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Region Oriented 3D-Segmentation of NMR-Datasets: A Statistical Model-Based Approach

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ABSTRACT

We present a three-stage method for segmenting NMR-datasets of the head into 3D-regions corresponding to different brain matter classes, liquid containing structures, cranium, and background. Our technique works from the beginning with 3D-regions, whose internal 'grey' values as well as shapes are described by stochastic models. The first phase starts by assuming the entire dataset as consisting of only one region, and then recursively extracts those areas which are not compatible with this hypothesis. During this step, special emphasis is given to the problem of accurately locating the region surfaces. In the second stage, a Bayes classifier groups the regions into different categories, like brain matter, liquid, cranium, and background. Classification errors are corrected largely automatically during the third stage by applying simple knowledge about the topological relationships between the classes.

INTRODUCTION

The partitioning of medical 3D-datasets into regions corresponding to different tissue classes or to anatomical organs is a necessary prerequisite for various further processing stages of the data, e.g. for 3D-display of organs or for obtaining quantitative information [1] [2] [3] [4] [5] [6] [7]. The success or failure of these processing steps thus depends crucially on the performance of the segmentation algorithm by which the partition is generated.

A particularly complex task is the partitioning of datasets generated by nuclear magnetic resonance (NMR) imaging, since different objects of interest are generally not characterized by nonoverlapping ranges of their respective grey values\textsuperscript{*}. Thresholding, which can be used for separating bones, soft tissue and background in X-ray computer tomography, is therefore not adequate for NMR volume data, so that more sophisticated methods have to be used.

We describe a segmentation technique which is based on a statistical model of the NMR-dataset to be processed. In contrast to edge-based approaches (e.g. [7] [8]), our procedure is region oriented. The technique requires no preprocessing like (edge preserving) smoothing (cf. [3] [4]). In order to take into account properly the 3D-structure of the datasets, our technique works from the start with 3D-regions, whose textures and typical shapes are characterized by an appropriate stochastic model.

Our segmentation procedure consists of three stages: Firstly, the volume of original NMR-data is partitioned into a (large) number of homogeneous elementary regions (primitives, low level processing). These regions are then grouped to anatomical objects by a parametric classifier. In the final stage, possible misclassifications are eliminated by applying simple knowledge about the spatial relationship between the objects of interest.

Since only the first step of the procedure works directly on volume elements (voxels) whereas the remaining two stages are operating with regions, the accuracy in locating object surfaces is primarily

* The notion 'grey value' is used for the representation of the scalar or vectorial measured value of NMR-parameter(s) like $T_1$, $T_2$ in a slice.
determined by this first step (cf. e.g. [4], where low level processing is described as playing a key role for analysis). The main part of our paper will hence be devoted to a description of the initial partitioning.

THE INITIAL SEGMENTATION

The purpose of segmentation is to subdivide the data volume into homogeneous regions. A homogeneous region is one whose internal grey values are described by a stationary random process, of which the distribution is in turn characterized by parameters like region mean and variance.

We start by hypothesizing the complete data set to be homogeneous, that is, we assume the entire data volume as consisting of only one region. The basic idea of our approach is to extract those (threedimensional) areas from this volume which are not compatible with the one-region hypothesis (null hypothesis). Since the parameters of the marginal distribution for the grey values can be estimated from this region only conditioned on the null hypothesis, we can formulate explicitly the likelihood for the null hypothesis only. Thus, significance testing is the appropriate statistical tool for this inhomogeneity extraction [9] [10].

To be more specific, let us assume that global statistics, e.g. the sample mean, have been computed from all grey values of the initial region. To find locations which are not compatible with the null hypothesis, we search the whole region for voxels where local statistics - e.g. the local mean - deviate significantly from overall statistics. Those voxels where inhomogeneities occur are marked, and new regions are created by connected sets of these marked voxels. The result is a partition consisting of some major regions, a slice of which is depicted in Fig. 1. The individual global parameters for each of these regions can now be computed. This process of comparing local statistics against global ones, and the subsequent 3D-connected component analysis, are termed object detection.

The rather coarse partition of Fig. 1 is refined by recursively applying the inhomogeneity extraction to each newly detected region. The finer the partition becomes, the more the process 'learns' about the composition underlying the dataset, and hence, the more 'delicate' are the inhomogeneities which can be revealed. The segmentation process comes to an end when no more significant inhomogeneities can be detected. This is usually the case after 4 iterations.

There are, however, two disadvantages coupled with the segmentation scheme as far as it is described above, which can be revealed by a close examination of Fig. 1: Firstly, some region borders (surfaces, in fact) are misplaced from their 'true' locations. This is due to the fact that the local test statistics for each voxel have to be computed from a finite neighbourhood. Determining the size of this neighbourhood involves a trade-off between the 'reliability' of the significance test, and spatial resolution. The larger this neighbourhood is, the more reliably can local statistical parameters be estimated, but also, the more severe is the blurring effect introduced.

Secondly, region boundaries also might tend to be somewhat noisy between regions which differ only slightly in their respective statistics. The reason for this is that we have so far only considered the region internal grey values, but not the region shapes.

As already pointed out in the introduction, the impact of misplaced and noisy region surfaces on the final segmentation result might be rather serious, since they cannot be corrected during later processing stages. Thus, to locate the region surfaces accurately — as far as this is permitted by partial volume artifacts — we apply after object detection a procedure termed surface relaxation. This relaxation compensates possible smearing effects by examining for each voxel situated at a region border whether it fits better to one of the neighbouring regions. If this turns out to be the case, the voxel is reassigned accordingly. Since the global statistics of all regions involved are known at this stage, this procedure is robust, so that we can afford to consider single voxels, avoiding smearing measurement windows.

By working on border voxels, this procedure predominantly influences the shapes of regions by altering their surfaces. We have thus incorporated here a model for region shapes, which tends to smooth region
surfaces in statistically 'uncertain' areas. After application of surface relaxation the partition of Fig. 2 emerges.

The next iteration step of the segmentation can now be started by renewed object detection. The flow chart of the algorithm is given in Fig. 3. Object detection and surface relaxation, as well as our stochastic model for the datasets, shall now be discussed in detail.

**THE STOCHASTIC MODEL FOR NMR-DATASETS**

We consider the volume covered by the 3D-dataset \( Y = \{y_{ijk}\} \) as a composition of 3D-regions \( R_n \). The grey values inside each individual region are supposed to be samples from a spatially uncorrelated Gaussian random field, which is described by its mean \( m_n \) and variance \( \sigma_n^2 \) (cf. [11]). To represent the partition \( Q \), that is, the spatial ensemble of regions \( R_n \), a label \( q_{ijk} \) is assigned to each voxel \((i,j,k)\). The underlying 'hidden' process which governs the composition of the label array is modeled by a threedimensional Gibbs/Markov random field (cf. [11] [12] [13] for the 2D-case). As will be shown later, this enables us to favour the development of partitions consisting of smoothly shaped regions during the process.

**OBJECT DETECTION**

Let a partition \( Q \) for our NMR-dataset \( Y \) be given. This might be the initial one-region partition, or one of the partitions emerging during the recursive process. For each region, we estimate the global mean and global variance by the Maximum Likelihood estimates

\[
\hat{m}_n = \frac{1}{N_n} \cdot \sum_{y_{ijk} \in R_n} y_{ijk}, \quad \hat{\sigma}_n^2 = \left( \frac{1}{N_n} \cdot \sum_{y_{ijk} \in R_n} y_{ijk}^2 \right) - \hat{m}_n^2
\]

(1)

where \( N_n \) denotes the size of region \( R_n \). The purpose of object detection is to locate those areas inside each region \( R_n \) which are unlikely to stem from the distribution \( N(\hat{m}_n, \hat{\sigma}_n) \). Two different features which can be used to test the homogeneity hypothesis are described in the following.

**Testing the local mean**

First, an error dataset \( E = \{e_{ijk}\} \) is computed by normalizing the region internal grey values according to
with \( n \) indicating the region \( R_n \) to which voxel \((i,j,k)\) is assigned. On the assumption that the null hypothesis \( H_0 \) is correct at \((i,j,k)\), \( e_{ijk} \) obeys a zero mean Gaussian distribution \( N(0,1) \) with unit variance. Inside a small window of dimension \( d \times d \) which slides through each error slice \( k \), we compute the local average

\[
\mu_{ijk} = \frac{1}{d^2} \sum_{\text{window}} e_{xyz}
\]

and assign it to the center voxel \((i,j,k)\).

Assuming that no inhomogeneity is present within the window, \( \mu_{ijk} \) comes from a zero mean Gaussian distribution \( N(0,d^{-1}) \) with variance \( d^{-2} \), that is

\[
p(\mu_{ijk}|H_0) = \frac{d}{\sqrt{2\pi}} \cdot \exp(-\frac{d^2}{2} \cdot \mu_{ijk}^2)
\]

With this distribution known, we define a positive threshold \( t \) such that the event of \( |\mu_{ijk}| \) exceeding \( t \) is an unlikely one \([10 \, p.229]\). The probability \( P(|\mu_{ijk}| > t | H_0) \) of the unlikely event is the significance level \( s \) of the test. In practice, the local average is compared against \( t \) and \(-t\), with \( t \) determined such that \( P(\mu_{ijk} > t | H_0) = P(\mu_{ijk} < -t | H_0) = s/2 \) (see Fig. 4). Each location \((i,j,k)\) with \( |\mu_{ijk}| > t \) is marked as an inhomogeneity. In doing so, we use a positive mark if \( \mu_{ijk} > t \), and a negative one if \( \mu_{ijk} < -t \). New regions are formed by performing a 3D-connected component analysis on these marked voxels. The connected component analysis is carried out based on a threedimensional first order neighbourhood (see Fig. 5, and cf. \([14 \, p.42]\)).

Experimentally, a significance level between \( s = 10^{-5} \) and \( s = 10^{-4} \) in connection with a window size of \( d = 5 \) was found to give good results (Fig. 1). It is noteworthy that the significance testing can be performed in parallel.

**Object detection using a sufficient statistic**

So far, we have only tested the local mean to find out whether the transformed random variable \( e_{ijk} \) originates from the distribution \( p(e_{ijk}|H_0) = N(0,1) \). One could now assume a case where \( e_{ijk} \) obeys another zero mean Gaussian distribution \( N(0,\sigma) \) with a variance \( \sigma^2 \) other than one. Using only the local average as feature would not be sufficient to make a decision, so that one would have to test the variance as a second feature, too. However, regarding

\[
p(e_{ijk}|H_0) = N(0,1) = \frac{1}{\sqrt{2\pi}} \cdot \exp(-\frac{e_{ij}^2}{2})
\]

which depends only on \( e_{ijk}^2 \), it turns out that it should be sufficient to derive a test for \( e_{ijk}^2 \) (cf. \([10 \, p.73]\)). Hence, we alter the test described in the previous section insofar as we compute the square sum of normalized grey values inside our sliding window, that is

\[
e_{ijk}^2 = \sum_{\text{window}} e_{xyz}^2
\]

which, under the assumption of zero mean, is proportional to the local variance estimate of \( e_{ijk} \). Assuming the null hypothesis is true, \( e_{ijk}^2 \) obeys a \( \chi^2 \)-distribution with as many degrees of freedom as there are...
voxels inside the local test window. The significance test is carried out as illustrated in Fig. 6: After defining a significance level $s$, we compute a lower threshold $t_1$ and an upper threshold $t_u$ according to $P(\epsilon_{ijk}^2 > t_u | H_0) = P(\epsilon_{ijk}^2 < t_1) = s/2$. Marking the voxels, and the subsequent 3D-connected component analysis are carried out as already described.

As already pointed out, a partition $Q_0$ which emerges when object detection has been applied can be refined with respect to the accuracy of the localization of the 3D-region borders (surfaces). This is carried out by altering $Q_0$ until it matches the given data set $Y$ best. This 'best match' is assessed based on the Maximum a posteriori criterion, that is, we try to maximize the a posteriori density $p(Q|Y)$ by an appropriately modified partition $Q$ (cf. e.g. [15] [16]). This posterior density can be split into the product

$$p(Q|Y) = \text{const} \cdot p(Y|Q) \cdot p(Q)$$

where $p(Y|Q)$ denotes the likelihood of the data set for a specific partition $Q$, and $p(Q)$ the a priori density for the partition. Both these expressions shall now be derived in detail.

Let $\bar{y}_n$ denote the vector whose components are the grey values $y_{ijk}$ inside region $R_n$. Since we model these components as being generated by a 'white' Gaussian process with mean $m_n$ and variance $\sigma_n^2$, we obtain for the likelihood of $\bar{y}_n$

$$p(\bar{y}_n|m_n, \sigma_n^2) = \left(\sqrt{2\pi\sigma_n^2}\right)^{-N_n} \cdot \exp\left\{ -\frac{1}{2\sigma_n^2} \sum_{y_{ijk} \in R_n} (y_{ijk} - m_n)^2 \right\}$$

Replacing the unknown mean and variance by equation (1) we obtain

$$p(\bar{y}_n|m_n, \hat{\sigma}_n^2) = \left(\sqrt{2\pi\hat{\sigma}_n^2}\right)^{-N_n} \cdot \exp\left( -\frac{N_n}{2} \right)$$

* Strictly speaking, this is only true if the estimates of region mean and variance in equation (2) are replaced by the true parameters. However, since these estimates are derived from an entirety much larger than the small local window, we view them as sufficiently close to the unknown mean and variance.
The likelihood \( p(Y|Q) \) is then given by
\[
p(Y|Q) = \prod_{\{n\}} p(\bar{y}_n, \bar{m}_n, \bar{\sigma}_n^2)
\]
with the product comprising all regions of the partition \( Q \).

The prior density \( p(Q) \) can be used to assign different probabilities of occurrence to different partitions. In order to prefer partitions consisting of regions with locally smooth surfaces, we have to find a probability measure related to surface smoothness such that a segmentation \( Q \) consisting of smoothly shaped regions is more likely to occur than other ones. This is possible by modelling the label array \( Q \) as a sample of a three-dimensional second order Gibbs/Markov random field (cf. for the 2D-case [12] [13] [17]). To give an expression for the distribution \( p(Q) \), we have to consider pairs of adjacent voxels, which are termed cliques. The different types of cliques which occur on the 3D-lattice are depicted in Fig. 7. These voxel pairs may either lie completely within a region, or they are situated across a region border. The border cliques are characterized by their voxels carrying different labels, and are thus termed 'inhomogeneous cliques', whereas voxel pairs inside regions are referred to as 'homogeneous cliques'.

To each clique \( c_i \) a potential \( V(c_i) \) is assigned, which depends only on the labels of the clique’s voxels. In order to measure the smoothness of region borders, we define the potentials as follows:
- \( V(c_i) = A, A > 0 \) for all inhomogeneous cliques oriented parallel to the \( i \)- or \( j \)-axis (both voxels belonging to the same slice, types \( a, b \) in Fig. 7).
- \( V(c_i) = C, C > 0 \) for all diagonally oriented inhomogeneous cliques with both voxels belonging to the same slice (types \( c, d \)).
- \( V(c_i) = E, E > 0 \) for all inhomogeneous cliques oriented parallel to the \( k \)-axis (type \( e \) in Fig. 7, both voxels belong to different slices).
- \( V(c_i) = F, F > 0 \) for all diagonally oriented inhomogeneous cliques with both voxels belonging to two different slices (types \( f, g, h, i \) in Fig. 7).
- \( V(c_i) = 0 \) for all homogeneous cliques.

Modeling the partition as being generated by the above mentioned Gibbs random field leads to the following expression for its distribution \( p(Q) \):
\[
p(Q) = \text{const} \cdot \exp\left\{-n_A A + n_C C + n_E E + n_F F\right\}
\]
with \( n_A, n_C, n_E, \) and \( n_F \) denoting the numbers of inhomogeneous cliques occurring in \( Q \) with potentials \( A, C, E, \) and \( F \), respectively.

This a priori density exhibits the desired properties: The smoother the region surfaces are in a partition, the lower are the numbers that \( n_A, n_C, n_E, \) and \( n_F \) of border voxel pairs (inhomogeneous cliques) occurring in that partition, and hence, the higher is the prior probability associated with that partition.

The different clique potentials shall reflect the interaction between the two voxels belonging to a clique, which is the lower, the farther the two voxel centers are apart. We relate the potentials as follows:
\[
C = \frac{A}{2}, \quad E = \frac{A}{r^2}, \quad F = \frac{A}{r^2 + 1}
\]
where \( r \) is the ratio between intra-slice resolution and inter-slice resolution. The potentials are thus reciprocally proportional to the squared distance of the voxel centers of a clique. If \( r = 1 \), the elongated voxels in Fig. 7 become cube-shaped, and we have \( A = E, \) and \( C = F = A/2 \).

Combining equations (9),(10),(11) leads to an explicit expression of equation (7), so that we can now discuss the implementation of the algorithm.
Implementation

Modifying a partition $Q_0$ is carried out by a deterministic relaxation procedure: The whole data volume is scanned several times, with the scan direction being altered for every new scan. Whenever a border voxel is encountered, its label is tentatively replaced by the label(s) of the region(s) adjacent to it (maximal 6, see the neighbourhood of Fig. 5). Criterion (7) is recomputed for each replacement, and the label which turns out as the optimal one is assigned. In case the voxel's 'old' label is the best one, it is kept. If a label reassignment is carried out, the region parameters of the two involved regions are updated accordingly (asynchronous updating). This relaxation converges to a local maximum of (7). In practice, we terminate the relaxation when the average number of label changes per slice falls below a prespecified threshold, e.g. 300.

This inherently sequential procedure can be made parallel by 'synchronous updating', that is, region parameters are updated whenever a scan is completed.

It is important to note that recomputing (7) for each tentative replacement is considerably simplified by the strictly local one-voxel operations. The likelihood $p(Y|Q)$ of equation (10) can be decomposed into the term $p(\hat{Y}_k|\hat{m}_k, \hat{\alpha}_k^2) \cdot p(\hat{Y}_i|\hat{m}_i, \hat{\alpha}_i^2)$ corresponding to the two regions $R_k, R_i$ affected by the label replacing, and the 'rest' term $\prod_{n \neq k,i} p(\hat{Y}_n|\hat{m}_n, \hat{\alpha}_n^2)$ which is not affected.

For the evaluation of $p(Q)$, we note that replacing a voxel's label changes the potentials of only those voxel pairs (cliques) to which the considered voxel belongs (18 cliques for a second order 3D-Gibbs random field, see Fig. 8). Thus, the best label as specified by equations (7),(9),(10),(11) can be found without much computational effort. The main difference of this approach to Besag's ICM method [16] is that we only consider surface voxels, and further reduce the solution space by only allowing the labels of adjacent regions for a border voxel. Moreover, the classes of [16] are not necessarily contiguous, whereas our regions are.

Fig. 7 : Clique types for the Gibbs model

Fig. 8 : The 18 cliques, to which the shaded voxel belongs
THE DESCRIBED PARTITIONING ALGORITHM SUBDIVIDES THE DATA VOLUME INTO 3D-REGIONS (Fig. 9) WHOSE INTERNAL GREY VALUES ARE CHARACTERIZED BY STATIONARY RANDOM PROCESSES, THAT IS, BY PARAMETERS LIKE REGION MEAN AND VARIANCE (OR STANDARD DEVIATION). FOR GROUPING THESE REGIONS TO MEANINGFUL CLASSES, WE HENCE USE A BAYES RISK-MINIMIZING QUADRATIC GAUSSIAN CLASSIFIER [10] WITH THESE REGION PARAMETERS AS FEATURES. THIS ENABLES REGION CLASSIFICATION ACCORDING TO THE FIVE CLASSES WHITE BRAIN MATTER, GREY MATTER, LIQUID, SKIN AND BONE (CRANIUM), AND NON-NMR-SENSITIVE BACKGROUND.

THE CLASSIFIER IS TRAINED ON A FEW (2D)-SLICES OF THE DATA VOLUME BY STORING FOR EACH REGION OUT OF THE TRAINING SET THE INTERACTIVELY DEFINED CLASS LABEL \(i, i = 1 \ldots 5\). FOR EACH CLASS, MEAN AND VARIANCE OF THE TWO FEATURES CAN NOW BE ESTIMATED. THAT IS, WE ESTIMATE MEAN \(\bar{m}_i\) AND VARIANCE \(\text{var}_i(\bar{m})\) OF THE FEATURE 'REGION MEAN' FOR EACH CLASS \(i, i = 1 \ldots 5\) AND LIKewise \(\sigma_i\) AND \(\text{var}_i(\sigma)\) FOR THE FEATURE 'REGION STANDARD DEVIATION'. FURTHERMORE, THE PRIOR PROBABILITIES \(P(\omega_i)\) OF THE CLASSES ARE ESTIMATED. ASSUMING THE FEATURES AS INDEPENDENT [18 P.194] AND GAUSSIAN DISTRIBUTED, THE DISCRIMINANT FUNCTIONS ARE FOR \(i = 1 \ldots 5\) GIVEN BY

\[
g_i(\bar{m}, \sigma) = -\frac{1}{2} \ln(\text{var}_i(\bar{m}) \cdot \text{var}_i(\sigma)) - \frac{(\bar{m}_n - \bar{m}_i)^2}{2 \cdot \text{var}_i(\bar{m})} - \frac{(\sigma_n - \sigma_i)^2}{2 \cdot \text{var}_i(\sigma)} + \ln P(\omega_i) + \ln C_i
\]

\(C_i\) IS A COST TERM ASSIGNING INCREASED PENALTY IF A CLASSIFICATION ERROR IS MADE GIVEN THE TRUE CLASS \(i\) [CF. 19 CHAPTER 2]. SINCE OUR MAIN AIM IS TO RECOGNIZE AREAS BELONGING TO THE BRAIN, WE CHOSE \(C_i > 1\) FOR THE CLASSES WHITE MATTER AND GREY MATTER, AND \(C_i = 1\) FOR ALL OTHER CLASSES. EXPERIMENTALLY, \(C_i = 13\) FOR BRAIN MATTER TURNED OUT TO GIVE THE BEST CLASSIFICATION RESULTS. THE TRAINED CLASSIFIER MAY BE USED FOR NMR-DATA ACQUIRED WITH A SIMILAR MACHINE ADJUSTMENT AS THE TRAINING SET.

CORRECTION OF CLASSIFICATION ERRORS

DEPENDING ON THE TYPE OF THE INPUT DATA TO BE PROCESSED, THERE MAY STILL OCCUR SOME MISCLASSIFICATIONS. FOR INSTANCE, IN SCALAR \(T_2\)-WEIGHTED DATA SETS OF THE HEAD, THE EYES ARE USUALLY IN FEATURE SPACE NOT SEPARABLE FROM BRAIN MATTER, AND IN \(T_1\)-WEIGHTED DATA, PARAMETER DISTRIBUTIONS OF BRAIN MATTER OR CSF AND TISSUES SURROUNDING THE BRAIN CONSIDERABLY OVERLAP. IN BOTH CASES, REGIONS LYING OUTSIDE THE 'TRUE' BRAIN ARE ERRONEOUSLY CLASSIFIED AS BRAIN. AS LONG AS THESE FALSELY CLASSIFIED REGIONS ARE NOT CONNECTED TO CORRECTLY LABELED BRAIN REGIONS, THEY CAN BE CORRECTED AUTOMATICALLY USING SIMPLE KNOWLEDGE ABOUT THE SPATIAL RELATIONSHIP OF THE DIFFERENT CLASSES, E.G. BY RELABELING SMALL 'BRAIN' REGIONS SURROUNDED BY OTHER CLASSES. A SLICE OF A FINAL RESULT IS GIVEN IN FIG. 10.

RESULTS

THE DESCRIBED METHOD HAS BEEN APPLIED TO SEVERAL NMR-DATASETS CONSISTING OF AXIAL SLICES OF THE HEAD. FIGS. 1, 2, 9, 10 AND 11 HAVE BEEN COMPUTED FROM A \(T_2\)-WEIGHTED SEQUENCE CONSISTING OF 64 SLICES, WITH AN INTER-SLICE DISTANCE OF 2mm. FIGS. 12, 13, 14, AND 15 WERE GENERATED FROM A 128-SLICE SEQUENCE, AND FIG. 16 FROM A 112-SLICE SEQUENCE, EACH WITH 1.2mm INTER-SLICE RESOLUTION. THE SLICE SIZE WAS 256 \(\times\) 256 VOXELS. THE INITIAL SEGMENTATION COMPRISED 4 ITERATIONS. SURFACE RELAXATION WAS PERFORMED TWICE AFTER EACH OBJECT DETECTION, FIRST WITH RATHER HIGH VALUES FOR THE POTENTIALS \(A \approx 5\) IN ORDER TO ELIMINATE SPECKLES WHICH DIFFER ONLY SLIGHTLY FROM THEIR SURROUNDINGS, AND THEN WITH A REDUCED INFLUENCE OF THE SHAPE MODEL \(A \approx 0.7\). FOR EACH DATASET, THE CLASSIFIER HAS BEEN TRAINED ON 3 SLICES. APART FROM CLASSIFIER TRAINING, MANUAL INTERACTION WAS ONLY NECESSARY IN EYE-LEVEL SLICES TO CORRECT MISCLASSIFICATIONS IN THE AREA OF THE ORBITAL CAVITIES (CF. [7]) WHICH COULD NOT BE ADJUSTED AUTOMATICALLY.

Fig. 9: (Over-)segmented slice before region classification

Fig. 10: Slice of the final segmentation after classification and correction

Fig. 11: 3D-display of the brain surface, computed from 64 slices of the $T_2$-weighted sequence

Fig. 12: Slice 37 of a dataset consisting of 126 slices, final segmentation result
Fig. 13: Slice 54 of the 126-slice-dataset, final segmentation result

Fig. 14: 3D-image computed from the segmented dataset, with skin and cranium removed above eye level

Fig. 15: Brain surface as generated from the segmented dataset

Fig. 16: 3D-image of a head generated from 112 slices, opened by manipulations offered by the graphics software
CONCLUSIONS

We have developed a region based 3-step procedure for 3D-segmentation of NMR-datasets of the head. Our main concern was the initial partitioning algorithm, which operates on voxels and provides the elementary regions for subsequent steps to proceed with. The special importance of accurately localizing the region borders during the first step is reflected in the subalgorithm surface relaxation. The price for the robustness of the approach is increased computational effort, when compared to edge based segmentation methods. However, we point out that object detection as well as surface relaxation can be performed in parallel. Furthermore, a reduction of the computational demands might be possible by replacing the one-region-partition, with which we start, by a partition which has been obtained by simple grey level thresholding (slicing). This partition usually exhibits considerable irregularities such as spotty or highly wriggled regions. It is first subjected to a surface relaxation, before one or two iterations of Fig. 3 are applied. The required thresholds can be determined by a histogram mode analysis, or by a voxel classification.

A small amount of human interaction was required to correct classification errors which could not be adjusted automatically. It could be reduced by using multispectral data, or by integrating the segmentation technique as low-level part into a non-sequential knowledge-based control structure, e.g. of [4], which enables back tracking.

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REFERENCES


