MR Image Evaluation For Intensity Group Cluster Segmentation Of T1 And T2 Weighted Axial Sliced Section

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Citation

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Abstract

Segmentation of T1 and T2 weighted axial sliced section involves several stages, which are Image Enhancement, Feature Extraction and Classification. All the stages are not always necessary and sometimes segmentation can some times lead directly to specific diagnoses. Image enhancement is capable of improving the image appearance, (e.g., removal of noise, contrast stretching, etc) feature extraction emphasizes regions of interest, (e.g., emphasizing borders) segmentation separates emphasized structures from background, and classification recognizes/classifies the diagnosis.

Segmentation of medical imaging is a challenging task due to the complexity of the images, as well as to the absence of models of the anatomy that fully capture the possible deformations in each structure. Brain is a particularly complex structure, and its segmentation is an important step for derivation of computerized anatomical MR image, as well as pre- and intra-operative guidance for therapeutic intervention.

In this study we will evaluate the intensity of two MR sequences known as T1 and T2 weighted images in axial sliced section. Intensity group clustering algorithms is proposed to achieve further diagnosis for brain MR images, which has been hardly studied. This subjective study is to evaluate the clustering group intensity in order to obtain the best diagnosis as well as better detection for the suspected cases.

INTRODUCTION

The objects to be segmented from medical imaging are actual anatomical structures, which are often non rigid and complex in shape, and it exhibits considerable variability from one person to another. Combined with the absence of explicit shape models that capture the deformations in anatomy, it makes the segmentation task challenging. Magnetic resonance images are further complicated due to its limitations in the imaging equipment, like inhomogeneities in the receiver or transmitter coils which, leads to a non-linear gain artifact in the images, and large differences in magnetic susceptibilities of adjacent tissue leads to distortion of the gradient magnetic field, and hence a spatial susceptibility artifact in the images. In addition, the signal is degraded by the motion artifacts that may appear in the images due to movement of the subject and blood vessel during the scan.

The methods proposed include feature extraction, gray scale image segmentation, multispectral segmentation and clustering methods for anatomical images with additional recent efforts directed toward the mapping of functional metrics MR image (T1and T2) to provide locations of important functional regions of the brain as required for optimal surgical planning.

Other applications of MR image segmentation includes the diagnosis of brain trauma where white matter lesions, a signature of traumatic brain injury, may potentially be identified in moderate and possibly mild cases. These methods, in turn, may require correlation of anatomical images with functional metrics to provide sensitive measurements of brain injury.

MRI segmentation methods have also been useful in the diagnostic imaging of multiple sclerosis [$_1$], including the detection of lesions [$_2$], and the quantization of lesion volume using multispectral methods [$_3$].

In order to understand the issues in medical image segmentation, in contrast with segmentation of, say, images of indoor environments, which are the kind of images with which general purpose visual segmentation systems deal, we

need an understanding of the salient characteristics of medical images.

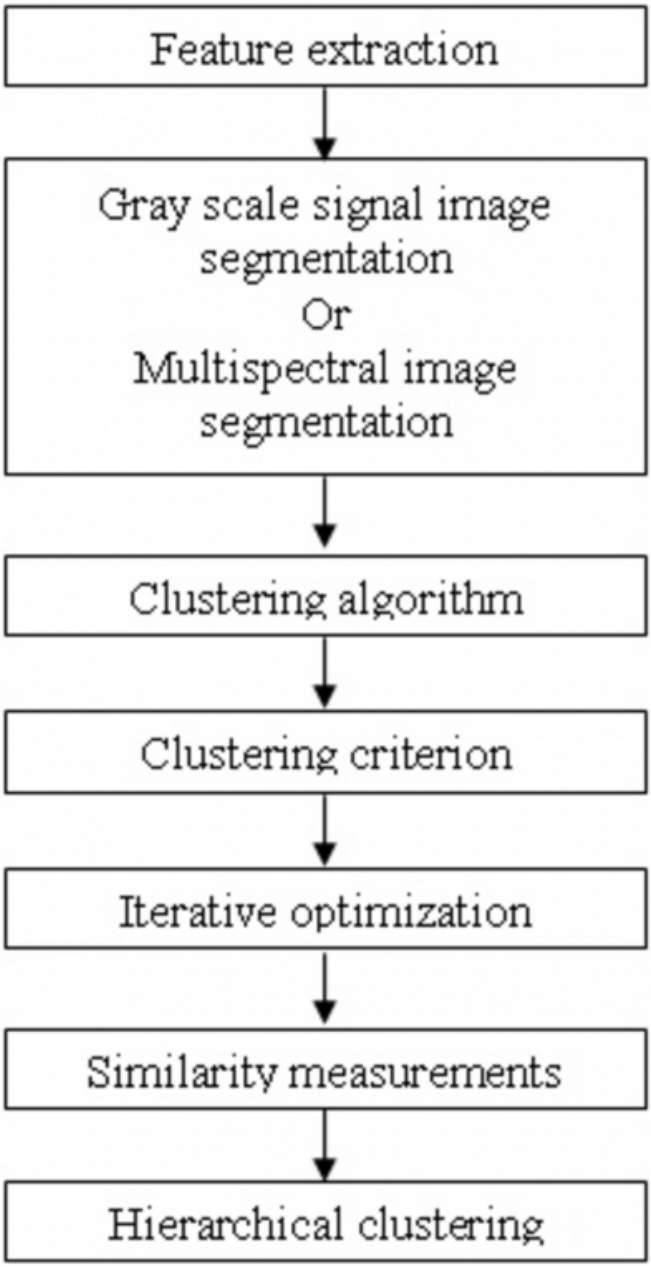
The application of our clustering algorithm is to map and identify important brain structures, in which it is important in navigating brain surgery. Contrast materials [4] have been suggested to provide better tissue specification and to identify actively the tissue distribution. Hence, segmentation methods need to include these additional image data sets. However in this study segmentation involving contract evaluation was not included. A similar progression of segmentation methods is evolving for the planning of surgical procedures primarily in neurological investigations [5], surgery simulations [6][7], or the actual implementation of surgery in the operating suite where both normal tissues and the localization of the lesion or mass needs to be accurately identified.

SEGMENTATION OF MR IMAGES

MR segmentation can be roughly divided into two categories: a single image segmentation, where a single 2D or 3D gray scale image is used, and multi-spectral image segmentation where multiple MR images with different gray scale contrasts are available.

Figure 1

Figure 1: proposed segmentation algorithm flow



FEATURE EXTRACTION

Segmentation of MR images is based on sets of features that can be extracted from the images, such as pixel intensities, which in return can be used to calculate other features such as edges and texture. Rather than using all the information in the images at once, feature extraction and selection breaks down the problem of segmentation to the grouping of feature vectors [8]. Selection of good feature is the key to successful segmentation [9]. The focus of the paper is not feature extraction, therefore simple but effective feature extraction method using entropy measures.

GRAY SCALE SINGLE IMAGE SEGMENTATION

The most intuitive approach to segmentation is global thresholding. One common difficulty with this approach is determining the value of the thresholds. Knowledge guided thresholding methods, where global thresholds are determined based on a goodness function describing the separation of background, skull and brain have been reported [3] [10]. The method is limited, and successful application for clinical use hindered by the variability of anatomy and MR data.

Combination with morphological [2] filtering is another method and boundary tracing [11], where the operator clicks on a pixel in a region to be outlined and the method then finds the boundary starting from that point. It is usually restricted to segmentation of large, well defined structures, but not tissue types.

Seed growing methods are also reported [12], where the segmentation requires an operator to empirically select seeds and thresholds. Pixels around the seed are examined, and included in the region if they are within the thresholds. Each added pixel then becomes a new seed.

MULTISPECTRAL SEGMENTATION

Supervised methods require a user supplied training set, usually found by drawing regions of interest on the images. Using maximum likelihood methods where multivariate Gaussian distributions are assumed [10] [13], statistics are calculated like mean and covariance matrices. The remaining pixels are then classified by calculating the likelihood of each tissue class, and picking the tissue type with the highest probability. Parametric methods are useful when the feature distributions for different classes are well known, which is not necessarily the case for MR images. k nearest neighborhood (KNN) has given superior results both in terms of accuracy and reproducibility compared to parametric methods [14]. Artificial neural networks also are commonly used [14] [15].

All supervised methods are operator dependent. Inter- and intra-operator variability has been measured and shown to be relatively large [15]. Because of this reason unsupervised methods may be preferred from a viewpoint of reproducibility.

CLUSTERING ALGORITHMS

Clustering [16] is an unsupervised way of data grouping using a given measures of similarity. Clustering algorithms attempt to organize unlabeled feature vectors into clusters or “natural groups” such as samples within a cluster are more similar to each other than to samples belonging to different clusters. Since there is no information given about the underlying data structure or the number of clusters, there is no single solution to clustering, neither is there a single similarity measure to differentiate all clusters, for this reason there is no theory, which describes clustering uniquely.

Pattern classification can be divided into two areas depending on the external knowledge about the input data. If we know the labels of our input data, the pattern recognition problem is considered supervised [17]. Otherwise the problem is called unsupervised. As pattern recognition studied, statistical pattern recognition is one of the chosen method. There are several ways of handling the problem of pattern recognition if the labels are given a priori. Since we know the labels, the problem reduces to finding features of the data set with the known labels, and to build a classifier using these features. The Bayes' rule shows how to calculate the posteriori probability from a priori probability. Assume that we know that a priori probabilities P (C_i) and the conditional densities P ($x \mid C_i$). When we measure x, we can calculate the posteriori probability P ($C_i \mid x$) as shown

Figure 2

$$P(C_i \mid x) = \frac{p(x \mid c_i)P(c_i)}{p(x)}$$

where

$$p(x) = \sum_{i=1}^{N} p(x \mid c_i)P(c_i)$$

The clustering problem is not well defined unless the resulting clusters are required to have certain properties. The fundamental problem in clustering is how to choose these properties. Once we have a suitable definition of a cluster, it is possible to evaluate the validity of the resulting clustering using standard statistical validation procedures.

There are two basic approaches to clustering, which are called parametric and nonparametric approaches. If the purpose of unsupervised learning is data description, then we can assume a predefined distribution function for the data set, and calculate the sufficient statistics, which will describe the data set in a compact way. For example, if we assume that the data set comes from a normal distribution N (M, ∑), which is defined as

Figure 3

$$N|_X(M,\Sigma) = \frac{1}{(2\pi)^{n/2}|\Sigma|^{1/2}}\exp(-\frac{1}{2}(X-M)^T\Sigma^{-1}(X-M))$$

The sufficient statistics are the sample mean M=E {X} and the sample covariance matrix ∑=E {XX^T}, which will describe the distribution perfectly. Unfortunately, if the data set is not distributed according to our choice, then the statistics can be very misleading.

Another approach to clustering is to group the data set into groups of points, which has strong internal similarities [18]. To measure the similarities we use a criterion function and seek the grouping that finds the extreme point of the criterion function.

CLUSTERING CRITERION

To define the clustering problem as follow, assume that we have N samples, i.e. $x_1...x_N$ we assume that the samples are not random variables, since the samples are fixed by the clustering algorithm [9]. The problem can be defined as to place each sample into one of L clusters, $w_i...w_i$ where L is assumed to be given. The cluster k to which the i^{th} sample is assigned is denoted by $w_{k(i)}$, where k (i) is an integer between 1...L, and i = 1...N.

A clustering C is a vector made of $w_{k(i)}$ and X is a vector made up x_i 's, that is,

Figure 4

$$C=[w_{k(1)}\dots w_{k(N)}]^T$$

and

$$X=[x_i\dots x_N]$$

The clustering criterion J is a function of C and X. and can be written as,

Figure 5

$$J(C,X)=J(w_{k(1)}\dots w_{k(N)};x_1\dots x_N)$$

The best clustering C should satisfy

Figure 6

$$J(C_0,X)=min|_C \text{ or } max|_C(J(C,X))$$

Depending on the criterion, only minimization will be considered, since maximization can always be converted to minimization.

ITERATIVE OPTIMIZATION

The input data are finite, therefore there are only a finite number of possible partitions. The clustering criterion can always be solved by exhaustive enumeration. However, in practice such an approach is not feasible, since the number of iterations will grow exponentially with the number of clusters and sample size where the number of different solutions are given approximately by $L^N...L!$

The basic idea in iterative-optimization is to find an initial partition and to move samples from one group to another as such a move will improve the value of the criterion function [15].

In general this procedure will guarantee local optimization. Different initial points will give different results. The simplicity of the method usually overcomes the limitations in most problems.

SIMILARITY MEASURES

In order to apply the clustering algorithm, we have to define how we will measure similarity between samples. The most obvious measurement of the similarity between two samples is the distance between them. The Lp norm is the generalized distance measure where p=2 corresponds to the Euclidean distance [20]. The Lp norm between two vectors of size N, is given as

Figure 7

$$L_p(x_1, x_2) = \left(\sum_{i=1}^{N} (x_1(i) - x_2(i))^p \right)^{\frac{1}{p}}$$

If this distance were a good measurement of similarity, then we would expect the distance between samples in the same cluster to be significantly less than the distance between samples in different clusters.

Another way to measure the similarity between two vectors is the normalized inner product, which is given as

Figure 8

$$s(x_1, x_2) = \frac{x_1^T x_2}{\| x_1 \| \| x_2 \|}$$

This measure is basically the angle between two vectors.

HIERARCHICAL CLUSTERING

To consider a sequence of partitions of the N samples into C clusters, first partition into N clusters, where each cluster contains exactly one sample. The next iteration is a partition into N-1 clusters, until all samples form one cluster. If the sequence has the property that whenever two samples are in the same cluster at some level, they remain together at all higher levels, then the sequence is called a hierarchical clustering. It should be noted that the clustering can be done in reverse order, that is, first all samples form a single cluster, and at each iteration more clusters are generated.

In order to combine or divide the clusters, measure the similarity in the clusters and dissimilarity between clusters commonly used distance measures [21] are as follows:

Figure 9

$$D_{\min}(C_1, C_2) = \min \| x_1 - x_2 \|$$

$$D_{\max}(C_1, C_2) = \max \| x_1 - x_2 \|$$

$$D_{avg}(C_1, C_2) = \frac{1}{N_1 N_2} \sum_{x_1 \in C_1} \sum_{x_2 \in C_2} \| x_1 - x_2 \|$$

$$D_{mean}(C_1, C_2) = \| m_1 - m_2 \|$$

All of these measures have a minimum-variance flavor, and they usually give the same results if the clusters are compact and well separated. However, if the clusters are close to each other, and the shapes are not basically hyperspherical, very different results may be obtained.

RESULTS AND DISCUSSION

Typical MR images of brain with axial sliced, as shown in Figure 1 were processed by clustering segmentation method. Thirteen segmented brain MR images were obtained for different intensity groups values. Tested results, gained by subjective measures mentioned above, are shown in Figure 2 and 3.

Figure 10

Figure 2: T1 weighted MR image

White matter gray matter cerebrospinal meninges original

Figure 11

Figure 3: T2 weighted MR image

White matter gray matter cerebrospinal meninges original

In total, 13 regions-of-interests (ROI) have been marked to define clinically interesting tissue parts, such as skin, bone, meninges, white and gray matter. Delineation of the tissue is best in the post contrast images, i.e., the tissue -ROI was defined by multi regions enhancement in post contrast images and then transferred to the pre-contrast relaxation time images However this feature has not studied in this

paper. From the T1 and T2 images the listed images each ROI were calculated. The clustering and classification method used in this study is based on discriminate tests on a layer hierarchical decision.

For the subjective result, Table 2 and 3 summarizes the result from the evaluation made by a radiologist from University Putra Malaysia Medical Center (UPMMC) MR images. The diagram below shows the intensity distribution area verses the number of slices. Each region of interest in brain anatomy has been monitored and studied according to subjective aspects.

In general the 13 slices of the clustering segmented group was studied, where the regions of interest was examined according to the intensity differences and subtracted slices where done individually from the original T1 and T2 weighted images.

From the illustrated two diagrams, first diagram is a segmentation of T1 weighted MR image. Each slice has been segmented to 13 clustered intensity groups. However each group will carry the particular intensity of weighted vector values. The ratio of intensity distribution of a particular vector value illustrated under the area shown, according the number of slice, where each ratio under the area can present a sequence of that value in a number of slice. For example, skin value is shown in most of the region in the original image.

The second diagram is the segmentation of T2 weighted MR image where slice has been segmented to 13 clusters of intensity groups as well. According to intensity values and the area of distribution, comparison between T1 and T2 has been made.

From the respected result we obtained, the clustered segmentation intensity groups has relative connection between the two MR T1 and T2 weighted images. The first of 13 slice distribution images presented, the following diagram, skin intensity values is the most covered area for the entire respected slice.

Basically the skin can be threshold effectively in MR image, but our study is to clarify the intra cranial diagnosis, which are made during MR image acquisition by the specialist. Differential diagnosis is also considered in this study.

Figure 12

Diagram 1: T1 weighted MR image intensity area values groups versus slice number

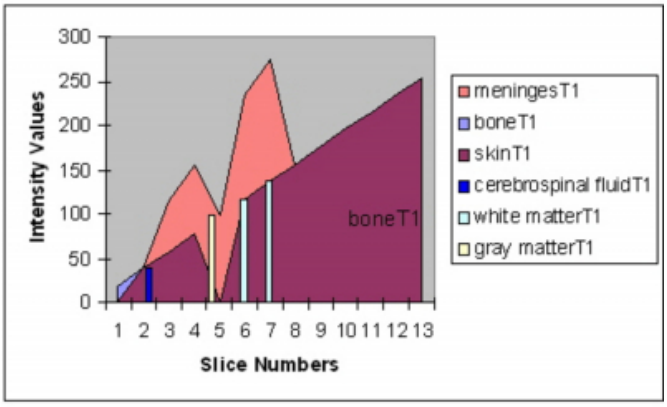
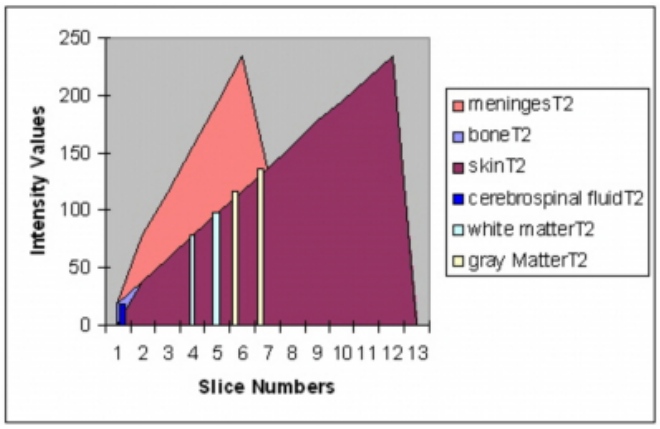


Figure 13

Diagram 2: T2 weighted MR image intensity area values groups versus slice number



To study each case individually it can clearly be seen that the intensity grouped area or region of interest have its ratio during the clustering segmentation. From the illustrated diagrams 1 and 2, we evaluate each clustered case individually and make the subjective clusterization for comparison purposes between T1 and T2 weighted MR images.

Subjective evaluation by viewers is still a method commonly used in measuring image quality. The subjective test emphatically examines fidelity and at the same time considers image intelligibility. When taking subjective test, viewers focus on the difference between segmented image and the original image. Once they notice such details, the information clustered accurately can be accepted. The representative subjective method is Mean Opinion Score (MOS) [$_1$]. It has two kinds of scores: one is T1 table and

another T2 table and made a comparison between the relative intensity values with the number of sliced. Two examples are shown below in Tables. Each viewer compares the reconstructed image with the original one to decide which level it belongs to and gives the score.

Figure 14

Table 1: for T1 weighted MR image, intensity values versus number of sliced

No. of Slice	1	2	3	4	5	6	7	8	9	10	11	12	13
Intensity values	19	39	58	78	98	117	137	156	176	196	215	235	255
Skin	-	√	√	√	-	√	√	√	√	√	√	√	√
Bone	√	-	-	-	-	-	-	-	-	-	-	-	-
Meninges	-	-	√	√	√	√	√	-	-	-	-	-	-
Gray matter	-	-	-	-	√	-	-	-	-	-	-	-	-
White matter	-	-	-	-	-	√	√	-	-	-	-	-	-
Cerebrospinal fluid	-	√	-	-	-	-	-	-	-	-	-	-	-

Figure 15

Table 2: for T2 weighted MR image, intensity values versus number of slice

No. of Slice	1	2	3	4	5	6	7	8	9	10	11	12	13
Intensity values	19	39	58	78	98	117	137	156	176	196	215	235	255
Skin	-	√	√	√	-	√	√	√	√	√	√	√	-
Bone	√	-	-	-	-	-	-	-	-	-	-	-	-
Meninges	-	√	√	√	√	√	-	-	-	-	-	-	-
Gray matter	-	-	-	-	-	√	√	-	-	-	-	-	-
White matter	-	-	-	√	√	-	-	-	-	-	-	-	-
Cerebrospinal fluid	√	-	-	-	-	-	-	-	-	-	-	-	-

From the clustered method, the results after analyzing the data, the skin, bone and meninges from T1 and T2 weighted MR images shows that the intensity value for the clustered segment slice to be loosely distributed with in the region of interest from the intensity values as well as with in the same number of slice distribution.

On the other hand after a subjective examination we find that the gray matter, white matter and cerebrospinal fluid, has the differences in the number of slice but carries the same intensity values, where the clustering groups segmentation has the intensity values distribution in a separate slice. Slice examination for region of interest carries the range from one slice another, depending on clustering groups from T1 and T2 weighted MR images. The range distribution can present to us the characteristics of weighted MR image, which can guide us to the right diagnosis for the radiologist.

CONCLUSION

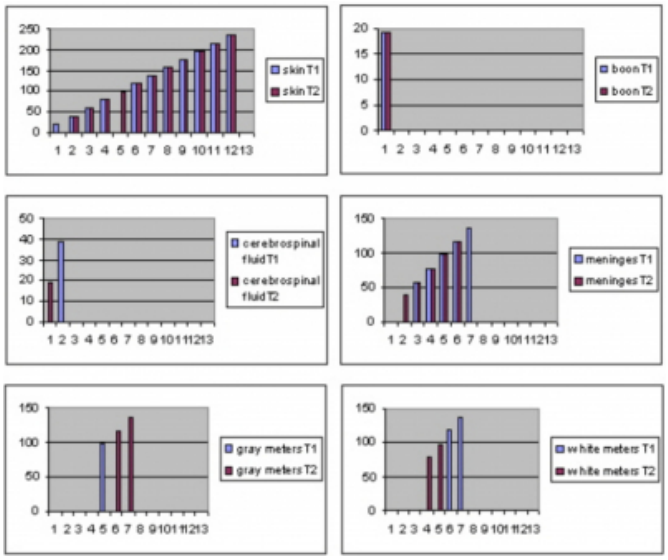
The proposed study of clustering segmentation methods gives the flexibility to radiologist to analyze and monitor the patient according to specific region of interest with in the brain.

Study on the criteria for image quality evaluation is a meaningful but has complicated task. The criteria can be used to evaluate the clustering algorithm and to guide the design of segmentation algorithms. Subjective MR image clustering and classification algorithm can reflect the quality of region of interest of T1 and T2 images approximately.

Clustered values must be above certain value if the segmented image reaches the level of segmentation quality. The quality of segmentation slice images depends on intensity distribution values over the MR image surface groups. The quality examined subjectively by radiologists where the values of intensity between (19 to 255 for T1 and T2 weight) for brain axial sliced section from different brain depth of the MR images respectively. The results indicated that segmentation from slice 1 to 13 was acceptable for the evaluation of the axial brain anatomy and subsequently may aid further pathlogical diagnosis.

Figure 16

Diagram 3: T1 & T2 weighted MR image intensity area values groups versus slice numbers comparison



References

1. Wells, W.M., Grimson, W.E.L., "Adaptive segmentation of MRI data," IEEE Trans. on Med. Imag., V15, N4, p429-442, 1996.
2. Ritter, G.X., Wilson, J.N., Handbook of Computer Vision Algorithms in Image Algebra, CRC Press, Boca Raton, FL, 1996.
3. Jackson, E.F., Narayana, P.A., Wolinksy, J.S., Doyle, T.J., "Accuracy and reproducibility in volumetric analysis of multiple sclerosis lesions," Journal of Computer Assisted Tomogrophy, V17, p200-205, 1993.
4. Tjuvajev, J.G., Macapinlac, H.A., Daghighian, F., Scott, A.M., Ginos, J.Z., Finn, R.D., Kothari, P., Desai, R., Zhang, J., Beattie, B., Graham, M., Larson, S.M., Blasberg, R.G., "Imaging of brain tumor proliferative activity with Iodine-131-Iododeoxyuridine," Journal of Nuclear Medicine,

V35, p1407-1417, 1994.
5. Zhang, J., "Multimodality imaging of brain structures for stereoactic surgery," Radiology, V175, p435-441, 1990.
6. Hu, X.P., Tan, K.K., Levin, D.N., Galhotra, S., Mullan, J.F., Hekmatpanah, J., Spire, J.P.,"Three-dimensional magnetic resonance images of the brain: Application to neurosurgical planning," Journal of Neurosurgery, V72, p433-440, 1990.
7. Sandor, S., Leahy, R.M., "Surface-based labeling of cortical anatomy using a deformable database," IEEE Transactions on Medical Imaging, V16, N1, p41-54, February 1997.
8. Zadech, H.S., Windham, J.P., "Optimal linear transformation for MRI feature extraction," IEEE Trans. on Med. Imag.,V15, N6, p749-767,1996.
9. Principe, J., Xu D., and Fisher, J.,"Information theoretic learning," in Unsupervised Adaptive Filtering, Ed. S. Haykin, John Wiley & Sons, New York, 2000.
10. Liang, Z., "Tissue classification and segmentation of MR images," IEEE Eng. Med. Biol., V12, p81-85, 1993.
11. L. Lemieux, G. Hagemann, K Krakow, and F.G. Woermann, "Fast, Automatic Segmentation of the Brain in T1-weighted Volume Magnetic Resonance Image Data," Proc. SPIE Medical Imaging 1999: Image Processing, K. Hanson, ed., 3661, pp.152-160, SPIE, 1999.
12. Robb, R.A., Visualization methods for analysis of multimodality images," Functional Neuroimaging: Technical Foundations, Orlando, FL, Academic Press, p181-190, 1994.
13. Karhunen, J., "Optimization criteria and nonlinear PCA neural networks," IEEE International Conference on Neural Networks, V2, p1241-1246, 1994.
14. Wang, Y., Adali, T., "Quantification and segmentation of brain tissues from MR images: A probabilistic neural network approach," IEEE Trans. on Image Processing, V7, N8, p1165-1180, 1998.
15. Davatzikos, C., Bryan, R.N., "Using a Deformable Surface Model to Obtain a Shape Representation of the Cortex," Technical Report, Johns Hopkins University, Baltimore, 1996.
16. M.S. Atkins and B. Mackiewich, "Fully automatic segmentation of the brain in MRI," IEEE Transactions on Medical Imaging, 17(1), pp. 98-107, 1998.
17. S. Smith, "Robust automated brain extraction", In Sixth Int.Conf. on Functional Mapping of the Human Brain, page 625. 2000.
18. Grossberg, S., "Adaptive pattern classification and universal recording: II. Feedback, expectation, olfaction, and illusions," Biological Cybernetics, V23, p187-202, 1976.
19. Giedd J.N., Blumental J., Jeffries N.O., Castellanos F.X., Liu H., Zijdenbos A., Paus T., Evans A.C., Rapoport J.L, "Brain development during childhood and adolescense: a longitudinal MRI study," Nature Neuroscience, V2, p861-863, 1999.
20. Dahmen J, Keysers D, Motter M, et al.: An automatic approach to invariant radiograph classification. Procs BVM-01:337-341, L¨ubeck, Germany, March 2001.
21. Dahmen J, Keysers D, Ney H, et al.: Statistical image object recognition using mixture densities. Journal of Mathematical Imaging and Vision 14(3):285-296, May 2001.

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