ABSTRACT
In this paper, we propose a new approach to segmentation of 3D CT images, which is aimed at texture-based segmentation of organs or disease diagnosing. The extension of Haralick 2D texture feature to the 3D domain was studied. Calculation of separate co-occurrence matrix for each voxel in the 3D image is proposed. The co-occurrence matrix is calculated from all voxels in a small rectangular window around the voxel. This makes it possible to segment given 3D image as opposed to calculating the feature for the pre-segmented regions of an image. Consequently, such features can be used to search for very small regions with different texture properties (like tumours). A set of abdomen CT images is used for evaluation of the proposed approach. The segmentation method we used is model-based, using Gaussian Mixture Model. EM algorithm is used for learning the parameters of mixture model from training data-set.

KEY WORDS
texture features, Haralick features, 3D image analysis, image segmentation, CT images, Gaussian mixture, model-based decision-making, EM algorithm

1. Introduction
Texture-based image analysis using medical images is covered by many theoretical as well as practical papers. We concentrate on analysis of 3D images using texture features. This area is starting to be of main interest in last years. Specifically, we are studying new possibilities in texture feature-based analysis that are opened with the availability of 3D images.

Texture features are often used instrument for image analysis especially for medical images [1]. Texture features are variables calculated from given image region in order to characterise the region texture. In 2D texture analysis of medical images, Haralick features are often used [2, 3, 4]. In our research, we studied specific 3D extension of Haralick features in order to effectively use the three-dimensional CT scans of abdomen area. To verify usability of proposed extension of 3D Haralick texture features, we have used the features constructed, for the segmentation of abdomen area. The method used for segmentation uses model-based learning and maximum-likelihood decision-making. The model applied, is Gaussian mixture model [5]. Standard EM algorithm is used for estimation of its parameters [6].

In Section 2 we describe the specific implementation of Haralick texture features in 3D domain for 3D CT, MRI or any other 3D images available. This is the actual contribution of this paper. In Section 3 we describe the method how these features can be used for image segmentation. This was already presented in [5, 3, 7]. Section 4 shows the example of medical data segmentation. CT data of abdomen were segmented using 3D features.

It should be noted, that in practical application more different methods should be used and the results should be merged. Section 3.3, describes merging with different probabilistic method using Bayes formula.

2. Extension of Haralick Features to 3D Domain
Haralick 2D texture features, are statistics calculated from co-occurrence matrix. This matrix is computed from pixel intensity (gray-level or in case of CT the power intensity) values in a given region. The reason, why the co-occurrence matrix is so widely used in image analysis, is that it represents characteristics of the texture in a given region. Haralick features are statistics defined to emphasize certain texture properties. The co-occurrence matrix consists of numbers, that are counts of co-occurrences of the same gray-scale colour (intensity) in two pixels separated by oriented separation vector. Number of intensity values have to be finite and relatively small, in order to have any co-occurrences in the co-occurrence matrix. Number of intensity value is called “quantization constant”, and denoted by q.

We define original image by the 2D intensity matrix P with intensities p_{a,b} quantized to q intensities. Region where Haralick features, are to be calculated is defined by the set R of two-component vectors. For given separation vector \bar{s} = s_1, s_2, the co-occurrence matrix C is defined by its components c^{(s)}_R(i, j) with following equation:

\[
c^{(s)}_R(i, j) = \frac{\text{card} \{ \bar{u} \in R : p_{\bar{u}} = i; p_{\bar{u}+\bar{s}} = j \}}{\text{card} R}
\] (1)
where $i, j \in \{1, 2, \ldots, q\}$.

Haralick features are calculated as statistics, from the matrix $C$. As originally presented by Haralick [8] and mostly used thereafter, co-occurrence matrix is calculated for the region of interest $R$ (or for the whole image), in order to evaluate the texture on the whole region. Then the image needs to be pre-segmented by another method, in order to separate regions of interest. Because of that, features calculated from co-occurrence matrix calculated for the whole region, can not be easily used for segmentation of the image. It is why we are investigating the possibility to calculate co-occurrence matrix based Haralick features locally for every pixel. It is possible to calculate this matrix on reasonable small window around every pixel of the image, thus having co-occurrence matrix for each pixel instead of having only one number for the big region. Then, features can be calculated for every pixel of the image. The problem of this approach is, that co-occurrence matrix have to be filled with reasonably big values, otherwise it does not distinguish different regions very well. In order to achieve this, the window size around the pixel of interest, should be relatively big. However if the window size is too big, than even distant pixels influence features belonging to the pixel of interest, which means that for bigger windows, features will be blurred. To illustrate the idea about the size of the window, see figures 2 to 4 for comparison of window-based Haralick features for different window sizes.

In 2D case, the window size will have either insufficient size to produce useful Haralick features or it will be too big and will produce blurred feature image. However, the idea of local co-occurrence features and local images can be adopted much better for 3D images. In 3D case, the window area can be made big enough to fill the co-occurrence matrix of reasonable size. As we show in section 4, for $q = 8$ and window size between $5 \times 5 \times 5$ to $11 \times 11 \times 11$ the texture features are determining the texture very well. From Information Theory point of view, we are employing the fact that in 3D space, the information about

Figure 1. CT scan layer of the abdominal part of the human body.

Figure 2. Haralick feature (entropy) calculated for image in figure1. Window size $w = 1$, quantization constant $q = 8$.

Figure 3. Haralick feature (entropy) calculated for image in figure1. Window size $w = 2$, quantization constant $q = 8$.

Figure 4. Haralick feature (entropy) calculated for image in figure1. Window size $w = 4$, quantization constant $q = 8$. 
the texture around given voxel, is significantly closer to
given texture as opposed to 2D space, where the information
about texture is displaced too far from the pixel of inter-
est. The conclusion from this is, that while co-occurrence
based features like Haralick features in 2D domain are only
usable to describe texture in bigger area, in 3D images they
can be used to characterise every single voxel.

For 3D image, the intensity array $P$ is defined by in-
dividual intensities $p_{x}$, for $\vec{v} = (x, y, z)$. Same as in 2D
case, $p_{x}$ are quantized to $q$ intensities. Co-occurrence ma-
trix $C_{\vec{v}}(i, j)$ is defined by its components $c_{\vec{v}}(i, j)$. The
separation vector is $\vec{s} = (s_{1}, s_{2}, s_{3})$. Window $W(\vec{v})$ of the size
$2w + 1$ around the voxel $\vec{v}$ is defined as:

$$W(\vec{v}) = \{ \vec{u} \in I : \vec{u} \leq \vec{v} + \vec{w}; \vec{u} \geq \vec{v} - \vec{w}; \} \quad (2)$$

where $\vec{w} = (w, w, w)$ and $I$ is the whole image region. The
co-occurrence matrix is defined like this:

$$c_{\vec{v}}(i, j) = \frac{\text{card} \{ \vec{c} \in W(\vec{v}) : p_{\vec{c}} = i; p_{\vec{c} + \vec{s}} = j \}}{\text{card} W(\vec{v})} \quad (3)$$

Having the co-occurrence matrix $C$ with components
c(i, j) calculated, Haralick features can be computed using
formulas given below. At first, statistics have to be defined:

$$\mu_{x} = \sum_{i=1}^{q} \sum_{j=1}^{q} (i-1)c(i, j)$$

$$\mu_{y} = \sum_{i=1}^{q} \sum_{j=1}^{q} (j-1)c(i, j)$$

$$\text{var}_{x} = \sum_{i=1}^{q} \sum_{j=1}^{q} (i-1 - \mu_{x})^{2}c(i, j)$$

$$\text{var}_{y} = \sum_{i=1}^{q} \sum_{j=1}^{q} (j-1 - \mu_{y})^{2}c(i, j)$$

$$c_{x}(i) = \sum_{j=1}^{q} c(i, j)$$

$$c_{y}(j) = \sum_{i=1}^{q} c(i, j)$$

$$c_{x+y}(k) = \sum_{j=1}^{q} \sum_{l \in \{1, \ldots, q\} : i+j=k} c(i, j)$$

$$c_{x-y}(k) = \sum_{j=1}^{q} \sum_{l \in \{1, \ldots, q\} : i-j=k-1} c(i, j)$$

$$HXY = -\sum_{i=1}^{q} \sum_{j=1}^{q} c(i, j) \log c(i, j)$$

$$HX = -\sum_{i=1}^{q} c_{x}(i) \log (c_{x}(i))$$

$$HY = -\sum_{j=1}^{q} c_{y}(j) \log (c_{y}(j))$$

$$HXY1 = -\sum_{i=1}^{q} \sum_{j=1}^{q} c(i, j) \log (c_{x}(i)c_{y}(j))$$

$$HXY2 = -\sum_{i=1}^{q} \sum_{j=1}^{q} c_{x}(i)c_{y}(j) \log (c_{x}(i)c_{y}(j))$$

where $c_{x+y}(k)$ is defined for $k = 1, 2, ..., 2q - 1$ and
c_{x-y}(k) for $k = 1, ..., q$.

Haralick features, we considered in this paper follow:

entropy: $-\sum_{i=1}^{q} \sum_{j=1}^{q} c(i, j) \log c(i, j)$

**Texture contrast:** $\sum_{i=1}^{q} \sum_{j=1}^{q} |i - j| c(i, j)$

**Texture correlation:** $\sum_{i=1}^{q} \sum_{j=1}^{q} \frac{(i-1-\mu_{x})(j-1-\mu_{y})c(i, j)}{\sqrt{\text{var}_{x} \text{var}_{y}}}$

**Texture homogeneity:** $\sum_{i=1}^{q} \sum_{j=1}^{q} \frac{c(i, j)}{1+|i-j|}$

**Inverse difference moment:** $\sum_{i=1}^{q} \sum_{j=1, j \neq i}^{q} \frac{c(i, j)}{|i-j|}$

**Maximum probability:** $\max_{i=1, j=1, \ldots, q} c(i, j)$

**Uniformity of energy:** $\sum_{i=1}^{q} \sum_{j=1}^{q} c(i, j)^{2}$

**Contrast:** $\sum_{i=1}^{q} \sum_{j=1}^{q} (k-1)^{2}c_{x-y}(k)$

**Sum average:** $\sum_{k=1}^{2q-1} \sum_{i=1}^{q} \sum_{j=1}^{q} c_{x+y}(k)$

**Sum entropy:** $-\sum_{i=1}^{q} \sum_{j=1}^{q} c_{x+y}(k) \log (c_{x+y}(k))$

**Difference entropy:** $-\sum_{i=1}^{q} \sum_{j=1}^{q} c_{x-y}(k) \log (c_{x-y}(k))$

**Variance:** $\sum_{i=1}^{q} \sum_{j=1}^{q} (i-1-\mu_{x})^{2} c(i, j)$

**Information measure of correlation A:** $\frac{\text{H}(X) \text{H}(Y)}{\text{H}(X + Y)}$

**Information measure of correlation B:** $(1 - \exp(-2(HXY - HXY)))^{2}$

**Maximal correlation coefficient:**

The 2nd eigenvalue of matrix $Q$ given by its elements

$q(i, j) = \sum_{k=1}^{q} \frac{c(k,i)c(k,j)}{c_{x}(i)c_{y}(j)}$

The total number of Haralick texture features considered
is 15. In different papers [8, 2], more features can be
found. However, we found out that for our data, the addi-
tional features have the strong correlation with features al-
ready defined above. For several features among these
defined above, division by zero may occur. Such cases have
be NaN dealt with. For few features, defining 0 log 0 to be equal
to its limit 0 may help. In other cases, adding a very small
value to denominator is acceptable technical solution.

Haralick texture features presented here can be further
parametrised by three parameters. Those parameters are,
separation vector $\vec{s}$, quantization constant $q$ and win-
dow size $w$. We assume that medical data are isotropic,
so only absolute value of the separation vector $\vec{s}$ is im-
portant, not its direction. Co-occurrence vectors can be cal-
culated for all 6 directions in 3D space ("up", "down", "left",
"right", "forward", "backward") and average them together
(it is already suggested by Haralick in [8]). This approach
adds more data, what makes the co-occurrence matrix bet-
ter statistics of underlying texture.

3. Use of 3D Features for Image Segmentation

Texture features are statistics, which distinguish between
different types of image texture. In order to perform im-

age segmentation, another method have to be used, which makes the actual image segmentation using these features. The method described here uses database of 3D images which have known segmentation. Specifically, for every voxel of the 3D image, we know which type of tissue it belongs to. The segmentation algorithm learns the value of features for every type of tissue in consideration. This is called “learning phase” and it is described in subsection 3.1. Features are fitted to given parametrised model and for every tissue type, different set of parameters. It is why, this approach is also called, model-based. Segmentation of unknown image is done in “inference phase” as described in subsection 3.2. For every voxel, decision-making is done using parametrised models found in learning phase. The inference is based on maximum likelihood

3.1 Learning phase

We assume that there are \( m \) types of tissue indexed by \( t = 1, 3, \ldots, m \). Let voxel at coordinates \( \vec{v} \) belongs to tissue type \( t \). This will be denoted as \( M(\vec{v}) = t \). Feature vector \( f(\vec{v}) \) is assumed to be random variable with given conditional probability density function, conditioned by the value of \( M(\vec{v}) \). Then the the model for feature \( f(\vec{v}) \) is defined as:

\[
p(f(\vec{v})|M(\vec{v}) = t) = \sum_{i=1}^{n} \frac{\alpha_i(t)}{(2\pi)^{\frac{n}{2}}|C_i(t)|^{\frac{1}{2}}} \times \\
\times \exp \left[ -\frac{1}{2}(f(\vec{v}) - \mu_i(t))^T C_i^{-1}(t)(f(\vec{v}) - \mu_i(t)) \right]
\]

where \( p(f(\vec{v})) \) is multi-dimensional probability density function of the feature vector \( f(\vec{v}) \) from pixel in region with diagnosis \( t \). \( n \) is number of components of the mixture, \( \alpha_i(t), C_i(t), \mu_i(t) \), are unknown parameters of the Gaussian mixture, that are estimated by EM algorithm in learning step. Number \( d \) is dimension of the feature vector.

Probability density function (pdf) \( p(f(\vec{v})) \) is the model for feature vector \( f(\vec{v}) \). The goal of the learning phase is to find the estimate for the set of parameters \( \alpha_i(t), C_i(t), \mu_i(t) \), for given data \( f(\vec{v}) \) from the above-mentioned database of known diagnoses.

The parameter \( n \), which is the number of Gaussian pdf’s in the mixture, is taken arbitrarily. The choice of \( n \) does not affect performance of the algorithm, if sufficiently big value is selected. For our application, we used \( n = 7 \). Bigger values did not bring any significant improvement of the method.

3.2 Inference phase

The inference is done for every voxel in diagnosed image. The value of probability density function \( p(f(\vec{v})|M(\vec{v}) = t) \) is calculated for every image and for every diagnosis \( t \). As a result, for every feature vector \( f(\vec{v}) \), numbers \( p(f(\vec{v})|M(\vec{v}) = 1), p(f(\vec{v})|M(\vec{v}) =\)

\[\text{Figure 5. Heart (lighter) and liver region (darker) manually selected on the CT scan layer of the abdominal part of the human body. Illustrates correct segmentation for image in figure 1}\]

\[2), \ldots, p(f(\vec{v})|M(\vec{v}) = m) \] represent likelihood, and estimated diagnosis is found by maximising over all \( m \) diagnoses.

3.3 A note on merging results with different probabilistic methods

It is assumed, that the method described in this paper would be combined with another segmentation method, to make successful segmentation. As we prove in this paper, the information included in texture allows to segment an image. However, medical images can contain many other sources of information. Some of them have the probabilistic form. It means that the result of the other method have the form \( p_{OM}(M(\vec{v}) = t) \). We can use it as prior information for our method and posterior information will be given by Bayes formula:

\[
p(M(\vec{v}) = t) \propto p(f(\vec{v})|M(\vec{v}) = t)p_{OM}(M(\vec{v}) = t)
\]

Symbol \( \propto \) denotes proportionality to, which means, that proper normalisation constant needs to be calculated in order to get probability function in left-hand side of formula. Instead of maximising likelihood, result is obtained by maximising posterior probability function over all models.

As an example of good prior information, probabilistic atlas of organs can be taken.

4. Application for Medical CT Data Segmentation

We segmented the set of full abdomen images from 10 patients. Resolution was approximately \( 512 \times 512 \times 240 \). For all of them, the diagnosis was known. 8 patients have been put into the learning data set and two patients, were used
for testing. Fifteen Haralick texture features were used as described in section 2. In addition raw intensity value was used. Haralick co-occurrence texture features were used with window sizes $w = 2$ and $w = 4$ (note the definition of $w$ in 2). In all our experiments, the value of quantization constant $q = 8$. The absolute value of separation vector used was 1.

In order to evaluate texture-based segmentation only, no other form of post-processing was used. It would obviously improve segmentation, if we used the fact that organs are contiguous. However, what was contribution of texture feature segmentation method, and what was contribution of the other method. In practical application, combination of more methods would be beneficial. As described in section 3.3, results of this probabilistic method can be easily merged with results of another probabilistic method.

Figure 1 shows layer of the CT scan of abdominal part of the human body. It is only one of many layers of the 3D image. The goal in this case was segmentation of heart and liver (and the surrounding tissue). It is quite hard to distinguish liver and heart only from the gray level value (which is proportional to CT intensity) of the figure 1. Also there are many other types of tissue in abdominal cavity with the same gray level as liver and heart. Three types of tissue, were modelled: heart, liver, other tissue. In in figures 2 to 4, which show the value of one of features, the heart and liver region is already very well distinguishable. The gray level (which is proportional to the value of one feature), is different for the heart and liver region, which indicates substantial difference in texture of those two regions.

The result of segmentation is in the figure 6. For comparison, correct segmentation in the figure 5.

The second subject in the training set was used to detect and distinguish the liver and stomach regions. Because both regions had approximately same gray level (CT intensity), it was hard to see easily the difference in the original image (Figure 7). After calculating features and performing segmentation as described in section 3, the segmentation obtained, is in figure 9.
The extension of Haralick features was proposed, that calculates Haralick texture feature for every voxel of the original image. Let us note that they might not be correct from the texture point of view. From tables 1 and 2 We can see, that in both cases the two types of tissue are separated very well. There are only very few mis-detections between the two types of tissue. Some mis-detections with “other tissue” might be due to different texture in the border of given organ.

### 5. Conclusion and Further Research

The extension of Haralick features was proposed, that calculates Haralick texture feature for every voxel of the original image. The method was verified with the set of abdominal CT images of 10 subjects. Results were acceptable, considering that only described texture features and raw CT intensity value was used. In real applications, the texture only based method would not be practical, but suitable combination with probabilistic atlas of organs would be used. This is especially easy since result of the method is in form of probability of given organ, so Bayes formula gives straightforward way to combine it with another probability-based methods like probabilistic atlas. Also, practical segmentation applications need a post-processing, that would take into account the fact, that any organ is contiguous region.

In connection with model-based probabilistic segmentation algorithm, this makes the method usable for searching for the tissue with given texture (like tumours), without the need to select suspicious regions in advance by another method.

In further research, we would like to try to improve calculation of the local co-occurrence matrix Instead of simple summing over rectangular window, we would like to use different weighting functions over co-occurrences around the voxel of interest.

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