

Fuzzy Model-based Algorithm for 3-D Bone Tumour Analysis

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Abstract: In this paper, a new fuzzy model based algorithm for 3-D bone tumour segmentation in MR series is introduced. The presented segmentation procedure is based on a modified fuzzy connectedness method. The there required fuzzy affinity values are estimated using a fuzzy inference system, whose fuzzy membership functions are structured on the basis of gaussian mixture model of analyzed image regions. The 3-D fuzzy tumour model is generated using different MR modalities acquired during a single examination. The segmentation abilities of prototype system have been tested on a MR database consisting of 27 examinations composed of two different sequences each.

1 INTRODUCTION

According to (Davies et al., 2009; Husband and Reznik, 2004), bone tumour is an abnormal growth of cells within a single bone, spreading to another one, muscles or soft tissue in their surroundings. They are usually found in children and young adults and their early diagnosis can be crucial for the treatment applied. The diversity of bone tumours in children still features many diagnostic and therapeutic problems. Determination of their nature requires experience and close collaboration of specialists from various areas. Despite the significant progress of imaging techniques, many cases are diagnosed too late.

The bone tumours diagnostics is mostly based on Magnetic Resonance (MR) imaging, where during a single examination, series in different MR modalities are acquired. However, different tumour types vary in their appearance even in the same modality. Largely only the comparative radiological analysis taking into consideration several acquired series enables a reliable diagnosis.

Due to the fact, that bone tumours are quite rare, the problem of their segmentation is not often discussed in literature. Varied intensity levels in MR sequences constituting different tumours cause the described segmentation methods (Ma et al., 2005; Zhao et al., 2004; Pan and Li, 2003) to be dedicated to one tumour type only. A wide range of currently available imaging techniques differentiates the segmentation procedure to dynamic MR based (Zhao

et al., 2004; Zhao et al., 2003) as well as static MR based (Ma et al., 2005; Pan and Li, 2003) techniques. All the procedures presented in the mentioned papers combine the information coming from different MR modalities. The segmentation algorithm proposed in (Ma et al., 2005) is based on fuzzy connectedness analysis developed by (Rosenfeld, 1979; Udupa and Samarasekera, 1996) and is commonly used in different medical applications (Pednekar et al., 2008; Udupa et al., 2002). The fuzzy connectedness principles have been tested in dozens of studies in past 15 years.

There exist different fuzzy logic based techniques dedicated to medical applications described in literature (Yamaguchi et al., 2010; Hata et al., 2000; Tolia and Panas, 1998). The fully automated fuzzy topology method used for brain image analysis is proposed in (Mari and Dellepiane, 1996). Brain analysis investigating its morphological changes based on a combination of Bayesian classification with Gaussian Mixture Model (GMM) and fuzzy active surface is presented in (Yamaguchi et al., 2010).

The differences in grey intensity levels building bone tumours areas depending on their location in the human body make reliable automatic segmentation and direct application of mentioned procedures impossible. Therefore, this paper presents a new segmentation algorithm combining GMM and fuzzy inference systems in the fuzzy connectedness procedure, insensitive to tumour type and location in the body. The developed 3-D segmentation method,

based on the previously segmented tumour as well as surrounding tissues regions on a single slice, adopts the fuzzy inference system parameters to enable the analysis of the whole study.

Radiological diagnostic of bone tumours relies on comparative analysis of different MR images acquired during one examination. With this in mind, in the presented methodology a parallel analysis of two different MR series is applied.

In the following section, a short introduction to the fuzzy connectedness-based segmentation procedure is given. In section 3 the membership functions structured based on GMM are described. Section 4 introduces the used fuzzy inference system and section 5 presents the developed algorithm. Discussion concerning performed experiments and obtained segmentation results is given in section 6. Then, the last section (section 7) concludes the work and presents some plans for the future.

2 FUZZY CONNECTEDNESS BASED SEGMENTATION

The idea of fuzzy connectedness analysis in image processing and image segmentation has been given in works (Rosenfeld, 1979; Udupa and Samarasekera, 1996). The there presented methodology operates on multidimensional, multifeature sets of data, being connected and ordered. The points classified into an object are strongly connected with some relations having relatively lower values, when it comes to points outside the object. In medical image segmentation a multifeature data set often consists of grey intensity levels of pixels (or voxels – in volumetric data) in acquired CT, MR, US etc. studies. The image fusion methods applied afterwards make it possible to simultaneously analyse them all. In the presented study only MR data of bone tumours are collected, however the multifeature dataset is constructed with different MR modalities, namely T2-weighted, T1-weighted, T1-weighted contrast enhanced, etc.

Then, the segmentation procedure takes into consideration local similarities of the analyzed voxels, exploring their position $\underline{e} = (e_x, e_y, e_z)$ and gray intensity levels $I^d(\underline{e})$, where $d = \{1, \dots, D\}$ is the dimensionality of feature space.

Fuzzy connectedness of two image points is estimated on the basis of their fuzzy relation – fuzzy affinity κ

$$\kappa = \{((\underline{e}, \underline{d}), \mu_\kappa(\underline{e}, \underline{d})) : (\underline{e}, \underline{d}) \in C \times C\}, \quad (1)$$

where $\mu_\kappa \in [0, 1]$ is the fuzzy affinity membership function of spels (spatial elements) \underline{e} and \underline{d} . The

reflexive: $\mu_\kappa(\underline{e}, \underline{e}) = 1$ and symmetric: $\mu_\kappa(\underline{e}, \underline{d}) = \mu_\kappa(\underline{d}, \underline{e})$ fuzzy affinity is mostly given as

$$\mu_\kappa(\underline{e}, \underline{d}) = \mu_\alpha(\underline{e}, \underline{d}) \cdot g(\mu_\omega(\underline{e}, \underline{d}), \mu_\psi(\underline{e}, \underline{d})), \quad (2)$$

where μ_α is the functional form of adjacency relation α and μ_ω , μ_ψ are intensity-based and intensity gradient-based components of the affinity, respectively. There are different forms of (2) discussed in (Udupa et al., 2002), from which the most popular in medical applications is the weighted gaussian variant

$$\mu_\kappa(\underline{e}, \underline{d}) = \mu_\alpha \cdot (w_1 H_1(\underline{e}, \underline{d}) + w_2 H_2(\underline{e}, \underline{d})), \quad (3)$$

with parameters w_1 and w_2 denoting positive constants fulfilling

$$w_1 + w_2 = 1. \quad (4)$$

Components H_1 and H_2 are defined as:

$$H_1(\underline{e}, \underline{d}) = \exp\left(-\frac{1}{2\sigma_1^2} \left(\frac{I(\underline{e})+I(\underline{d})}{2} - \lambda_1\right)^2\right), \quad (5)$$

$$H_2(\underline{e}, \underline{d}) = \exp\left(-\frac{1}{2\sigma_2^2} (|I(\underline{e}) - I(\underline{d})| - \lambda_2)^2\right).$$

Pairs λ_1 , σ_1 and λ_2 , σ_2 are the expected parameters of the segmented object, describing its gray intensity and gradient.

To determine the relations of spels \underline{e} and \underline{d} the concept of digital path has been introduced (Udupa and Samarasekera, 1996). A nonempty path p_{ed} from $\underline{e} = \underline{e}^{(1)}$ to $\underline{d} = \underline{e}^{(m)}$ is any sequence of elements $\langle \underline{e}^{(1)}, \underline{e}^{(2)}, \dots, \underline{e}^{(m)} \rangle$, such that for any $i \in [1, m-1]$ pair $\langle \underline{e}^i, \underline{e}^{(i+1)} \rangle$ a link exists. The strength of a path is given by the strength of its weakest link (with the smallest affinity). The strength of the "strongest" paths between two image points (spels) \underline{e} and \underline{d} describes their connectedness.

Finally, the fuzzy κ -connectedness relation K between two image points \underline{e} and \underline{d} is given as follows

$$\mu_K(\underline{e}, \underline{d}) = \max_{p_{ed} \in P_{ed}} [\mu_N(p_{ed})], \quad (6)$$

where

$$\mu_N(p_{ed}) = \min_i \{\mu_\kappa(\underline{e}^{(i)}, \underline{e}^{(i+1)})\}. \quad (7)$$

Fuzzy affinity scene ℓ_o with respect to object's starting point \underline{o} is then given by

$$\ell_o(\underline{e}) = \mu_K(\underline{o}, \underline{e}). \quad (8)$$

Then, the segmented fuzzy object $O(\underline{o})$ containing starting point \underline{o} is obtained using the thresholding procedure on scene ℓ_o . The problem of threshold selection is solved by introducing the second object, treated as a background region with its own seed point \underline{b} . Therefore, spel \underline{e} belongs to object $O(\underline{o})$ if $\mu_K(\underline{o}, \underline{e}) > \mu_K(\underline{b}, \underline{e})$. The already described approach

is called the Relative Fuzzy Connectedness method and it is discussed in detail in (Udupa et al., 2002; Udupa and Samarasekera, 1996). To solve the shortest path problem the authors use the dynamic programming approach, which in (Carvalho et al., 1999) has been replaced by the Dijkstra's Algorithm. In the later FC applications (Saha and Udupa, 2001) also the single seed points belonging to the object as well as the background have been replaced by the seed points sets.

In cases of clearly visible tissues and sharp enough edges the already described FC-based segmentation method yields very good results. Based on the selected seed points areas the required intensity and intensity gradient parameters are there easy to estimate. The pathologies, like soft tissue tumours, with a more complex structure can be segmented applying a clustering based FC analysis presented in (Badura et al., 2011). The analysed image data are first clustered and the obtained clusters parameters are then utilised in the FC step.

The idea introduced in this paper is to adopt the fuzzy connectedness approach to multifeature bone tumour analysis. The presented methodology is based on two different MR modalities. Two exemplary images of a bone cyst on coronal Short Time Inversion Recovery (STIR) and Fast Spin-Echo (FSE) T1-weighted series are shown in Figure 1. In the radiological diagnosis the comparative analysis of both the series is utilised. Due to this fact, first, different 3-D multifeature clustering procedures (McLachlan and Peel, 2000; Heo and Gader, 2010) have been applied. However, none of the implemented multifeature algorithms has yielded satisfactory final segmentation results. Therefore, a fuzzy inference system simulating experts reasoning, described in the following sections, has been developed.

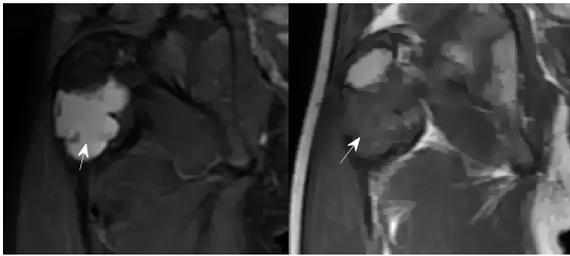


Figure 1: A bone cyst visualised on a single slice coming from two different MR coronal series: left – STIR, right – FSE T1-weighted.

Let us assume that there are two reference regions selected on a single slice: tumour area and the background, respectively. The areas are then transferred into both the analyzed modalities. Let the already given regions constitute the expert knowledge. Due to

the fact that the grey intensity levels constructing the tumours areas vary depending on the analyzed lesion and its location in the patients body, the fuzzy rules and dictionary are adaptively created for each single tumour case. The varying grey intensity levels building tumour as well as background areas on both MR sequences are described using the Gaussian Mixture Model. The obtained models are then used both in a fuzzy system dictionary and the rules base. The crisp value at the output of the developed fuzzy inference system is the fuzzy affinity value $\mu_K(\underline{a}, \underline{e})$.

3 GAUSSIAN MIXTURE MODEL

Gaussian Mixture Model (GMM) is a semi-parametric technique, which enables estimating a probability density function with a mixture distribution (McLachlan and Peel, 2000; Dempster et al., 1977), defined as a weighted sum of its components.

Let be a set of N vectors $\underline{x}_n = [x_n^1, x_n^2, \dots, x_n^D]^T$, $n \in \{1, \dots, N\}$, where D is the dimensionality of feature space. Consider a mixture model with K ($K > 1$) components in R^n for $n \geq 1$. The probability density function of vector \underline{x} in the mixture is given as

$$p(\underline{x}) = \sum_{k=1}^K \pi_k p_k(\underline{x}), \quad (9)$$

where $p_k(\underline{x})$ is the density of k -th component and $\pi_k \in [0, 1]$ are the mixing proportions coefficients fulfilling

$$\sum_{k=1}^K \pi_k = 1. \quad (10)$$

In the Gaussian Mixture Model each group of the data is assumed to be generated by a normal probability distribution

$$p_k(\underline{x}) = \frac{1}{(2\pi)^{\frac{D}{2}} \det(\Sigma_k)^{\frac{1}{2}}} \exp \left\{ -\frac{1}{2} (\underline{x} - \lambda_k)^T \Sigma_k^{-1} (\underline{x} - \lambda_k) \right\}, \quad (11)$$

where λ_k and Σ_k are the parameters of D -dimensional normal probability distribution $N(\lambda_k, \Sigma_k)$, mean values vector and covariance matrix, respectively.

The maximum likelihood estimator of parameter $\Theta = \{\Theta_1, \Theta_2, \dots, \Theta_K\}$, where $\Theta_k = \{\lambda_k, \Sigma_k\}$, of a parametric probability distribution is found using the Expectation-Maximization (EM) algorithm (Dempster et al., 1977). Since the EM procedure is dedicated to incomplete data sets analysis, it iteratively alternates between finding the greatest lower bound to the likelihood function, making guesses about the complete data and then maximizing this bound by finding the Θ that maximizes $p(\underline{x}|\Theta)$ over Θ .

The EM algorithm requires starting points as well as clusters number selection. The required parameters are estimated applying the unsupervised cascade clustering procedure and Kernelised CS cluster validity measure discussed in detail in (Czajkowska et al., 2012).

In the proposed segmentation procedure the adaptively generated bone tumour as well as background model constitute the basis for fuzzy inference system. The obtained components parameters are used in the fuzzy dictionary, which defines the membership functions of fuzzy rules. The combination of different components building particular image regions is the basis for fuzzy rules generation.

4 FUZZY INFERENCE SYSTEM

There exist different fuzzy reasoning systems described in literature (Yamaguchi et al., 2010; Hata et al., 2000; Siler and Buckley, 2005) and also applied to medical tasks. The basic structure of such systems consists of three components: dictionary defining the membership functions, base of fuzzy IF-THEN rules and reasoning mechanism.

Historically the first fuzzy control system, based on Zadeh's formulations from 1973, was introduced by Mamdani in 1976. The input numbers are there translated into linguistic terms and the fuzzy rules map them onto linguistic terms describing the system output. Then, the output linguistic terms are translated back into the numbers. The procedures of translations are known as fuzzification and defuzzification, respectively. A typical fuzzy rule in such a system is constructed as follows:

$$\begin{array}{l} \text{IF input1 is } A_i^1 \text{ AND input2 is } A_i^2 \\ \text{THEN output is } B_i \end{array} \quad (12)$$

It tries to formulate the expert knowledge using some linguistic rules. An exemplary rule dedicated to the task of bone tumour segmentation can be simply described as:

$$\begin{array}{l} \text{"IF the intensity level of the area} \\ \text{in } T2 - \text{weighted series is } \mathbf{very\ high} \\ \text{AND the intensity level of the area} \\ \text{in } T1 - \text{weighted series is } \mathbf{very\ low} \\ \text{THEN the analyzed region} \\ \text{might be a tumour"} \end{array} \quad (13)$$

There are different combinations of grey intensity levels suggestive of bone tumour defined by the experts and consequently different linguistic rules connected with them. Simultaneously, there exists a set of linguistic rules defining the healthy tissues. The developed fuzzy inference system attempts to describe the majority of them.

Let the fuzzy sets in the fuzzy premises of i -th rule be given as A_i^1 and A_i^2 , respectively and the fuzzy set in the conclusion of i -th rule is denoted as B_i . In the exemplary radiologist reasoning rule, the fuzzy sets A_i^1 and A_i^2 are given as "high" and "low" and B_i as "might be tumour".

The fuzzy control algorithm developed by Mamdani is based on two concepts: fuzzy implication and compositional rule of inference (Kickert and Mamdani, 1978). Assume two fuzzy sets: A of the universe of discourse \mathbb{X} and B of \mathbb{Y} defined by their fuzzy membership functions μ_A and μ_B . The membership function of a fuzzy implication S : "IF A then B " is then defined as

$$\mu_s(x, y) = \min[\mu_A(x); \mu_B(y)], \quad x \in \mathbb{X}, y \in \mathbb{Y}. \quad (14)$$

For such given implication S , fuzzy set B' of the universe of discourse \mathbb{Y} inferred by a given fuzzy set A' of \mathbb{X} , has a membership function estimated as

$$\mu_{B'}(y) = \max_x \min[\mu_{A'}(x); \mu_s(x, y)], \quad x \in \mathbb{X}, y \in \mathbb{Y}. \quad (15)$$

In fuzzy systems found in research applications there are different rules describing one phenomenon. When the rules conditions are matched, a set of actions will be activated. Each rule, with the antecedent non-zero matching degree, contributes an output with the activation value equal to it. The final system output taking into consideration all the activated rules is constructed using an aggregation operation. Its most common implementation is operator max, however there exist different aggregation operators found in real applications, like algebraic sum or the bounded product.

Coming back to the bone tumours analysis, the already described fuzzy system is used in the fuzzy connectedness analysis in order to estimate the fuzzy affinity value of the spels connection, instead of the functions given by (4) and (5).

5 ALGORITHM

Before the segmentation procedure begins, thanks to the positioning information provided by the DICOM header, the positions of voxels belonging to the two analysed MR series are matched.

The segmentation procedure starts on the basis of exemplary region selection performed by an expert. The automated part of analysis begins with the adaptive 3-D filtering method (Perona et al., 1994). The there required parameters are adaptively estimated based on the assumptions given in (Positano et al.,

2000). The goal of this analysis step is firstly the reduction of noise and thereby an increase in the signal-to-noise or contrast-to-noise ratios while maintaining the edge lines. Secondly, as a result of smoothing the objects areas the number of groups in the clustering procedure, being the next step, decreases and the analysis is not sensitive to outliers.

The main part of performed analysis constitutes of four steps discussed in previous sections, whose combination is shown on the block diagram in Figure 2.

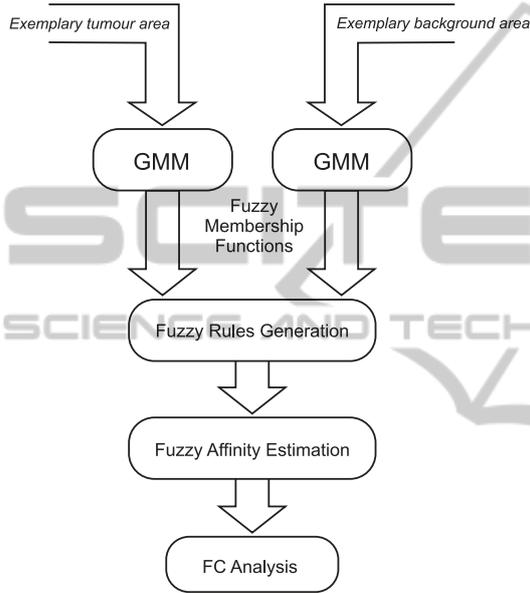


Figure 2: The flow chart of 3-D bone tumours segmentation procedure

First, based on the reference expert selections, personalized GMMs of bone tumour and background areas are generated. The detailed discussion of the algorithm is given in section 3. Let the obtained GMMs of tumour area be given as $G_t^{1,2}$ and of the background as $G_b^{1,2}$, respectively. Both GMM pairs are the sets of mixture components parameters θ and voxels C classified into each of K_t or K_b groups

$$\begin{aligned} G_t^i &= (\theta_{1_t}^i, C_{1_t}^i), (\theta_{2_t}^i, C_{2_t}^i), \dots, (\theta_{K_t}^i, C_{K_t}^i), \\ G_b^i &= (\theta_{1_b}^i, C_{1_b}^i), (\theta_{2_b}^i, C_{2_b}^i), \dots, (\theta_{K_b}^i, C_{K_b}^i), \end{aligned} \quad (16)$$

where index $i = \{1, 2\}$ refers to two simultaneously analysed MR sequences.

Based on them, the input membership functions describing the intensity levels constituting tumour as well as background areas are defined. An exemplary set of membership functions obtained for a bone cyst in STIR and T1-weighted sequences (Figure 1) is visualised in Figure 3. The membership functions defined for the tumour area are marked with the black

solid lines and the membership functions defined for the background are given by the grey dashed lines.

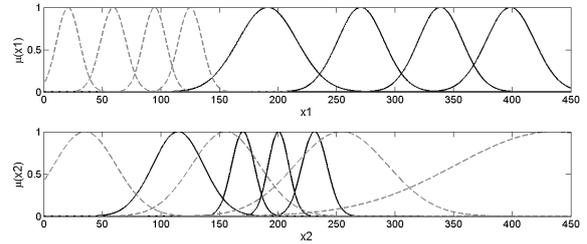


Figure 3: An exemplary set of membership functions generated for a bone cyst in STIR (top) and T1-weighted (down) sequences. The membership functions defined for the tumour area are marked with the black solid lines and the membership functions defined for the background are given by the grey dashed lines.

Since the fuzzy connectedness analysis is used in the segmentation step, the system inputs should cause two adjacent spels to obtain their affinity value. The functions given by (4) and (5) take into consideration the mean intensity value $0.5(I(\underline{e}) + I(\underline{d}))$ and gradient $|I(\underline{e}) - I(\underline{d})|$. Since the attempts of modelling gradient values characterising tumour or healthy tissues have not provided any useful information, the inputs to the fuzzy system are defined as $x_i = 0.5(I^i(\underline{e}) + I^i(\underline{d}))$.

Two membership functions in the conclusions of rules are shown in Figure 4. The output of the system is the affinity value of two adjacent spels. The membership function visualised using the black solid line defines the "high" affinity and the dashed line defines the "low" affinity of spels connection. Moreover, to reduce the computation time associated with the relative FC analysis, the meaning of "big" affinity value is "it might be tumour". Based on the graph of the functions in Figure 4, the threshold defining the tumour area can be set to 0.45.

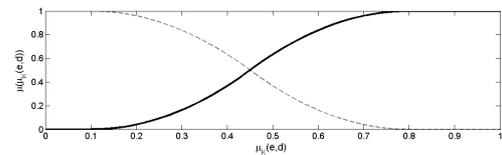


Figure 4: An exemplary set of membership functions on the output of the fuzzy inference system. The black solid line defines the tumour and the grey dashed line represents the background.

Let the fuzzy sets in premises referring to $G_t^{1,2}$ and $G_b^{1,2}$ are given as $A_{k_t}^i$ and $A_{k_b}^i$, and the fuzzy sets in conclusions as B_h – "high" and B_l – "low". Then, on the basis of sets $G_t^{1,2}$ and $G_b^{1,2}$ and all the positions of voxel \underline{c} the unique fuzzy rules R_l^i , $l \in \{1, 2, \dots, L\}$ and R_p^i , $p \in \{1, 2, \dots, P\}$ defining tumour and non-tumour

areas, respectively, are generated as follows:

- 1: **if** $\underline{c} \in T$ **and** $\underline{c} \in C_{k_t}^1$ **and** $\underline{c} \in C_{k_t}^2$, where T is the set of reference tumour voxels **then**
- 2:

$$R_t^l : \text{IF } x1 \text{ is } A_{k_t}^1 \text{ AND } x2 \text{ is } A_{k_t}^2 \\ \text{THEN } \mu_K(\underline{e}, \underline{d}) \text{ is } B_h \quad (17)$$

- 3: **end if**
- 4: **if** $\underline{c} \in T$ **and** $\underline{c} \in C_{k_b}^1$ **and** $\underline{c} \in C_{k_b}^2$, where T is the set of reference background voxels **then**
- 5:

$$R_b^p : \text{IF } x1 \text{ is } A_{k_b}^1 \text{ AND } x2 \text{ is } A_{k_b}^2 \\ \text{THEN } \mu_K(\underline{e}, \underline{d}) \text{ is } B_l \quad (18)$$

- 6: **end if**

For each pair of the adjacent voxels the output linguistic value is then translated into their fuzzy affinity. In the defuzzification step the center of gravity method is employed. Using the precomputed affinity tables, the multiseeded FC algorithm described in (Badura et al., 2011) is performed.

To reduce the false positive regions in the case when the tumour is connected with the healthy tissues having similar characteristics, a convex hull-based postprocessing technique is applied. Starting from the reference slice the there obtained tumour convex hull is then mapped into the adjacent slices. The comparison of areas of tumour like regions covered and uncovered by the convex hull provides the information concerning the final segmentation results.

6 EXPERIMENTS AND RESULTS

To evaluate the ability of developed methodology, the database consisting of 27 examinations of 18 patients studies has been used. The therein contained cases have included 5 types of bone tumours: *chondromas*, *Ewing's sarcomas*, *osteosarcomas*, *bone cysts* and *chondrosarcomas*. In total, 413 pairs of slices have been analysed. An individual pair have consisted of T1-weighted, T1-weighted contrast enhanced and fat saturated, T2-weighted or STIR sequences in different MR projections: axial, sagittal and coronal. The FC threshold values have been set to 0.45 and 0.5.

All the obtained results have been discussed with an expert, who judged them on each slice in each examination. As a result the obtained image regions have been divided into three classes: true positive (TP) – the coherent areas containing a correctly indicated tumour, false positive (FP) – a coherent region containing healthy tissues incorrectly classified as tumorous, false negative (FN) – a coherent region con-

taining tumour areas incorrectly classified as healthy tissue.

The accuracy of presented segmentation procedure has been estimated based on the following similarity coefficient

$$DV = \frac{FP + FN}{TP + FN}, \quad (19)$$

yielding the value equal 0 when the segmentation results are fully correct. The obtained DV value for the bone tumours database has been equal to 0.12, which is sufficient for computer assisted diagnosis systems.

Exemplary results for 3 different types of bone tumours are shown in Figures 5 - 7.

The original fuzzy connectedness algorithm (FC1) described in (Udupa et al., 2002) as well as its modification (FC2) developed in (Badura et al., 2011) were used to compare the obtained results, which were categorized into two groups: the segmentation results in the homogeneous and in-homogeneous image series. The numerical results (DV values) are summarized in the Table 1, where the last column (FIS) provides the results obtained using the proposed methodology. The first row of Table 1 shows that the segmentation results obtained for homogeneous image data are comparable with other methods. The second row proves a superiority of the proposed method over another approach described in literature, which results are insufficient for computer assisted diagnosis systems and not acceptable by a radiologist.

Table 1: Accuracy of different segmentation procedures – DV coefficient.

	FC1	FC2	FIS
Homogeneous Series (22) DV	0.16%	0.13%	0.13%
In-homogeneous Series (5) DV	0.6%	0.5%	0.11%

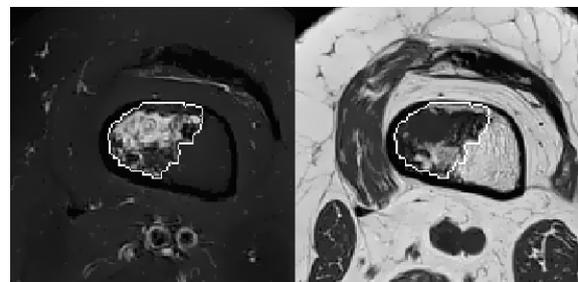


Figure 5: Final segmentation results of knee Enchondroma visualised on a single slices of axial MR series: left – T2 Blade FS, right – T1 TSE.

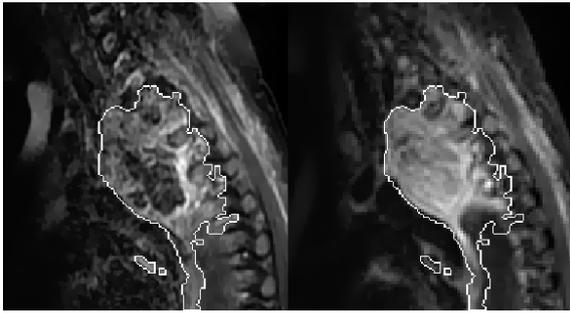


Figure 6: Final segmentation results of spines Ewing's sarcoma visualized on a single slices of sagittal MR series: left – T1+C SE FS, right – STIR.



Figure 7: Final segmentation results of tibias Osteosarcoma visualized on a single slices of coronal MR series: left – T2 FRFSE FS, right – T1 FSE.

7 CONCLUSIONS

This paper introduces a 3-D multifeature bone tumours segmentation method in MR images. The insensitive to bone tumour location and type algorithm combines Gaussian Mixture Model and fuzzy inference system in the fuzzy connectedness analysis. The proposed procedure has been tested on the database of real bone tumour cases consisting of 27 examinations of 18 patients, a single examination containing two different MR series. The obtained segmentation results encourage to further develop this method. The presented system provides a basis for developing an adaptively learning algorithm, training being based on the currently analysed and verified cases. The problem still remaining to be solved is the normalisation of MR sequences so that they can be compared. The plans for further work take into consider-

ation expanding the database with new tumour cases and involving in the analysis new features like texture. The detailed radiological consultation will enable developing fuzzy IF-THEN rules base and reasoning mechanism. In order to improve the segmentation results some fuzzy rules interpolation technique is also planned to be introduced.

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