A Comparative Analysis Of Clustering Based Brain Tumor Segmentation Techniques

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Abstract: Image segmentation of human brain is commonly used for clear-cut partitioning of gray and white matter, cerebral spinal fluid and skull in the image. Several image segmentation strategies have been proposed from the early stages of image processing. Clustering is one of the most popular among them. In this work k-mean, Fuzzy c mean and Genetic algorithm based clustering techniques has been studied and comparative analysis has been done in terms of mean and variance of segmented tumor, and inter and intra cluster distance of the centers for individual algorithm. The accuracy of each method is also compared with the ground truth image. The implemented clustering methods are further compared based on some segmentation metric. Here the BRATS-12 dataset is used for testing the algorithms, which consists 27 high grade tumor and 15 low grade tumor MRI images. Each MRI image is given with four different modalities such as T1, T2, FLAIR and T1+C. The database also consist four ground truth segmented images for each image. The ground truth images are prepared by the four different observers.

Index Terms: brain tumor, clustering, fuzzy c-mean, genetic algorithm, k mean, segmentation.

I. INTRODUCTION

Image segmentation is the process of dividing an image into specific sections based on different levels of certain parameters to clearly identify objects from the original image. Brain image segmentation is very critical and sensitive as it is related with the human life. Hence, it further requires minimum segmentation error. There can be two measure types of image segmentation. One is block based and another is layer based. The block based segmentation can be broadly classified into the following two categories.

This paragraph of the first footnote will contain the date on which you submitted your paper for review. It will also contain support information, including sponsor and financial support acknowledgment. For example, "This work was supported in part by the U.S. Department of Commerce under Grant BS123456."

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i) Region Based
ii) Edge Base or Boundary Base
The region based segmentation further classified in the following categories [1].
i) Clustering
ii) Split and Merge
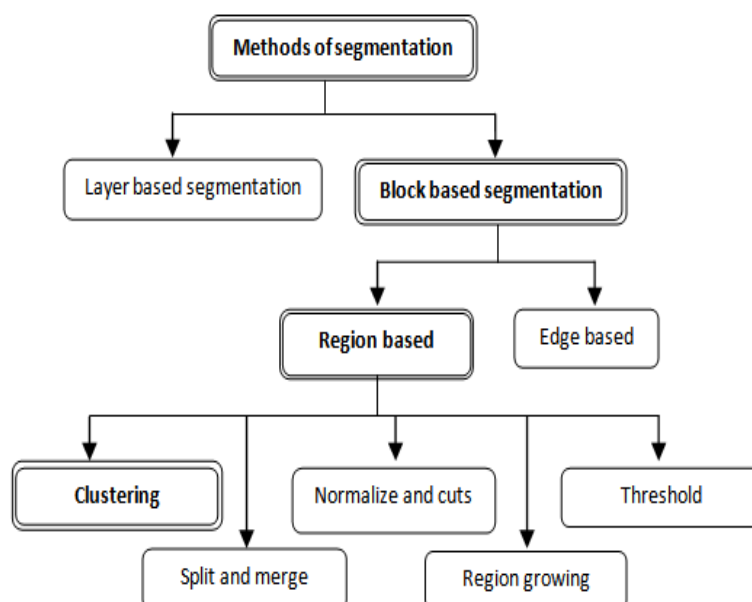iii) Normalized cuts
iv) Threshold

Figure 1: Types of segmentation

Clustering is widely used for segmenting medical images. Clustering algorithms are used to partition a dataset into a certain number of group, subsets or categories, where the data members of each group are similar while the data members from different group are not [2]. Different researchers adopted different clustering techniques for medical image segmentation. Among them k-mean, fuzzy c-mean and genetic algorithm based clustering techniques are most popular.

K-mean has been chosen as clustering approach by several researchers because of its simplicity. In k-means, there are k number of clusters (where, k≥ 2) and each data item belongs to any one of those clusters with the minimum mean (of?). Ming-Ni Wu, Chia-Chen Lin and Chin-Chen Chang [3] proposed a color based k mean clustering segmentation technique for brain tumor detection. In some later work color converted k-mean clustering segmentation technique [4] is proposed by Li-Hong Juang and Ming-Ni Wu. J. Vijay and J. Subhashini also used k-mean clustering algorithm [5].

In k-mean fuzzy clustering, whether a data item will belong to a cluster or not shall depend together on the probability that the data item is to be a member of a cluster and on the fuzziness coefficient in the membership function. Thus, k-mean fuzzy clustering allows a data item to be a member of more than one cluster. For this reason k-mean fuzzy clustering remains a good choice for image segmentation.

Although genetic algorithm is basically inspired from the biological sciences, but Mr. Ujjwal maulick and Sanghamitra bandyopadhyay [13] has shown in their work that it can be effectively used as a clustering technique. Further, G Rajesh Chandra and Kolasani Ramchand H Rao used genetic algorithm based clustering [14] for brain tumor segmentation with an effective success rate 97%.

N. Nandha Gopal and M. Karnan used fuzzy k- mean along with genetic algorithm and particle swam optimization techniques [7]. On the other hand support vector machine classifier is also associated with fuzzy c means by Parveen and Amritpal Singh [9]. Further, M. Shasidhar, V. Sudheer Raja and B. Vijay Kumar modified the fuzzy c mean algorithm to minimize convergence time [10] by using a comprehensive feature vector space to do the segmentation. A. Rajendran and R. Dhanasekaran also used region based fuzzy clustering in their work [11]. In some other work [8] region growing method is also integrated with the fuzzy clustering. Even not only brain, fuzzy c mean is also used to segment lung tumor [12]. Again, Garima Singh and M.A. Ansari use Naive Bayes classifier and SVM to determine whether there is tumor or not [6].

II. METHODS

A. k-mean Algorithm
1. Take input image of size r*c and convert it into grayscale
2. Set number of required cluster (k)
3. Partition the intensity range of input image equally into number of required clusters(k) by identifying the cluster having minimum distance for each pixel of input image and include the pixel intensity into its corresponding cluster set
4. Update the partition value of each cluster i.e. Cluster[k] as mean of its cluster set
5. If previous cluster partition value is not equal to current cluster partition value then go to step 4.

$$\text{Cluster[k]} = \text{Min intensity} + \frac{\text{Max intensity} - \text{Min intensity}}{\text{Total no. of clusters}} * \text{k} \quad (1)$$

6. Distinguish pixels of each cluster set with distinct intensity in image matrix.
7.

B. fuzzy c-mean Algorithm

1. Take input image of size [r, c] and convert it into grayscale.
2. Convert image into a 1D array of size [1, r*c] i.e. ARR[r*c].
3. Set value for fuzziness i.e. m and number of cluster required i.e. nc.
4. Choose initial centroid for each cluster randomly i.e. Centroid[j]=random, for j=1 to nc.
5. Compute membership function i.e. MFN for each pixel in ARR[i] against each centroid in Centroid[j] as:

$$MFN_{ij} = 1 \div \sum_{k=1}^{nc} \left(\frac{d_{ij}}{d_{ik}}\right)^{\frac{2}{m-1}} \quad (2)$$

Where d_{ij}= Distance between ARR[i] and Centroid[j]

6. Now Calculate new centroid as:

$$\text{Centroid[j]} = \frac{\sum_{i=1}^{c*r}(MFN_{ji})^{m} * ARR[i]}{\sum_{i=1}^{c*r} MFN_{ji}} \quad (3)$$

7. If difference between previous and current centroid is greater than .001 then go to step 5.
8. For each cluster identify the cluster with minimum MFN and distinguishcorresponding pixel in ARR[r*c] with distinct intensity.
9. Revert the updated 1D array i.e. ARR[r*c] to 2D image matrix.

C. Genetic Algorithm (GA) based Clustering

GA based clustering offers an effective technique to find the appropriate cluster centers. A new population with a better fitness value is generated in each iteration. In other words it actually optimizes the similarity metric of the cluster. Here in this case the chromosomes are consisting of four floating point value representing the cluster centres. The population is initialized with four chromosomes. This technique randomly selects two chromosomes for crossover and mutation to generate a new chromosome and it is repeated for 4 times. The termination criterion is set to 100th iteration.

Chromosome representation

Here the chromosome string consist of four randomly generated number in the range between 0 and maximum intensity value of the input image.

Example:

Chromosome_1=[32.3816 120.809 207.7545 230.9769]

Population initialization

The population consists of 4 chromosomes. There can be any number of chromosomes in the population, but for simplicity here only 4 chromosomes is taken.

Fitness computation

Fitness computation is done into two phase. In the first phase the clustering is performed by assigning each point to the appropriate cluster with centre z_j.

$$x_i \in c_j$$

Then new cluster centres are determined by computing the mean of each corresponding cluster.

In the second phase the actual computation of fitness function is performed as follows.

$$\mu = \sum_{i=1}^{k} \mu_i$$

$$\mu_i = \sum_{x_j \in c_i} |x_j - z_i|$$

And the fitness function is defined as $f = 1/\mu$ that means for minimum distance (μ) it maximizes f.

i. Selection

A range of value is assigned to each chromosome for selection based on their fitness value such that to make the sum of total range is equal to 1. In the next step an random number is generated and the corresponding chromosome is selected in which it lies.

ii. Crossover

Two chromosomes is selected by selection process. As it is considered here that the chromosomes are consist of 4 floating point numbers, so the crossover point(cp) is determined by generating a random number between 1 and 3. Then the new chromosome is obtained by coping values 1 to cp positions of 1st selected chromosome and (cp+1) to 4 values from 2nd selected chromosome.

iii. Mutation

In mutation process any one of the values in the chromosome is modified. It is done by determining the mutation point in the similar way by generating a number between 1 to 4 and a value x is added to the corresponding value in the chromosome. Where x varies from -10 to +10.

Termination criteria

Genetic Algorithm is a NP Complete problem. It always leads to better solution, but the best solution cannot be achieved in real time. Instead it is suitable to optimize the solution. Here the solution is optimized up to 100th iteration.

III. RESULT AND DISCUSSION

All three above discussed clustering algorithms has been implemented in MATLAB 13. In this section the result of these algorithms are discussed with comparative analysis. The comparison is done based on the clustering metric and segmentation metric. In case of clustering metric, the comparison has been shown in terms of inter-cluster distance and intra-cluster distance, where inter-cluster distance measures how pixels are co-related within a cluster and intra-cluster distance measures how two or more clusters are related. It is always desirable to minimize the inter-cluster distance and maximize the intra-cluster distance. Equation (4) is used to compute intra-cluster distance as follows.

$$\sum_{i,j=1}^{k} |c_i - c_j| \qquad (4)$$

Where $i \neq j$, c_i and c_j represents centroid of ith and j^{th} cluster respectively and k is the number of cluster. And for the kth cluster the inter-cluster distance computed as below.

$$\frac{\sum_{i=1}^{n} |c_k - x_i|}{n} \qquad (5)$$

Where $x_i \in c_k$ and n is the total number of elements in cluster k.

On the other hand for segmentation metric, two different measure approaches has been applied. Firstly, the comparison is given in terms of mean(μ) and variance(σ^2) of segmented tumor. The following equations are used to evaluate mean and variance.

$$\mu = \frac{\sum x_i}{n} \qquad (6)$$

$$\sigma^2 = \frac{\sum (x_i - \mu)^2}{n} \qquad (7)$$

Where $x_i \in c_4$ and 'n' is the total number of intensities in cluster 4.

Table 1 clustering metric results of fuzzy c mean

Cluster wise Inter cluster Distance	Intra-cluster Distance	Mean of segmented Area	Varience of segmented Area
6,6,1,23	78.31226985	173.9043478	93.55942029
8,9,5,1	41.80807445	92.5908142	29.03038738
8,6,1,7	51.20115052	114.0051037	44.46251994
15,2,11,8	64.25361816	137.9640206	80.82467162
20,8,2,7	68.65604344	154.1303879	72.24946121

Table 2: clustering metric results of k mean

Cluster wise Inter cluster Distance	Intra-cluster Distance	Mean of segmented Area	Varience of segmented Area
3,9,14,18,	77.45287505	168.9377818	73.13165014
2,11,8,15,	64.22515616	137.3928571	82.66573661
1,7,6,8,	51.02930397	114.0051037	44.46251994
1,6,6,23,	76.15119969	172.7380282	93.6
2,8,6,20,	61.41783622	137.3942857	61.33142857

Table 3 : clustering metric results of GA based clustering

Cluster wise Inter cluster Distance	Intra-cluster Distance	Mean of segmented Area	Varience of segmented Area

3,11,14,7,	98.2147	179.5409	63.118
4,11,13,8,	78.1063	151.7681	40.733
1,7,7,5,	54.3939	106.1115	83.279
1,7,10,17,	83.0902	146.9651	52.144
2,9,12,12,	85.3040	153.2177	161.69

Secondly, the comparison shows the Volume Error(VE), Coefficient of Similarity(COS), Spatial Overlap(SO), Under Segmentation Rate(USR) and Over Segmentation Rate(OSR) of the segmented output image of each algorithm with respect of four different observers of the BRATS dataset. The equations for these metric are given below.

Volume Error, $VE = \frac{2(S-GS)}{(S+GS)}$ (8)

Coefficient of Similarity, $COS = 1 + \frac{(GS \cap S)}{GS}$ (9)

Spatial Overlap, $SO = \frac{2(GS \cap S)}{(S \cup GS)}$ (10)

Under Segmentation Rate, $USR = |GS - (S \cap GS)|$ (11)

Over Segmentation Rate, $OSR = |S - (S \cap GS)|$ (12)

As per above discussion the following results are obtained.
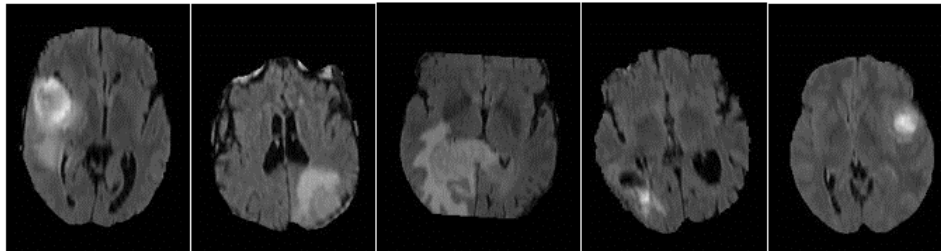

Figure 2 : Image H1, Image H2, Image H3, Image H4, Image H5(left to right)

Table 4: Comparison based on segmentation metric for image H1

Algorithm	Observer	VE	COS	SO	USR	OSR
c-mean	Observer1	0.235646	1.87183	1.545564	283	552
	Observer2	0.251401	1.876446	1.560132	267	583
	Observer3	0.232192	1.867475	1.531932	295	546
	Observer4	0.135941	1.791217	1.309113	561	351
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
GA	Observer1	0.211551	1.830163	1.41928	375	478
	Observer2	0.229428	1.832022	1.424723	363	513
	Observer3	0.218206	1.815813	1.377845	410	495
	Observer4	0.12445	1.744325	1.185536	687	311
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
k-mean	Observer1	0.099005	1.643569	0.948915	787	189
	Observer2	0.10236	1.655715	0.975559	744	193
	Observer3	0.092805	1.643306	0.948344	794	178
	Observer4	0.048871	1.560104	0.777979	1182	105

Table 5 : Comparison based on segmentation metric for image H2

Algorithm	Observer	VE	COS	SO	USR	OSR
c-mean	Observer1	0.922985	1.956616	1.83368	60	2319
	Observer2	0.963577	1.97	1.883495	39	2381
	Observer3	0.846242	1.91169	1.675423	139	2207
	Observer4	0.864159	1.957018	1.835158	64	2217
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
GA	Observer1	0.999079	1.965293	1.865828	48	2713
	Observer2	1.038893	1.976923	1.909774	30	2778
	Observer3	0.924226	1.92122	1.707892	124	2598
	Observer4	0.944194	1.963062	1.857513	55	2614

	Observer	VE	COS	SO	USR	OSR
k-mean	Observer1	0.955786	1.963847	1.860433	50	2486
	Observer2	0.996288	1.976154	1.906837	31	2550
	Observer3	0.879288	1.919949	1.703529	126	2371
	Observer4	0.902411	1.956347	1.83269	65	2395

Table 6 : Comparison based on segmentation metric for image H3

Algorithm	Observer	VE	COS	SO	USR	OSR
c-mean	Observer1	0.384515	1.938986	1.769979	195	1475
	Observer2	0.478308	1.9541	1.824456	131	1753
	Observer3	0.312978	1.922549	1.712467	271	1248
	Observer4	0.218055	1.861523	1.513467	569	936
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
GA	Observer1	0.786271	1.974969	1.90232	80	4089
	Observer2	0.875037	1.982481	1.931129	50	4401
	Observer3	0.698804	1.990283	1.961506	34	3740
	Observer4	0.57504	1.961791	1.852789	157	3253
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
k-mean	Observer1	0.384515	1.938986	1.769979	195	1475
	Observer2	0.478308	1.9541	1.824456	131	1753
	Observer3	0.312978	1.922549	1.712467	271	1248
	Observer4	0.218055	1.861523	1.513467	569	936

Table 7 : Comparison based on segmentation metric for image H4

Algorithm	Observer	VE	COS	SO	USR	OSR
c-mean	Observer1	0.02814	1.404603	0.507213	802	27
	Observer2	0.034503	1.464439	0.604911	625	30
	Observer3	0.431493	1.889163	1.600887	45	211
	Observer4	0.020316	1.261266	0.300524	1541	27
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
GA	Observer1	1.163623	1.751299	1.203329	335	3282
	Observer2	1.233474	1.793488	1.315341	241	3368
	Observer3	1.654468	2	2	0	3888
	Observer4	0.973981	1.569032	0.79531	899	3107
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
k-mean	Observer1	0.033161	1.409057	0.514232	796	32
	Observer2	0.038857	1.470437	0.615126	618	34
	Observer3	0.436805	1.903941	1.649438	39	216
	Observer4	0.023979	1.264142	0.304336	1535	32

Table 8 : Comparison based on segmentation metric for image H5

| Algorithm	Observer	VE	COS	SO	USR	OSR
c-mean	Observer1	1.561763	1.808411	1.356863	246	8275
	Observer2	1.547775	1.796421	1.32342	273	8245
	Observer3	1.441772	1.804577	1.346097	333	7942
	Observer4	1.572131	1.788933	1.302872	267	8315
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
GA	Observer1	0.516971	1.548287	0.755365	580	693
	Observer2	0.480643	1.551081	0.760679	602	658
	Observer3	0.337311	1.512911	0.689818	830	523
	Observer4	0.530428	1.546245	0.751495	574	706
	Observer	**VE**	**COS**	**SO**	**USR**	**OSR**
k-mean	Observer1	0.327306	1.404984	0.507813	764	353
	Observer2	0.29991	1.40343	0.505371	800	332
	Observer3	0.178502	1.377347	0.465099	1061	230
	Observer4	0.32928	1.411858	0.518666	744	352
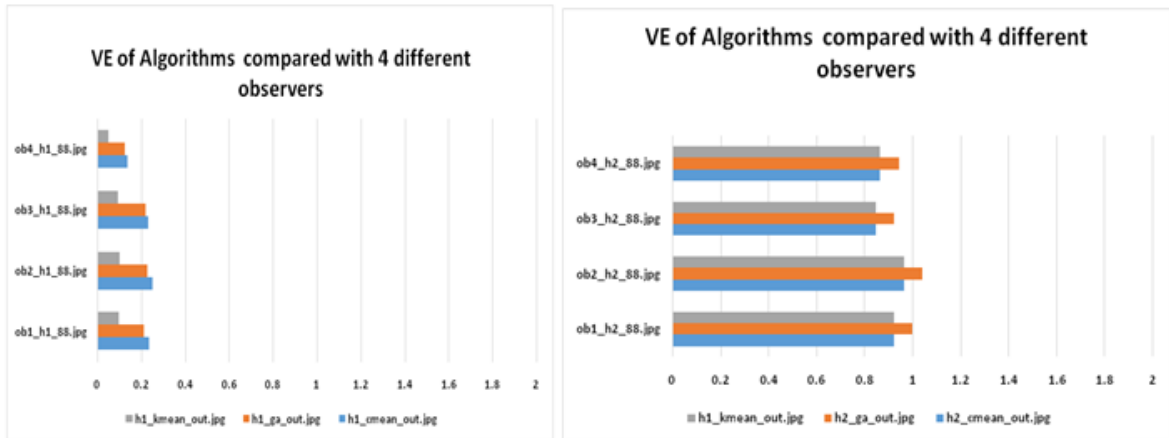
Figure 3 : volume error for Image H1and H2
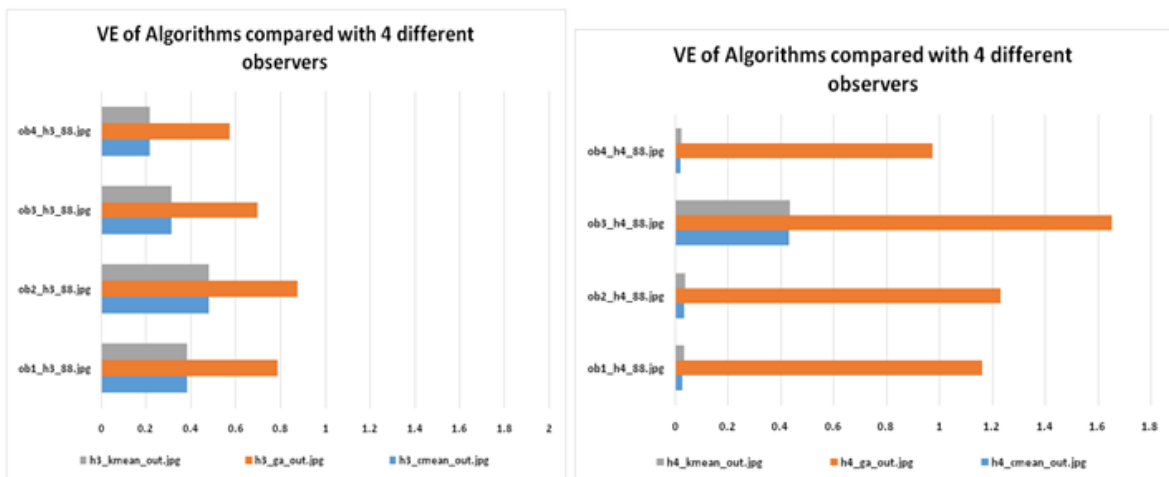
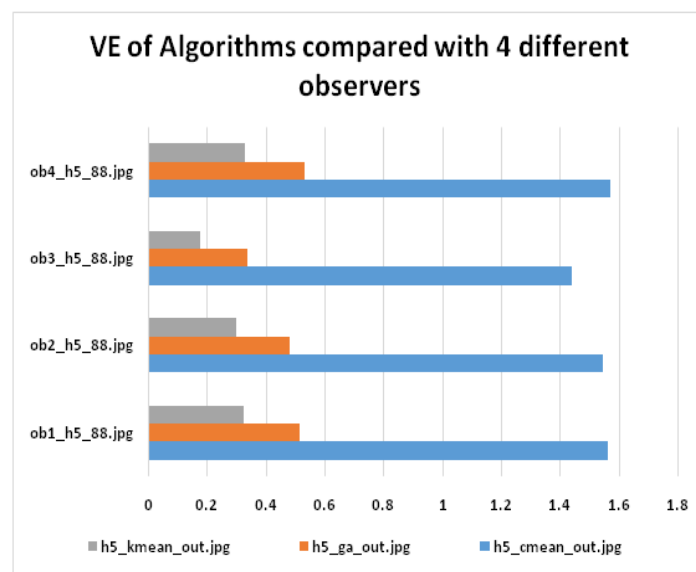**Figure 4 : volume error for Image H3 andH4**

Figure 5 : volume error for Image H5

IV. CONCLUSION

In this work k-mean, c-mean and GA based clustering are studied, implemented and analyzed individually based on the same data set. By analyzing the facts, it can be concluded that clustering efficiency is totally depends on characteristics of data. Different clustering approach gives best result for different images. Therefore only clustering based approach alone can not give best result, rather some additional approach along with clustering should be adopted for getting the best result in every case.

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