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Automatic attribute threshold selection for morphological connected attribute filters

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ABSTRACT

Attribute filters allow enhancement and extraction of features without distorting their borders, and never introduce new image features. In attribute filters, till date setting the attribute-threshold parameters has to be done manually. This research explores novel, simple, fast and automated methods of computing attribute threshold parameters based on image segmentation, thresholding and data clustering techniques in medical image enhancement. A performance analysis of the different methods is carried out using various 3D medical images of different modalities. Though several techniques perform well on these images, the choice of technique appears to depend on the imaging mode.

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1. Introduction

Connected filters [1–3] have found application in medical image processing [4–10], image segmentation and reconstruction [11–15], object detection and recognition [16,17], document analysis [18], characters recognition [19] video processing [20], color processing [21,22] as well as remote sensing [23–27]. In most of these applications, the processing is directed towards classification or enhancement of regions of meaningful objects with respect to the application. In biomedical applications these objects might be tumors, kidney stones or aneurysms, whereas in remote sensing, the objects of interest may be roads, different types of buildings or vegetation, or damage caused by floods, landslides or earthquakes.

Early examples of connected operators include openings and closings by reconstruction [28,29] and area openings and closings [30]. These were generalized to the larger class of attribute openings, closings, thickenings, and thinnings [31], which together are called grey-scale attribute filters. For recent reviews see [1,32].

In attribute filters [31,20] filtering is based on properties of the desired image features. They work by computing some property, or *attribute* of image components, and preserving only those

components which have the desired attribute values. An example of an attribute filter is shown in Fig. 1, in comparison to a classical morphological filter. As can be seen, in the connected case, image components can either be removed or remain intact but new ones do not emerge. This is a desirable property in many applications.

In the simplest form proposed in [31,20], attributes are compared against an *attribute-threshold*. Features with attributes above (or below) the threshold are preserved, the rest are removed. Choosing ‘the best’ attribute threshold λ is done manually, which is subjective. Alternatively, a range of thresholds is used, e.g. to perform multi-scale analysis [33,25]. For filtering purposes, a single threshold is generally needed. Usually the threshold is obtained interactively [8] through trial and error. This is particularly tedious if the dynamic range of the attributes is large. Choosing ‘the right’ λ is important because it determines what is retained or rejected, besides the filtering criteria. Indeed, all the problems in classical, grey-level threshold selection [34,35] occur in attribute threshold selection as well.

As there is a vast literature on threshold selection [36–43], it is only natural to explore the possibilities of adapting *grey-level* threshold selection techniques to *attribute* threshold selection. Therefore, we developed several automatic attribute threshold selection methods, by adapting conventional automatic grey-level thresholding techniques as well as data clustering techniques. Note that thresholding in the literature has been used as a pixel-level image processing procedure but never used for classification of regions or objects in an image, as it is in this work. Some

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Fig. 1. Left is the original image, middle is a structural opening with disk of radius=20, which exhibits distorted borders and emergence of new features, Right is connected operator (area opening at threshold $\lambda=100$), which shows no border distortion and regions are removed in their entirety.

preliminary results on blood-vessel enhancement were previously presented in [44]. In this paper we extend this research to include more threshold selection methods, and test these on 3D medical images of different modalities.

In principle, these techniques should work perfectly for all images but in this research the focus is 3D medical image enhancement and filtering. Two fundamental aspects of medical imaging make enhancement and filtering a difficult problem. The first aspect is the imaging process itself. The imaging process may fail to separate the anatomical feature of interest from its surroundings. The second fundamental aspect that makes filtering a difficult problem is that it needs to cope with the complexity and variability of the human anatomy. Manual selection of optimal processing parameters in medical imaging becomes complex, time-consuming and unfeasible when there are large numbers of images of varying quality, as often happens in medical images. Automatic choice of optimal parameter values is highly desirable.

The organization of the paper is as follows. Attribute filters are discussed briefly in Section 2. Section 3 discusses various threshold selection methods. Performance evaluation of the methods on various 3D medical images and document analysis are covered in Section 4. Performance is evaluated on noise suppression in document analysis and in 3D medical data sets. We show that several automatic techniques obtain threshold values close to those selected manually. In the case of document analysis, we show that for certain methods the resulting output image has an image quality similar to that of the best manual selection. Conclusions are given in Section 5.

2. Attribute filtering

In the following, a binary image X is considered a subset of some universal E . Foreground pixels are members of X , background pixels are in $E \setminus X$, where $\setminus$ denotes set difference. A grey-scale image is a function $f: E \rightarrow T$, with T being the totally ordered set of grey levels (usually $T \subseteq \mathbb{Z}$).

In the binary case, attribute filters [31] retain those connected components of an image which meet certain attribute criteria. After computing the connected components of X , i.e. the maximal connected subsets of X , some property or attribute of each component is computed. A threshold is usually applied to these attributes to determine which components are retained and which removed. Thus, the criterion Λ , usually has the form

$$\Lambda(C) = \text{Attr}(C) \geq \lambda \quad (1)$$

with C being the connected component, $\text{Attr}(C)$ some real-valued attribute of C and λ the attribute threshold.

Formally, attribute filters rely on connectivity openings γ_x , $x \in E$. In the binary case $\gamma_x(X)$ returns the foreground component to which x belongs if $x \in X$ and $\emptyset$ otherwise. After extracting the

connected components using connectivity openings, a trivial filter ψ^Λ based on attribute criterion Λ is applied to each. These are defined as

$$\psi^\Lambda(C) = \begin{cases} C & \text{if } \Lambda(C) \text{ is true} \\ \emptyset & \text{otherwise.} \end{cases} \quad (2)$$

The attribute filter ψ_Λ based on criterion Λ is then defined as

$$\psi_\Lambda(X) = \bigcup_{x \in X} \psi^\Lambda(\gamma_x(X)) \quad (3)$$

In other words, $\psi_\Lambda(X)$ returns the union of all connected components which meet the criterion Λ .

Breen and Jones [31] build grey scale variants of binary filters by the standard method of threshold decomposition [45]. This means that for a grey scale image f , we compute these attributes for the connected components of threshold sets $X_h(f)$, defined as

$$X_h(f) = \{x \in E \mid f(x) \geq h\}. \quad (4)$$

In principle, we can apply the binary filter to each threshold set and stack the results. A more efficient approach uses the Max-Tree [20] data structure. The nodes C_h^k , with k being the node index and h the gray level of the Max-Tree represent connected components for all threshold levels in a data set. These components are referred to as *peak components* and are denoted as P_h^k . The root node represents the set of pixels belonging to the background, and each node has a pointer to its parent. An example of a Max-Tree is given in Fig. 2. Each node contains a reference to its parent, its original and filtered grey level and its attribute value or values in the case of vector-attribute filtering [46].

2.1. Attribute filter design

When designing an attribute filter, there are three points to consider in the binary case, and four in the grey-scale case. The first is which attribute to choose. Much work has been done developing attributes and algorithms to compute them efficiently [31,20,33,8,9,47]. In most cases a single attribute is computed for each component, but extensions to vector-attribute filters have been made [46,48].

The second point to consider is the which connectivity to use. This determines what constitutes a connected component, and therefore at what aggregation level in the image we are applying our attribute computation. Though in most cases we use 4 or 8 connectivity in 2D and 6 and 26 in 3D, the morphological connectivity theory developed in [49,50], and in particular for attribute filters in [51] allows more advanced choices of what constitutes a connected object.

The third consideration is that of the attribute criterion. In our case we will consider only the form in (1) (or its negation). This means that we are only left with the choice of the attribute threshold λ .

Fig. 2. An example of a Max-Tree representation of a simple 4-level image.

Finally, in the grey-scale case, when using non-increasing criteria, we also need to choose the filter's decision rule.

In this paper, we focus on single attribute filters with 8-connectivity in 2D and 26-connectivity in 3D, but the methods developed are equally applicable in other connectivities. In the grey scale case we also have the choice of decision rule, and this is fixed to the subtractive rule. Again, the methods should in principle work with other rules as well.

2.2. Attribute computation

The filtering process is separated into four stages: construction, attribute computation, filtering and restitution. During the construction phase, the Max-Tree is built from the flat zones of the image. To construct a Max-Tree, a variety of fast algorithms is available [20,52,53]. During the construction of the tree, attributes can be computed on the fly, but the order of their computation is dependent on the tree construction. The Max-Tree construction and attribute computation can also be separated, allowing computation of different attributes with a single tree construction [8].

A number of 3D scale, translation and rotation invariant attributes exist. Many are based on moments, like non-compactness, elongation, flatness, sparseness, radial moments [47,8] or non-moment based like sphericity [9] or size based like volume or surface area. The performance of each attribute in terms of filtering can depend on the imaging modality, image characteristics, application or other factors.

In the current work we focus on the non-compactness attribute [8] which is robust to noise and has several applications in a number of imaging modalities. The non-compactness attribute is minimal for a sphere and rapidly increases with object elongation. To compute non-compactness of connected components in a scale-invariant manner, the classical two pass algorithm approach [31,20] was used by Westenberg et al. [8] based on the moment-of-inertia tensor, which is equivalent to the covariance matrix multiplied by the number of voxels in a connected component (C). It can be computed efficiently for each node of the Max-Tree by simply computing, $\sum x, \sum y, \sum z, \sum xy, \sum xz, \sum yz, \sum x^2, \sum y^2, \sum z^2$ and volume. Each of these is easily updated incrementally. Several moment-invariants can be computed from the moment-of-inertia tensor. The non-compactness attribute $N(C)$ is

$$N(C) = \frac{I(C)}{V^{5/3}(C)} \quad (5)$$

where $I(C)$ is the trace of the moment-of-inertia tensor and $V(C)$ is the volume of the connected component C .

The radial moment sphericity attribute [47] uses a multi-pass algorithm. This attribute is also comparably robust and resilient to noise, but can also be generalized to higher moment orders without performance degradation. It is based on computing roundness of connected components using radial moments. For each connected component, we first compute the centroid coordinates $(\bar{x}, \bar{y}, \bar{z})$ and the volume of the node $V(C)$. The radial

moment attribute $\psi_\beta(C)$ is then computed as

$$\psi_\beta(C) = \frac{3}{(2\beta+3)^{3/(2\beta+3)}(4\pi)^{2\beta/(2\beta+3)}\mu_{r,2\beta}^{3/(2\beta+3)}(C)} V(C) \quad (6)$$

where

$$\mu_{r,2\beta}(C) = \sum_{(x,y,z) \in C} ((x-\bar{x})^2 + (y-\bar{y})^2 + (z-\bar{z})^2)^\beta \quad (7)$$

Radial moments are maximal for a sphere and decrease rapidly with elongation.

Having computed the attributes, the tree is processed during the filtering phase. Based on the attribute value $Attr(P_h^k)$ of a node C_h^k , the algorithm takes a decision on whether to preserve or to remove the node. This is done by associating a criterion T to the attribute function $Attr$. Two classes of strategies exist: (1) pruning strategies, which remove all descendants of C_h^k if C_h^k is removed, and (2) non-pruning strategies in which the parent pointers of C_h^k children are updated to point at the oldest surviving ancestor of C_h^k . Salembier et al. [20] describe four different decision rules to filter the tree: the *Min*, *Max*, *Viterbi* and *Direct* rule [20], other rules include *Subtractive* rule [33] and *Branches* rule [48,54]. In this research, the Subtractive rule used because it works best for medical image enhancement and image decomposition based on shape [33,7,8]. With the subtractive rule, a node C_h^k is removed if $Attr(P_h^k) \leq \lambda$ and its pixels are lowered by the same amount as C_h^k itself but its descendants are unaffected.

3. The methods

Hundreds of thresholding techniques are present in the literature. A number of studies [34,39,55,56] categorize global thresholding between four to six somewhat overlapping groups based on the information that is exploited. In each category, there is a *primary* technique upon which tens of others are built. We tried as much as possible to consider primary techniques in each category. However, due to the nature of the data sets, we further required that the choice of the technique in each category takes into account at least most of the following properties:

- Ease of implementation in the Max-Tree.
- Computational complexity in each category.
- Robustness to noise.
- Potential to handle higher dimensional attribute vectors.
- Potential for future multi-thresholding.

In this research we investigate six of these global thresholding techniques that follow broadly into five categories. (i) Histogram based approaches which analyze the peaks, valleys and curvatures of the smoothed histogram. Otsu's method [38] was chosen. (ii) Entropy-based methods which use the entropy of the foreground and background regions or the cross-entropy between the original and binarized image. We adapted a method by [40] to compute

maximum entropy. (iii) Clustering-based methods, where samples are clustered in two parts as background and foreground object or modeled as a mixture of two Gaussians. K-means [57] and Fuzzy c-means (FCM) [58] were considered. (iv) Region property-based methods which use edge detection or any other property of the image like pixel similarity. Robust Automatic Threshold Selection (RATS) [36] was investigated in this category. (v) Artificial Neural Networks are based on processing elements through learning. Most of the techniques under this category are supervised but when used in unsupervised fashion as a clustering method, vector quantization (VQ) [59], is the principle technique under this category. We discuss these methods only briefly and their implementation in the Max-Tree data structure. For more details about the techniques references are given.

3.1. Robust Automatic Threshold Selection (RATS)

RATS [36] is a simple fast, noise robust and automatic method for bi-level thresholding of grey scale images. Segmentation is obtained through detection of edges (gradients) of various regions by locating points of abrupt changes in image gray level intensity values. It is based on image statistics which can be computed without use of histograms. The basic idea is to choose the threshold at the intensity where the gradients are the highest on average. It computes an edge-weighted average of the image intensity, using the gradient of the image and in a noise free image the optimal threshold T is computed as

$$T = \frac{\sum w_g(i)f(i)}{\sum w_g(i)}, \quad (8)$$

where f is the input image, and w_g is the edge weight, computed from gradient g of f . Both f and g are defined on the image domain E . Several methods may be used to compute g and w_g . In particular, choosing edge weights w_g equal to the square of g is particularly effective [37]. RATS also allows local thresholding, in which a threshold T is computed on sub-domains of the image.

We adapt this by defining the attribute gradient Δ_A as along root path in the Max-Tree as

$$\Delta_A(C) = \frac{Attr(C) - Attr(par(C))}{f(C) - f(par(C))} \quad (9)$$

with $par(C)$ being the parent of node C in the Max-Tree, and $f(C)$ denotes the grey level of node C . As this is a one-sided gradient, it corresponds best to the mean $M_A(C)$ attribute value of C and $par(C)$, i.e.

$$M_A(C) = \frac{Attr(C) + Attr(par(C))}{2} \quad (10)$$

However, because most medical images are noisy, we compute an optimal attribute threshold as in [37] by using the square of the gradient. This gives better results with noisy images, by giving a higher weight to the high gradients. Thus, the optimal threshold T is computed as

$$T = \frac{\sum_{i=0}^{N-1} \Delta_A^2(C_i) M_A(C_i)}{\sum_{i=0}^{N-1} \Delta_A^2(C_i)}, \quad (11)$$

with N being the number of nodes in the tree.

The advantage of this technique is that it does not only depend on the attributes values alone but also differences between the attributes of adjacent nodes in the root path. This means sudden changes in attribute value become important. In principle, it should be possible to adapt this to local thresholding in the tree, similar to the approach in [60].

3.2. Maximum Entropy based classification (MaxEnt)

This method stems from information theory [61]. MaxEnt seeks to extract as much information from a measurement as is acceptable by the data's signal-to-noise ratio. Entropy thresholding of an image selects an optimum threshold value by choosing the pixel intensity from the image's histogram that exhibits the maximum entropy over the entire image. We adapted a method by [40] to compute maximum entropy. We considered attribute values of nodes as two clusters by clustering the histogram. The maximum entropy sum method is based on the maximization of the attribute measure between the two classes. Let $p_i = h[i]/N$ be an estimate of the probability node attribute, where i is the histogram bin index of the node's attribute and N is the number of nodes in the tree as before. Let T be the number of bins in the histogram. If we assume two classes of node attributes, $c1$ and $c2$, separated by threshold t (in terms of bin number) we have

$$p(c1) = \sum_{i=0}^t p_i, \quad p(c2) = \sum_{i=t+1}^{T-1} p_i,$$

as probabilities for each class. Kapur et al. [40] use two entropies

$$H_T = - \sum_{i=0}^{T-1} p_i \ln p_i \quad \text{and} \quad H(t) = - \sum_{i=0}^t p_i \ln p_i$$

to define an algorithm to determine the optimal threshold by maximizing

$$\psi(t) = \ln[p(c1)p(c2)] + \frac{H(t)}{p(c1)} + \frac{H_T - H(t)}{1 - p(c2)} \quad (12)$$

To compute an optimal threshold, we first compute the attributes for all nodes as before and sort them. We then compute a histogram (usually with about 1000 bins). Finally, we compute the entropy using (12) for each t , and select the attribute value corresponding to the value separating bin t and $t+1$.

This method, like all histogram based methods, has a common drawback of taking into account only the histogram information (ignoring the spatial details). As a result, such an algorithm may fail to detect thresholds if these are not properly reflected as valleys in the histogram.

3.3. Otsu based classification

Otsu's method [38] is one of most frequently used thresholding methods in various fields especially image segmentation. The method automatically performs histogram shape-based image thresholding by having two groups of a measured pixel property, one with one range of values and the other with another. This is not trivial because ranges usually overlap. But by minimizing the error of classifying a background pixel as a foreground one or vice versa, we minimize this overlap and make each cluster as tight as possible. As we adjust the threshold one way, we increase the spread of one and decrease the spread of the other. The goal then is to select the threshold that minimizes the combined spread.

The algorithm assumes that the image to be thresholded contains two classes of measured property then calculates the optimum threshold separating those two classes so that their combined spread (intra-class variance) is minimal. In Otsu's method we exhaustively search for the threshold that minimizes the intra-class variance or maximizing the between-class variance, defined as a weighted sum of variances of the two classes. We can define the within-class variance ($\sigma_{Wthn}^2(t)$) as the weighted sum of the variances of each cluster as

$$\sigma_{Wthn}^2(t) = n_{c1}(t)\sigma_{c1}^2(t) + n_{c2}(t)\sigma_{c2}^2(t) \quad (13)$$

with

$$n_{c1}(t) = \sum_{i=0}^t p(i) \quad \text{and} \quad n_{c2}(t) = \sum_{i=t+1}^{T-1} p(i),$$

$\sigma_{c1}^2, \sigma_{c2}^2$ are variances of the two classes, $\mu_{c1}(t)$ and $\mu_{c2}(t)$ are the means of clusters c1 and c2, respectively, and $[0, T-1]$ the attribute range. Computing this within-class variance for each of the two classes for each possible threshold involves a lot of computations. The easier and faster way is to subtract the within-class variance from the total variance of the combined distribution, we get the between-class variance ($\sigma_{btm}^2(t)$) computed as

$$\sigma_{btm}^2(t) = \sigma^2 - \sigma_{Wthn}^2(t) \quad (14)$$

this is equivalent to:

$$\sigma_{btm}^2(t) = n_{c2}(t)[\mu_{c2}(t) - \mu]^2 + n_{c1}(t)[\mu_{c1}(t) - \mu]^2 \quad (15)$$

with σ^2 being the combined variance and μ the combined mean. Notice that the between-class variance is simply the weighted variance of the cluster means themselves around the overall mean:

$$\mu = n_{c1}(t)\mu_{c1}(t) + n_{c2}(t)\mu_{c2}(t) \quad (16)$$

Substituting Eq. (16) into Eq. (15) gives

$$\sigma_{btm}^2(t) = n_{c1}(t)n_{c2}(t)[\mu_{c1}(t) - \mu_{c2}(t)]^2 \quad (17)$$

Otsu [38] computes an optimal threshold by maximizing the between-class variance $\sigma_{btm}^2(t)$. Now each potential threshold t depends only on the difference between the means of the two clusters, thus avoiding having to calculate differences between individual attributes and the cluster means.

The optimal threshold maximizes the between-class variance. We adapt this to attribute thresholding, by sorting the attributes in ascending order, and computing $\sigma_{btm}^2(t)$ for all attribute values present, and selecting the threshold that maximizes $\sigma_{btm}^2(t)$.

The advantage of this technique is that it is simple and easy to implement. However, it fails if the histogram is unimodal or close to unimodal.

3.4. K-means clustering

K-means [57] clustering is a method of cluster analysis which aims to partition N observations into k clusters in which each observation belongs to the cluster with the nearest mean. The procedure follows a simple and easy way to classify a given data set through a certain number of clusters k , fixed a priori. In general, finding the correct value for k can pose a problem. However, for selection of a single threshold in our 1-D case, we have $k=2$. This algorithm aims at minimizing an objective function, in this case a squared error function J defined as

$$J = \sum_{i=1}^n \|x_i - \mu_{\kappa(i)}\|^2 \quad (18)$$

where $\kappa(i)$ is the index of cluster centroid $\mu_{\kappa(i)}$ which minimizes the distance to x_i , i.e.

$$\kappa(i) = \underset{j=1}{\overset{k}{\operatorname{argmin}}} \|x_i - \mu_j\|. \quad (19)$$

The algorithm is as follows:

- Compute the attribute as in Section 2.
- Initialize the number of clusters to 2.
- Take any random attributes as the initial centroids.
- Iterate until convergence by:
 - Determining the Euclidean distance of each attribute to both centroids.
 - Group the node attributes based on minimum distance.

- Update the cluster centroids.

- Compute the point of inter-cluster separation.

The optimal threshold is the point of inter-cluster separation which is equivalent to the mid-point between final centroids after convergence. This method can be generalized to multiple clusters most easily.

The main advantages of this algorithm are its simplicity and speed which allows it to run on large data sets. One disadvantage is that it does not yield the same result with each run sometimes, since the resulting clusters depend on the initial random assignments. Also, a fixed number of clusters can make it difficult to predict what k should be. In the current paper we restrict ourselves to $k=2$.

3.5. Fuzzy c-means clustering (Fuzzy)

Fuzzy c-means (FCM) [58,62] is a method of clustering which allows one piece of data to belong to two or more clusters. While in hard clustering an entity belongs only to one cluster, in fuzzy clustering entities are allowed to belong to many clusters with differing degrees of membership. Usually, membership functions are defined based on a distance function, such that membership degrees express proximities of entities to cluster centers.

Areas of application of fuzzy cluster analysis include for example data analysis, pattern recognition, and image segmentation. The fuzzy c-means (FCM) algorithm is one of the most widely used methods in fuzzy clustering. It is based on the concept of fuzzy c-partition [62] summarized as follows. Suppose $X = \{x_1, \dots, x_n\}$ is a set of a given data where each data point $x_k (k=1, \dots, n)$ is a vector in $\mathbb{R}^D$. Let $\mathbb{U}_{mn}$ be the space of real $m \times n$ matrices and m be an integer, such that $2 \leq m < n$. Then a fuzzy m -partition space of X is the matrix P_{mn} such that

$$P_{mn} = \{U = (u_{ik}) \in \mathbb{U}_{mn} \mid u_{ik} \in [0, 1]\} \quad (20)$$

$\Leftrightarrow$

$$\sum_{i=1}^m u_{ik} = 1, \quad \forall k \in \{1, 2, \dots, n\} \quad (21)$$

where u_{ik} is the membership value of x_k in cluster $i \in \{1, 2, \dots, m\}$.

The aim of the FCM algorithm is to find an optimal fuzzy c-partition and corresponding prototypes minimizing the objective function $J_w(U, C; X)$

$$J_w(U, C; X) = \sum_{k=1}^n \sum_{i=1}^m (u_{ik})^w \|x_k - c_i\|^2 \quad (22)$$

where $C = (c_1, \dots, c_m)$ is a matrix of unknown cluster centers $c_i \in \mathbb{R}^D$, $\|x_k - c_i\|^2$ is a Euclidean measure between a data point x_k and the cluster center c_i and $w \in [1, \infty)$ is a constant that influences the membership values. To minimize criterion J_w , under the fuzzy constraints defined in Eq. (21), fuzzy partitioning is carried out through an iterative optimization of the objective function J_w , with the update of membership u_{ik} and the cluster centers c_i by:

$$u_{ik} = \left[\sum_{j=1}^m \left(\frac{\|x_k - c_i\|^2}{\|x_k - c_j\|^2} \right)^{(2/(w-1))} \right]^{-1} \quad (23)$$

$$c_i = \frac{\sum_{k=1}^n u_{ik}^w x_k}{\sum_{k=1}^n u_{ik}^w} \quad (24)$$

Iteration will stop when:

$$\max_{i,k} \{u_{ik}^{j+1} - u_{ik}^j\} < \epsilon \quad (25)$$

where ϵ is a termination criterion between 0 and 1, whereas j are the iteration steps. This procedure converges to a local minimum

or a saddle point of J_w . We adapted this method by computing the optimal threshold T by considering nodes' attributes as belonging to two clusters.

The algorithm is as follows:

- Compute the attribute as in Section 2.
- Initialize the number of clusters to 2.
- Set ϵ and cluster membership threshold.
- Initialize $U = [u_{ik}]$ matrix, for the values of the memberships of attribute points.
- At each k -step: calculate the centers vectors using Eq. (24).
- Update the matrix U using Eq. (23) and membership.
- Iterate until $\{u_{ik}^{j+1} - u_{ik}^j\} < \epsilon$.

The optimal threshold is computed as the mid-point between the final cluster centroids as before, 'crispifying' the cluster membership. This method can be generalized to multiple clusters easily as well.

3.6. Vector quantization

Vector quantization (VQ) [59,63] is a quantization technique from signal processing which allows the modeling of probability density functions by the distribution of prototype vectors. It works by dividing a large set of points (vectors) into groups having approximately the same number of points closest to them. Each group is represented by its centroid point. Centroids are called codevectors and the regions they represent are called encoding regions. The set of all codevectors is called the codebook and the set of all encoding regions is a partition of the data space.

The idea behind VQ is that given a vector source with its statistical properties known, a distortion measure and the number of codevectors find a codebook and a partition which result in the smallest average distortion. A vector quantizer maps k -dimensional vectors, $X = \{x_{m,i} : m = 1, 2, \dots, k, i = 1, 2, \dots, k\}$ in the vector space R^D into a finite set of vectors $Y = \{y_i : i = 1, 2, \dots, N\}$, N is assumed to be sufficiently large so that all the statistical properties of the source are captured by the training sequence. Associated

with each codeword, y_i , is a nearest neighbor region called Voronoi region, defined as

$$V_i = \{x \in R^D : \|x - y_i\| \leq \|x - y_j\|, \forall j \neq i\} \quad (26)$$

The set of Voronoi regions partitions the entire space R^D such that:

$$\bigcup_{i=1}^N V_i = R^D \\ \bigcap_{i=1}^N V_i = \emptyset, \forall j \neq i$$

Let M be the number of codevectors and let $C = \{c_1, c_2, \dots, c_M\}$ represent the codebook. Each codevector is k -dimensional. Let V_n be the encoding region associated with each codevector such that the partition of the entire space is given by: $P = \{V_1, V_2, \dots, V_M\}$. For every $x_i \in V_n$ the respective encoding region, if $Q(x_i)$ is its approximation then:

$Q(x_i) = c_n$, given that $x_i \in V_n$. Assuming a squared-error distortion measure, the average distortion is given as

$$Ave_{dist} = \frac{1}{Nk} \sum_{i=1}^N \|x_i - Q(x_i)\|^2 \quad (27)$$

To compute vector quantization, we need to minimize Ave_{dist} . To satisfy Eq. (26), C and P should be solutions to Ave_{dist} .

Thus the encoding region V_n should consists of all vectors that are closer to c_i than any of the other codevectors.

The centroid condition is given as

$$c_i = \frac{\sum_{x_i \in V_i} X_i}{\sum_{x_i \in V_i} 1} \quad (28)$$

where $i = (1, \dots, N)$, c_i is average of all those training vectors that are in encoding region of V_i .

During implementation, at least one training vector belongs to each encoding region. Using [59] implementation solves the above two optimality criteria. The algorithm requires an initial codebook. This initial codebook is obtained by the splitting method. In this method, an initial codevector is set as the average of the entire

Fig. 3. Blood-vessel filtering on angiogram volume, showing maximum intensity projections of the original and filtered volumes for the different attribute threshold values from the methods in Table 1. (a) Original, (b) Manual, (c) Otsu, (d) RATS, (e) MaxEnt, (f) K-means, (g) Fuzzy, and (h) VQ.

Table 1
Computing attribute threshold value.

Data set	Manual	Otsu	MaxEnt	RATS	Kmeans	Fuzzy	VQ
angiolarge	2.55	0.025	2.025	2.128	2.30	2.30	2.28
mrt16_angio	2.70	0.020	6.30	0.80	0.80	0.79	0.76
mrt16_angio2	3.60	0.020	3.20	0.90	3.70	3.65	3.59
foot	1.2	0.25	1.95	0.61	0.61	0.60	0.60
prostate-stone	0.25	0.25	2.88	0.60	0.95	0.95	0.93
CT-Knee	0.80	0.25	3.66	0.74	2.70	2.72	2.35
angiolarge(kflat)	2.60	2.02	4.60	2.35	3.74	2.60	2.58
Document	0.65	0.31	0.65	0.85	0.40	0.40	0.40

training sequence. This codevector is then split into two. The iterative algorithm is run with these two vectors as the initial codebook. The final two codevectors are split into four and the process is repeated until the desired number of codevectors is obtained. The algorithm is summarized below:

- Compute the attribute as in Section 2.
- Set $\epsilon > 0$, which needs to be as small as possible.
- Set the number of codevectors $N=1$:
 - Calculate the centroid(c_1^*) using Eq. (28).
 - Calculate the average distortion(Ave_{dist}^*) using Eq. (27).

Fig. 4. Prostate-stone filtering on prostate-stone volume, showing maximum intensity projections of the original and filtered volumes for the different attribute threshold values from the methods in Table 1. (a) Original, (b) Manual, (c) Otsu, (d) RATS, (e) MaxEnt, (f) K-means, (g) Fuzzy, and (h) VQ.

Fig. 5. Bones filtering on CT-Knee volume, showing maximum intensity projections of the original and filtered volumes for the different attribute threshold values from the methods in Table 1. (a) Original, (b) Manual, (c) Otsu, (d) RATS, (e) MaxEnt, (f) K-means, (g) Fuzzy, and (h) VQ.

Fig. 6. Attribute histograms: (a, b, c, d, e, f) $k=0$, (g) $k=70$ and (h) $k=135$ showing the effect of the removal of low contrast features from the tree. (a) angiolarge, (b) mrt16_angio, (c) CT-knee, (d) prostate-stone, (e) foot, (f) mrt16_angio2, (g) angiolarge ($k=70$), and (h) prostate-stone ($k=135$).

- Split the attributes into two by setting the number of code-vectors ($N=2$):
 - Using the Euclidean distance measure cluster the vectors around each codevector.
 - Group the attributes based on the codevector that yields the minimum distance for each.
 - Update the new set of codewords by computing new codevectors.
 - Calculate and update the average distortion (Ave_{dist}^*).
 - Stop iteration if $Ave_{dist}^{i+1} - Ave_{dist}^i < \epsilon$.

The optimal threshold is the mean of final codevectors after convergence. This method can be generalized to multiple clusters easily as well.

The advantage of this classification technique is that the performance of how good or bad the clustering has been accurately done can be measured using signal-to-distortion ratio (SDR) which is given by:

$$SDR = 10 \log_{10} \frac{\sigma^2}{Ave_{dist}} (dB) \quad (29)$$

where σ^2 is the variance of the attributes and Ave_{dist} is the average squared-error distortion. The higher the SDR the better the performance.

4. Results and discussion

To test the performance of the methods, we ran tests on a number of 3D medical images of different modalities. We also asked 10 users to interactively find an optimal threshold for extracting objects from the data sets. The average manual value was used as the ground truth for comparison. For each data set, we performed quantitative comparison in noise suppression, filtering of objects of interest, enhancement of features, and computational timings for each algorithm.

4.1. Performance evaluation

The *angiolarge* courtesy of <http://www.volvis.org> is a 8 bits, $256 \times 256 \times 124$ magnetic resonance angiogram (MRA) with 361,463 peak components in the Max-Tree. The aim is to filter and enhance blood vessels while suppressing other features. The methods based on RATS, MaxEnt and the clustering techniques K-means, Fuzzy and VQ are closer to the manual threshold value. The Otsu threshold is too low because so many attribute values are close to zero, as shown in Fig. 6(a). The attribute histogram is skewed. Apparently, the other methods are not biased by this as can be seen in Fig. 3 and Table 1. By design Otsu performs well if the histogram is bimodal, which is not the case here. The other methods suppress noise well. All clustering techniques have very similar results and are slightly better than the others.

The *prostate-stone* is a 8 bits, $512 \times 512 \times 31$ 3D CT volume of a patient suffering from urolithiasis, with 124,477 peak components, courtesy of the Department of Radiology and Medical Imaging, University General Hospital of Alexandroupolis, Greece. The aim here is to filter out the kidney stone while suppressing the rest of the features. From Fig. 4 and Table 1, using the non-compactness attribute with the criteria of selecting structures that are less than λ , the kidney stone can be isolated. The users are able to obtain the value of $\lambda = 0.25$ which is the same as that of Otsu. The stone has been isolated by Otsu because the attributes histogram from Fig. 6 has two distinct peaks which Otsu can separate.

On the other hand, because of the distinct contrast of the attributes RATS performs relatively better as compared to the clustering techniques which clearly struggle.

The CT-Knee is a 8 bit, $379 \times 229 \times 305$ volume courtesy of <http://www.volvis.org>. The goal here is to enhance the bones but suppress the tissue. The number of peak components is 117,920. From Fig. 5 and Table 1, only RATS is able to perform like the manual technique. RATS achieves a value of $\lambda = 0.72$ compared to the mean manual of $\lambda = 0.80$. This can be attributed to the fact that there is a sudden change in attribute values in the transition from tissue grey level to bone grey levels. The other methods struggle with values either too low or high because of the many valleys and peaks in this attributes where estimating only 2 classes from it is difficult and inaccurate.

The *mrt16_angio* and *mrt8_angio2* are time-of-flight magnetic resonance angiograms (MRA) at 12 bits each courtesy of <http://www.volvis.org>. The data sets are $416 \times 512 \times 112$ and $256 \times 320 \times 128$ with 1,554,454 and 419,454 peak components computed, respectively. The goal here is to enhance the blood vessels. Time-of-Flight angiograms are very difficult to filter and very noisy. On the *mrt16_angio* all values from the methods are either too low or too high compared to the manual value of $\lambda = 2.7$. The higher values obtained by the clustering methods could be attributed to the cluster seen at very high attribute values in the histogram in Fig. 6(b).

By contrast, on *mrt8_angio2*, MaxEnt and the clustering methods K-means, Fuzzy and VQ are close or equal to the manually obtained value, and are more robust and resilient to noise while Otsu and RATS continue to struggle because of so many nodes' attribute values close to zero as seen Fig. 6(e).

The *foot* data set is a 8 bits, 256^3 voxel X-ray scan courtesy of <http://www.volvis.org>. The goal here is to enhance the bones. The number of peak components is 279,513 nodes. Using non-compactness with $\lambda = 1.2$, the manual value separates the bones from the tissue appropriately. The clustering techniques and RATS achieve values in the regions of 0.60 while Otsu technique at 0.25 is far too small which does not separate the bones from tissue

Fig. 7. The effect of k -flat filtering for $k=70$, using the same methods as in Fig. 3. (a) Original, (b) Manual, (c) Otsu, (d) RATS, (e) MaxEnt, (f) K-means, (g) Fuzzy, and (h) VQ.

(Table 1). The MaxEnt achieves a very high value though, which suppresses even the bones. On this data set all these automatic methods struggle, which can be attributed to the skewed distribution of attributes for this data set, see Fig. 6(f).

4.2. The effect of k -flat zones

To further improve the performance of the methods we adapted hyperconnectivity k -flat zones [18], which are connected regions of maximal extent, where the total grey level variation is not more than k . This restriction to grey-level range automatically restricts the size to which the regions can grow, yielding overlapping pseudo-flat zones which improves enhancement of internal details. The effect of using k -flat zones means that any node in the Max-Tree within k of an extremum is not considered

an independent entity and their attributes are ignored in any further computation (Fig. 7).

For our purposes, this removes a large number of low-contrast features which are predominantly noise from the computation of the optimal threshold. The effect of this can be seen in Fig. 6 bottom left. The number of nodes has been reduced substantially with nodes that do not contribute significantly to the object removed. The proper value of k depends on the data set and for *angiolar* a value of 70, while the *prostate-stone* using the radial moment attribute gave good results. The radial moment attribute is robust to noise as compared to other attributes on this data set but with $k=0$, the histogram is skewed to the left and therefore almost all the techniques struggle to isolate the kidney stone. However, when $k=135$, three of the automatic methods were able to isolate the stone as seen in Fig. 8, a higher k value means that we are only filtering very bright structures. This can be

Fig. 8. The effect of k -flat filtering using radial moment $\beta=5, k=200$. (a) Original, (b) Manual, (c) Otsu, (d) RATS, (e) MaxEnt, (f) K-means, (g) Fuzzy, and (h) VQ.

Fig. 9. User threshold variations.

Fig. 10. Automatic threshold variations.

explained by Fig. 6 bottom right. There is a clear separation of the two classes of attributes which these methods classify correctly. However, three other methods, Otsu, Entropy and K-means struggle to isolate the stone. This is due to the fact that the number of nodes and therefore attributes has significantly been reduced to a small number which limits the statistical properties needed to separate the two classes. The optimal size and shape of such an area is difficult to determine and histogramming over too small an area produces results which lose any statistical significance. From Table 1, the Otsu computed value increased by 900% at $k=70$ and by doing so we are improving the distribution of the histogram by making it less skewed (Fig. 6). The improvement was also reflected in filtering the *angiolarge* (Fig. 6) where the blood vessels were better filtered as compared to Otsu in Fig. 3. RATS appears to be quite robust to changes in k , but the results of K-means and MaxEnt became worse becoming too restrictive and showing substantial loss of small vessels, while Fuzzy and VQ compute the exact value of what the users obtained.

4.3. Threshold variations

To better understand the user variations in threshold values obtained plot of each user and their input is shown in Fig. 9. From Fig. 9, it is clear the variation between the users is very small on

only the document and prostate stone data set. While there is fair variation on the other data sets. This could be attributed to the fact that for users on the prostate stone and document data set, the filtering aim seems intuitive. For the document, they ensured that the salt and pepper is eliminated, while for the prostate stone, they would threshold until the stone was isolated. For the other data sets it was more subjective of what was the right value and there was no intuition of what was present in the data set. On the other hand, the automatic techniques, for almost every data set at least 2 methods agree on where the right threshold should be. However, for almost all data sets there is always a technique that completely deviates from the others, see Fig. 10. This is explained in Section 4.1.

4.4. Quality assessment of methods

The accuracy of filtering of medical images is very difficult to quantify in the absence of a *ground truth* filtering result for clinical data. Characterizing the performance of medical image filtering and enhancement approaches continues to be a challenge. In filtering, unlike segmentation, it is very hard to provide a ground truth. To provide a quantitative measure of the quality of these automatic methods in image filtering, and to show their applicability in a very different domain, we used an image of known ground truth, corrupted it substantially by adding salt and pepper noise to the image with noise density of 0.4 (Fig. 11) and filtered this image using the *non-compactness* attribute on all methods.

Performance analysis of each method is carried out using a number of metrics that have been proposed to measure image quality and fidelity in the literature. In this case we used: mean-squared-error (MSE), peak signal-to-noise ratio (PSNR) signal-to-noise ratio (SNR), visual signal-to-noise ratio (VSNR) [64] which quantifies the visual fidelity of images based on threshold properties of human vision, whereas universal quality index (UQI) [65] models any image distortion as a combination of loss of correlation, luminance distortion, and contrast distortion, and tries to mimic the human perception closely.

Results of the quantitative quality assessment are shown in Table 2 for the different methods. On the *document* data set, there is little difference between the original image and the three best methods (Manual, RATS and MaxEnt), as can be verified using UQI, where these three methods achieved a value of $UQI=0.91$. Despite the substantial corruption of the original image, two automatic methods are able to reconstruct the original image with greater accuracy. In terms of VSNR, RATS (37.54) outperforms manual selection (26.88) by quite a margin, whereas MaxEnt (27.31) achieves about the same level. However, the clustering techniques are not suitable for this kind of images. It should also be noted that the *area* attribute (corresponding to volume in 3D) reconstructs the document perfectly, but for consistency in this research we maintained the *non-compactness* attribute.

4.5. Computational timings

Using a standard Core 2 Duo E8400 at 2.0 GHz machine, we performed timings for the computation of each algorithm. This timing does not include the time to compute the attributes but rather the time it takes to compute the threshold. From Table 3, the manual technique takes considerable time to get the optimal threshold, as expected, and is not by any means faster than any automatic method on any data set tested. On almost all data sets, RATS, K-means, MaxEnt, VQ, and to some extent Otsu have comparable computational speed, while Fuzzy because of the many parameters and its design takes some time to converge, thus it is slower as compared to the other techniques. But what it lacks in speed it compensates with better performance in

Fig. 11. Document filtering of a page, filtered data set for the different attribute threshold values from the methods in Table 1. (a) Original, (b) Corrupted, (c) Otsu, (d) RATS, (e) Manual, (f) K-means, (g) Fuzzy, (h) MaxEnt, and (i) VQ.

Table 2
Visual quality assessment.

Metric	Manual	Otsu	MaxEnt	RATS	Kmeans	Fuzzy	VQ
MSE	539	3560	537	793	2998	2999	3001
PSNR	20.82	12.62	20.83	19.14	13.36	13.34	13.03
SNR	8.27	0.071	8.29	6.59	0.82	0.82	0.81
UQJ	0.91	0.65	0.91	0.91	0.66	0.61	0.64
VSNR	26.88	6.87	27.31	37.54	8.03	8.01	8.03

Table 3
Computing algorithms time (seconds).

Data set	Manual	Otsu	MaxEnt	RATS	Kmeans	Fuzzy	VQ
angiolarge	120	0.82	0.29	0.11	0.42	17.76	0.75
mrt16_angio	210	3.79	1.30	0.50	2.04	147	3.14
mrt16_angio2	145	1.00	0.32	0.11	0.54	35.0	0.96
foot	90	0.62	0.22	0.08	0.27	11.7	0.95
prostate-stone	60	0.35	0.14	0.07	0.19	9.12	0.51
CT-Knee	60	0.29	0.11	0.06	0.19	1.44	0.06
angiolarge(kflat)	50	0.04	0.03	0.1	0.03	0.95	0.60
Document	30	2.7	0.022	0.027	0.022	0.026	0.006

computing an optimal threshold on many data sets as compared some faster methods.

5. Conclusion

In this paper we presented methods for automatic computation of attribute threshold parameters. The methods are simple, fast and in several cases perform well against the manual interactive method. Which method performed best depended on the data set, probably due to the differing imaging modes. We also showed that the Otsu method can be further improved by using hyperconnectivity k -flat zones but this does introduce a new parameter to set. RATS performed well on three data sets but failed on the time of flight MRAs. Of the latter `mrt16_angio` was problematic to all methods which indicate that we need a different attribute in this case. Apart from automatic filtering, the methods could be used to guide the user rather than to prescribe a value especially when the attributes dynamic range is large.

In future, we consider multilevel thresholding which we believe improves the accuracy of attribute threshold computation and use of multiple attributes, e.g. using vector attribute filtering. Enhancement of the methods for accuracy, precision, and

computational speed as well as the amount of manual interaction should be possible by incorporating prior information or combining discrete and continuous-based enhancement methods. For increasing computational efficiency parallelizable methods appears to be promising.

It is unlikely that automated enhancement methods will ever replace physicians but are likely to become crucial elements of medical image analysis. Automatic enhancement methods will be particularly valuable in areas such as computer integrated surgery, where visualization of the anatomy is a critical component.

Conflict of interest

There no conflict of interest.

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