An Optimal iterative Minimal Spanning tree Clustering Algorithm for images

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Abstract:-Limited Spatial resolution, poor contrast, overlapping intensities, noise and intensity in homogeneities variation make the assignment of segmentation of medical images is greatly difficult. In recent days, mathematical algorithm supported automatic segmentation system plays an important role in clustering of imaging. The minimal spanning tree algorithm is capable of detecting clustering with irregular boundaries. In this paper we propose an optimal iterative minimal spanning tree clustering algorithm (OPIMSTCA).At each hierarchical level, it optimizes the number of cluster, from which the proper hierarchical structure of underlying data set can be found. The algorithm uses a new cluster validation criterion based on the geometric property of data partition of the data set in order to find the proper number of clusters at each level. The center and standard deviation of the cluster are computed to find the tightness of the individual clusters. In this paper we compute tightness of clusters, which reflects good measure of the efficacy of clustering. The algorithm works in two phases. The first phase of the algorithm produces sub trees. The second phase creates objective function using optimal number of clusters. The performance of proposed method has been shown with random data and then the new Cluster separation approach to optimal number of clustering. The experimental results demonstrate that our proposed method is a promising technique for effective optimal clusters.

Key words: Euclidean minimum spanning tree, clustering, eccentricity, center hierarchical clustering, sub tree, standard deviation, cluster separation.

1. INTRODUCTION

Cluster analysis is playing an important role in solving many problems in medical field, psychology, biology, sociology, pattern recognition and image processing. Due to the limitations in image equipments in MRI, the image has mainly three considerable difficulties: Noise, partial volume and intensity in-homogeneity .Also the image signals have highly affected by shacking of patient's body and patient's motion. So the medical MRI is seriously affected and it has improper information about the anatomic structure. Hence the segmentation of medical images is an important one before it to go for treatment planning for proper diagnosis. Automated segmentation methods based on artificial intelligence

A spanning tree is an acyclic sub graph of a graph G, which contains all vertices from G. The minimum spanning tree (MST) of a weighted graph is minimum weight spanning tree of that graph with the classical MST algorithms [2, 3, 4] the cost of constructing a minimum spanning tree is O (mlogn), where m is the number of edges in the graph and n is the number of vertices. More efficient algorithm for constructing MSTs have also been extensively researched [5,

techniques were proposed in (Clark etal.[1]).The image segmentation viewed as partition a given image into regions(or) segments such that pixels belonging to a region are more similar to each other than pixel belonging to different regions. We also require that these regions be connected so regions consist of neighboring pixels. Image segmentation used to partition a given image into a number of regions. So that each region corresponds to an object(intensity, color, texture…).Here we address the problem of segmenting a digital image into a set of disjoint regions such that each region is composed of nearby pixels with similar colors (or) intensities (or) spatial location.

6, 7].These algorithms promise close to linear time complexity under different assumptions. A Euclidean minimum spanning tree (EMST) is a spanning tree of a set of n points in a metric space (E^n).where the length of an edge is the Euclidean distance between a pair of points in the point set. MSTs have been used for data Classification in the field of pattern recognition (8) and image processing (9, 10, 11).we have also seen some limited applications in biological data analysis (12).One popular form these MST applications is called the single-linkage cluster analysis (13, 14, 15, 16).

Our study on these methods has led us to believe that all these applications have used the MSTs in some heuristic ways;eg.cutting long edges to separate clusters without fully exploring their power and understanding their rich properties related to clustering. Geometric notion of centrality are closely linked to facility location problem. The distance matrix D

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(data set) can Computed rather efficiently using Dijkstra's algorithm with time complexity $O(|V|^2 \ln |V|)$ (17).

The eccentricity of a vertex in G and radius $\rho(G)$, respectively are defined as

$$e(x) = \max_{y \in V} d(x, y) \text{ and } \rho(G) = \min_{x \in V} e(x)$$

The center of G is the set

$$C(G) = \{x \in V / e(x) = \rho(G)\}$$

The length of the longest path in the graph is called diameter of the graph G, $D(G) = \max_{x \in V} e(x)$.

The diameter set of G is

$$Dia(G) = \{x \in V / e(x) = D(G)\}.$$

An image pixels represents a mode on vertices and an edge reflects pair wise similarities between the pixels. we take a graph-based approach to segmentation. Let $G = (V, E)$ be an undirected graph with vertices $v_i \in V$, the set of elements to be segmented and $(v_i, v_j) \in E$ corresponding to pairs of neighboring vertices, each edge $(v_i, v_j) \in E$ has a corresponding weight $w(v_i, v_j)$, which is a non-negative measure of the dissimilarity between neighboring elements v_i and v_j weights of the edges are computed by a similarity function location, brightness and color. With this representation, the segmentation task can be solved by minimum spanning tree clustering methods.

In this paper, we will provide in-depth studies for MST based clustering. our major contributions include a rigorous formulation for Optimal iterative minimal spanning tree clustering algorithm(OPIMSTCA).we believe it is a good idea to allow users to define their desired similarity within a cluster and allow them to have some flexibility to adjust the similarity if the adjustment is needed. In this paper we propose optimal iterative minimal spanning tree clustering algorithm for image segmentation algorithm to address the issues of undesired clustering structure and unnecessary large number of clusters. Our algorithm works in two phases. The first phase construct the Euclidean distance based MST from the pixels of input image data, then creates subtree (cluster/regions) from minimum spanning tree (MST) by removes the inconsistent edges that satisfy the predefined inconsistence measure. The second phase optimal iterative minimal spanning tree algorithm, which produces optimal (or) best number of clusters with segmentation. The performance of proposed method has been shown with random data for images. Finally experimental results and conclusion we summarize the strength of our methods and possible improvements.

2. MINIMAL SPANNING TREE-BASED CLUSTERING ALGORITHMS

We will use a MST to represent a set of expression data and their significant inter-data relationships to facilitate fast rigorous clustering algorithm. Given a point set D in E^n ,the hierarchical methods stats by constructing a minimal spanning tree(MST) from the points in D.Each edge weight represents the distance ((or)dissimilarity) , $\| u - v \|$ between u and v,which could be defined as the Euclidean distance ,so we named this MST as EMST1.Next the average weight $\bar{w}$ of the edges in the entire EMST1 and its standard deviation σ are computed; any edge with $w_e > \bar{w} + \sigma$ (or)longest edge is removed from the tree. This leads to a set of disjoint subtrees $S_T = \{T_1, T_2, T_3 ....\}$ .Each of these subtrees T_i is treated as cluster.

3. OUR ALGORITHM,OPTIMAL ITERATIVE MINIMAL SPANNING TREE CLUSTERING ALGORITHM

The MST T into k subtrees $\{T_i\}_{i=1}^{k}$ to optimize a more general objective function is given by

$$J(U) = \sum_{i=1}^{k} \sum_{v \in T_i} \| v - c_i \| ,$$

where c_i is the center of T_i , $i = 1, 2.......k$.

that is to optimize the k-clustering so that the total distance between the "center" of each cluster and its data points is minimized-objective function for data clustering. The centers of clusters are identified using eccentricity of points. These points are a representative point for the each cluster (or) subtrees. A point c_i is assigned to a cluster i if $c_i \in T_i$, $i = 1,2....k$ .The group of center points $c_1, c_2 ......c_k$ are connected and again minimum spanning tree EMST2 is constructed. To each T_i calculate standard deviation, distance between the point of T_i and clusters center c_i .Thus the problem of finding the optimal number of clusters of a data set can be transformed into problem of finding the proper region (clusters) of the data set. Here we use the MST as a criterion to test the inter –cluster property based on this observation, we use a cluster validation criterion, called cluster separation (CS) in OPIMST clustering algorithm.

Cluster separation :(CS) is defined as the ratio between minimum and maximum standard deviation of clusters (subtrees),

$$CS = \frac{\delta\sigma_i}{\Delta\sigma_i} \quad , i = 1,2.......k \, ,$$

where $\Delta\sigma_i$ is the maximum value of standard deviation of clusters and $\delta\sigma_i$ is the minimum value of standard deviation clusters.

Then the CS represents the relative separation of centroids.The value of CS ranges from 0 to 1.A low value of CS means that the two centroids are too close to each other and the corresponding partition is not valid. A high CS value means the partitions of the data is even and valid. In practice, we predefine a threshold to test the CS.If the CS is greater than the threshold; the partition of the data set is valid. Then again partitions the data set by creating subtree (cluster/region).This process continuous until the CS is smaller than the threshold The CS criterion finds the proper binary relationship among clusters in the data space. The value setting of the threshold for the CS will be practical and is dependent on the dataset. The high the value of the threshold the smaller the number of clusters would be Generally, the value of the threshold will be > 0.8 [18].The given clusters the CS value < 0.8 and our OPIMST algorithm processing the results, the proper number of clusters/regions for the data set (pixel) is 2.Further more, the computational cost of CS is much lighter because the number of sub clusters is small. The created clusters/regions are well separated.

Algorithm: OPIMSTCA

Input : Image data (pixel value)
Output : optimal number of clusters
Let e1 be an edge in the EMST1 constructed from image data.
Let e2 be an edge in the EMST2 constructed form C.
Let w_e be the weight of e1.
Let σ be the standard deviation of the edge weights in EMST1.
Let S_T be the set of disjoint subtrees of EMST1.

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1. Create a node v, for each pixel of an image I.
2. Compute the edge weight using Euclidean distance from image data.
3. Construct an EMST1 from 2
4. Compute the average weight of $\bar{w}$ of all the edges from EMST1.
5. Compute the standard deviation $\sigma$ of the edges from EMST1.
6. $S_T = \phi$ , $n_c = 1$ , $C = \phi$ .
7. Repeat.
8. For each $e1 \in EMST1$.
9. If $(w_e > \bar{w} + \sigma)$ (or) current longest edge e remove e1 from EMST1.
10. $S_T = S_T \cup \{T'\}$// $T'$ is new disjoint subtrees (regions).
11. $n_c = n_c + 1$.
12. Compute the center $c_i$ of $T_i$ using eccentricity of points.
13. $C = \cup_{T_i} \in S_T \{c_i\}$.
14. Construct an EMST2 T from C.
15. Compute the standard deviation $\sigma(T_i)$.
16. $\delta\ \sigma(T_i)$ =get-min standard deviation.
17. $\Delta\ \sigma(T_i)$ =get-max standard deviation.
18. CS= $= \frac{\delta\sigma(T_i)}{\Delta\sigma(T_i)}$ , $i = 1,2......k$
19. Until $CS < 0.8$.
20. Merge the closest neighbor from EMST2.
21. Update the clusters points, repeat step 12 to step 20.
22. The following optimize the k-clustering objective function minimized, termination criterion is satisfied $\| J_t(U) - J_{t-1}(U) \| < \in$, where t is the iteration count and $\in$ is a thresholding value lies between 0 and 1.
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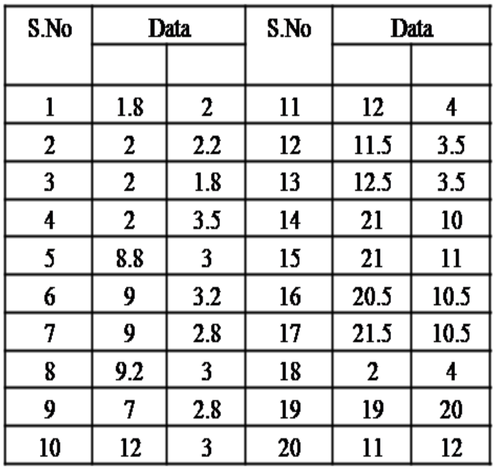
4. EXPERIMENTAL RESULTS

This section describes some experimental results on random data to the segmentation Performance of proposed method,

TABLE1: RANDOM DATA



S.No	Data		S.No	Data	
1	1.8	2	11	12	4
2	2	2.2	12	11.5	3.5
3	2	1.8	13	12.5	3.5
4	2	3.5	14	21	10
5	8.8	3	15	21	11
6	9	3.2	16	20.5	10.5
7	9	2.8	17	21.5	10.5
8	9.2	3	18	2	4
9	7	2.8	19	19	20
10	12	3	20	11	12

TABLE2: DISSIMILARITY MATRIX

	1	2	3	4	5	6	7	8	9	10
1	0	0.28	0.28	1.51	7.07	7.29	7.24	7.46	5.26	10.24
2		0	0.4	1.3	6.84	7.07	7.02	7.24	5.03	10.03
3			0	1.7	6.90	7.13	7.07	7.29	5.09	10.07
4				0	6.81	7.00	7.03	7.21	5.04	10.01
5					0	0.28	0.28	0.4	1.81	3.2
6						0	0.4	0.28	2.03	3.00
7							0	0.28	2	3.00
8								0	2.20	2.8
9									0	5.00
10										0
11										
12										
13										
14										
15										
16										
17										
18										
19										
20										

Table3: MINIMUM SPANNING TREE EDGES

Edge	Euclidean distance/weight	Edge	Euclidean distance/weight
{1,2}	0.28	{12,10}	0.71
{1,3}	0.28	{12,11}	0.71
{2,4}	1.3	{10,13}	0.71
{4,18}	0.5	{11,20}	8.06
{2,9}	5.03	{13,16}	10.63
{9,5}	1.81	{16,17}	1
{5,6}	0.28	{16,14}	0.71
{5,7}	0.28	{14,15}	1
{5,8}	0.4	{15,19}	9.21
{8,12}	2.35		

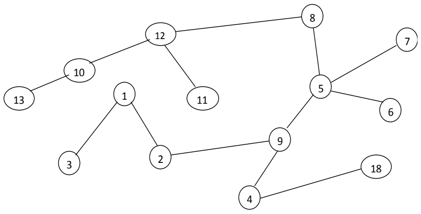


Figure1: Clusters connected through points-EMST1

Our OPIMSTCA constructs EMST1 from the dissimilarity matrix is shown in the figure1.The mean $\bar{w}$ and standard deviation σ of the edges from the EMST1 are computed respectively as 2.38 and 4.66.The sum of the mean $\bar{w}$ and standard deviation σ is computed as 7.04.This value is used to identify the inconsistence edges in the EMST1 to generate subtrees(clusters).based on the above value the edge having weight 8.06,9.21 and 10.63.By removing inconsistent edges from the EMST1,vertices(data points) in the EMST1 partitioned into four sets (four subtrees (or) clusters) T_1 , T_2 , T_3 and T_4 namely $T_1 = \{1,2,3,4,5,6,7,8,9,10,11,12,13,18,20\}$, $T_2 = \{14,15,16,17\}$, $T_3 = \{19\}$ and $T_4 = \{20\}$ is show in the figure 2.center point (vertex) for each of the each subtree is find using eccentricity of points (vertices).These center point (or) vertex is connected and again another minimum spanning tree EMST2(figure3) is constructed. To calculate the standard deviation each subtree using center. The maximum value of standard deviation of clusters $\Delta\sigma_i$ and the minimum value of standard deviation of clusters $\delta\sigma_i$, is find to compute cluster separation value. If the CS is greater than 0.8, then to remove the minimum edge weight of EMST2 .To update the clusters(subtree) vertices then to compute the center using eccentricity points(vertices).Finally the optimal iterative minimal spanning tree clustering algorithm produce, the optimal number of clusters 2.

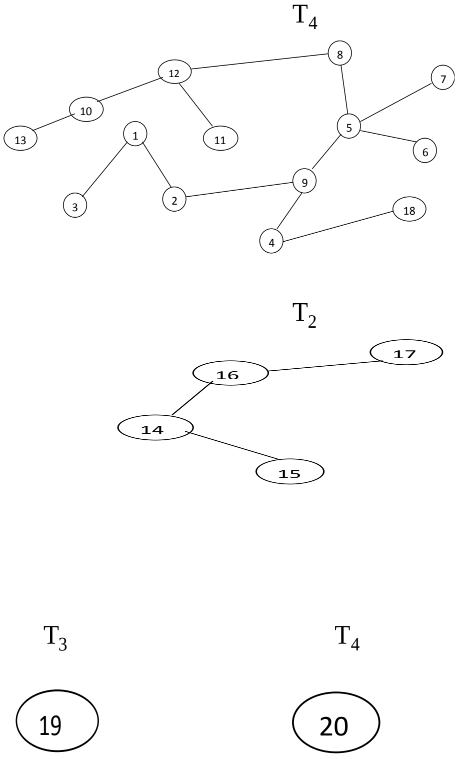


Figure2: Clusters connected through points- EMST1 (number of clusters 4)

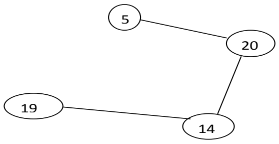


Figure3:EMST2 using four clusters center points. Center points: 5,14,19,20

Our algorithm OPIMST clustering algorithm, processing the optimal number of clusters Two.

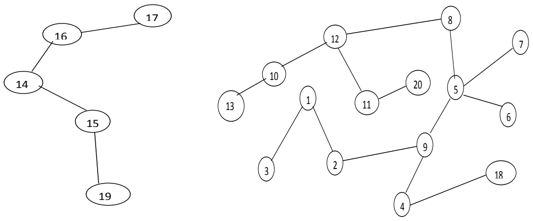


Figure: 4 OPIMST clustering algorithm, center 5 and16, $\delta\sigma_i = 2.94$ **and** $\Delta\sigma_i = 3.60$ $CS = 0.82 > 0.8$

5. CONCLUSION

In this paper proposed an optimal iterative MST clustering algorithm and applied to random data segmentation. The algorithm was formulated by introducing Euclidean distance function, eccentricity, and standard deviation of each cluster, with basic Objective function of the optimal iterative minimal spanning tree clustering algorithm to have proper effective segmentation in image. Our algorithm uses new cluster validation criterion based on the geometric property of partitioned clusters to produce optimal number of true clusters. The test result shows that the proposed method outperformed the base line methods. In future we will explore and test our proposed clustering algorithm in various domains and this work hopes that the proposed method can also be used to improve the performance of other clustering algorithm based on Euclidean distance functions.

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