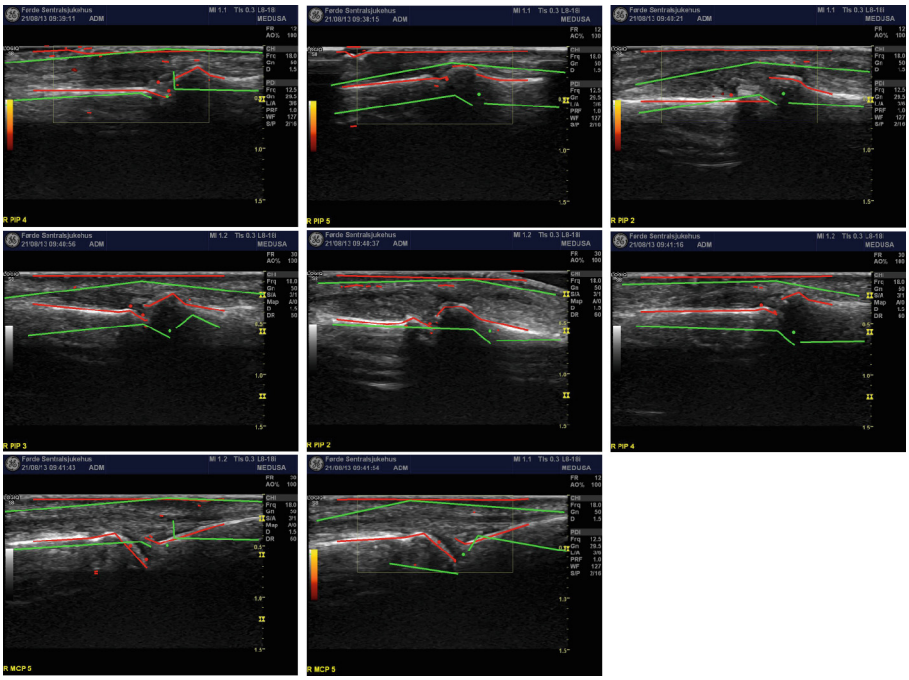

**Fig. 5.** Examples of image registration using CML. Each target image is shown with its annotation structure (red), and with a transformed center of the nearest matching cluster from CML (green) (Color figure online).

where $C(1), C(2), ...$ are structural descriptions, which are the cluster members. A cluster center $C^m$ is defined as

$$C^m = C(argmin_i \sum_{j=1}^{k} d^2(C(i), C(j))) \tag{5}$$

Each of the clusters resulting from this process defines a distinct class. A class model is the central element, or center of a cluster. Cluster *center* is defined as a cluster member for which the sum of squared distances to the remaining cluster members is minimal. A distance between a structural description $X$ and a cluster $C$, $D(X, C)$ is defined as the distance of this structural description from the cluster center $C^m$.

$$D(X, C) = d^2(X, C^m) \tag{6}$$

The set of all class models (cluster centers) is the Class Model Library. To identify the joint, skin and bones in an unlabeled image, the structural description of the image is compared with models in Class Model Library to find the nearest model and its mapping ($Map$) function, which identifies the features of the unlabeled structure. The following steps describe the proposed method for

clustering structural descriptions. The structural descriptions are referred to as samples.

1. Create an empty cluster, include in it the first sample, making this sample the cluster center.
2. If all samples have been processed, terminate. Otherwise, take the next sample, compare it (register) with the center of each cluster, and select the nearest cluster.
3. If the distance of the sample to the nearest cluster is greater than a threshold T, create a new cluster and include in it the sample, making the sample the cluster center. Otherwise, add the new sample to its nearest cluster and recompute the center for this cluster.
4. Go to Step 2.

**Example 1. Clustering.** For illustration, the first 24 of the 25 clusters, that resulted from the application of this method to a set of 85 annotated ultrasound images are shown in Fig. 4. Each sub-image of Fig. 4 shows one cluster. Each member of a cluster is shown using a different color. The same color is applied to all the features of a cluster member. The red color is used to draw the central element of each cluster.

**Example 2. Image Registration.** In a pilot image registration experiment, structural descriptions derived from images are matched with clusters from the CML. For each image, the structural description of the center of the nearest matching cluster is transformed according to $T$ given by Eq. 3, and overlaid on the image. Figure 5 shows images with annotations (red) and for each image an overlaid best matching cluster center transformed by $T$ (green). One can see, that orientation and position along the y-axis between the target and the reference structural descriptions are close, but in several cases there is a significant difference in the position along the x-axis. However, the position of the joint has not been used in the CML construction or in the image registration, and the results are expected to improve when it is included.

## 4 Conclusions

A Class Model Library is a set of models of structural descriptions of ultrasound images of joints, where a structural description represents skin and bones as polygonal chains. A Class Model Library is constructed from a set of ultrasound images with annotations which mark skin and bones in the images. Its purpose is to serve as a reference set for identifying skin, bones and a joint in an unannotated ultrasound image. An approach to constructing a Class Model Library has been presented. Its first part to obtain structural descriptions from the smooth curves that mark skin and bone features in the annotated ultrasound images, using polygonal chain approximation. The second part is a novel

unsupervised learning of class models by clustering the structural descriptions, where the minimal cost value of registration of structural descriptions is used as a measure of distance between structural descriptions and between clusters and structural descriptions. In continuation of this work a joint will be included in the structural description as one more feature, which should increase the registration accuracy, and a joint detector [10,11] will be used to find joint candidate location in an image. The presented approach is quite general. It is not limited to images of a joint and it should be useful for learning structural models of other anatomical structures, and it should work with other imaging modalities than ultrasound.

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