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Brain Tumor Detection of MRI Image using Level Set Segmentation and Morphological Operations

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Abstract – **In medical image investigation, one of the essential problems is segmentation of structural sections. In this paper we present a new concept of tumor detection and also validated segmentation of 2D MRI Data. This method on the appropriate setting of parameters can segment the tumor. This method unlike others does not require any initialization in the tumor. Also the effectiveness of this approach is demonstrated by quantitative evaluations and visualization of the segmentation results. First, the work was carried over to calculate the area of the tumor with single slice of MRI data set and then it is extended to calculate the area of tumor from multiple image MRI data sets. The fuzzy c-means clustering algorithm along with Self-Organizing MAP, Neural Network and thresholding and morphology is used for proper classification of medical data.**

Keywords – **Brain-Tumor, Fuzzy C-Means, MRI Data, Neural Network, Self-Organizing MAP.**

I. INTRODUCTION

Tumor is one of the most common brain diseases, so its identification and treatment have a vital importance for more than 400000 persons per year in the world (based on the World Health Organization (WHO) estimates). On the other hand, in modern years, expansions in medical imaging techniques allow us to use them in numerous dominions of medicine, for example, computer aided pathologies diagnosis, surgical planning, surgical guidance, statistical and time series (longitudinal) examination.

Brain cancer is one of the greatest deadly and obstinate diseases [1]. Tumors may be set in areas of the brain that are critical to run the body's vital tasks, this tumor cells infect other parts of the brain, establishing additional tumors that are too minor to spot with the usual imaging techniques. Sometimes, it's a hard to identify the Brain cancer's position such complications make it a difficult task to cure it for those people who has to fight with their life.

The physicians and cancer researchers compare imaging studies from cases similar to a selected patient or a drawn query region and create a similarity measure which is relevant [2]. It is important to perform complex statements with logical operations to combine different similarity measures and to specify different query regions, all without having expertise in MATLAB. It is also necessary to give the user an intuitive interface to specify a query region (whether on a study of a patient or on a brain atlas). The query region which can be drawn has also to consist of complex statements to specify a complete query region.

To obtain similarity between the drawn query region and the Region of Interest (ROI) such as the segmented tumor or edema, the voxel-set of the segmentations is stored in the database. A voxel-set of a segmented ROI belonging to one study contains about 20,000 voxels [3]. For efficient retrieval the Database model has to be well designed. It is important to achieve a fast retrieval of thousands of data in an acceptable time; therefore the database tables must be indexed to reduce search time.

One goal is to use machine learning methods to predict the locations of occult cancer cells to allow radiologists to refine the radiation therapy used to treat brain tumors; finding previous patients with similar tumors to a current patient and examining how the previous patients responded to treatment will help determine how to treat the current patient. Similarity based queries play an increasingly important role in medical training, research, and clinical decision making [4] [5].

Similarity based retrieval is used by physicians who want to compare imaging studies from either a new patient or a self-selected query to those from a database of prior patients to help them to specify diagnosis, the tumor growth, and potential treatment options. Therefore it is important to support interactive queries of the tumor dataset by physicians and cancer researchers. An interactive query which provides the opportunity to do queries based on text data and to combine them to image-based similarity queries is the basis for significant analysis. Therefore a database is needed to store both the text-based and image-based brain tumor data.

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II. BRAIN TUMORS

Brain tumors are abnormal masses in or on the brain. Tumor growing may appear as a result of uncontrolled cell proliferation, a failure of the regular shape of cell death, or both. Brain tumors can be either primary or secondary [5].

Primary tumors are composed of cells just like those that belong to the organ or tissue where they start. A primary brain tumor starts from cells in the brain. Maximum brain tumors in kids are primary, and at minimum half of all primary tumors create from cells of the brain that support the body's nervous system.

Tumors associated to the nervous system are called **Gliomas**, and they invent in the brain's glia cells. Central nervous system tumors constitute a heterogeneous group of diseases that vary from benign, slow-growing lesion to aggressive malignancies that can cause death within a matter of months if left unprocessed. All of these tumors has distinctive clinical, radiographic, and biologic appearances that dictate, in part, their supervision.

Benign tumors raise slowly and do not feast. Nevertheless, benign tumors are serious and can be life threatening; growing in a narrow space, a benign tumor be able to put force on the brain and compromise its function.

Malignant tumors grow quickly and can spread to surrounding tissues. "Malignancy" or "malignant" virtually always refers to cancer. In common, the glial neoplasms that are seen commonly in adults include low-grade tumors such as the infilterating astrocyoma, oligodendroglioma, and varied low-grade tumors. Intermediate-grade tumors include anaplastic astrocytoma and anaplastic oligodendroglioma, or diverse anaplastic tumors. The utmost malignant glial neoplasm is glioblastoma multiforme. A range of other tumors can be seen as well, such as meningioma and ependymoma. Brain tumors of infancy contain pilocytic astrocytoma, primitive neuroectodermal tumors such as medulloblastoma, ependymoma, and a variation of rare tumor categories such as the germ cell tumors and atypical rhabdoid tumors of the central nervous systems. The malignancy of brain tumor is not only dependent on the pathological malignancy, but also on the location, growth pattern and rate of growth. An otherwise benign tumor maybe located in an part of brain that comprise vital centers and therefore may cause great harm, rather than an extremely malignant tumor in an area that might be involved in abstract functions and may not cause symptoms for a long time. The position of the tumor is very important in the diagnosis as well. MRI cannot reliably separate between the different categories of tumors on imaging only, though merging the info with position can help in foreseeing the exact histology of the tumors.

Secondary tumors are made up of cells from another part of the body that has spread to one or additional parts. Secondary brain tumors are essentially composed of cancer cells from somewhere else in the body that have metastasized, or spread, to the brain, such as osteosarcoma (a primary bone tumor) or rhabdomyosarcoma (a primary tumor of muscle). These lesions tend to be rather well defined and may be more easily removed by surgery.

Brain tumors are relatively common tumors, especially in children. A tumor is any mass that conquers space. It is also called a space-occupying lesion (SOL). Not all tumors are cancer, and not all cancers are tumors.
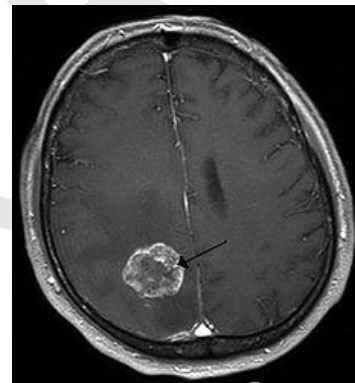

Figure 1: Brain image with a tumor [10]

III. PROPOSED METHOD

Image Acquisition

Images are obtained using MRI scan [6] and these scanned images are displayed in a two dimensional matrices having pixels as its elements. These matrices are dependent on matrix size and its field of view. Images are stored in MATLAB and displayed as a gray scale image of size 256*256. The entries of a gray scale image are ranging from 0 to 255, where 0 shows the total black colour and 255 shows the pure white colour. Entries between this ranges vary in intensity from black to white.

For experimental purpose 30 female and 30 male patients were examined, all patients have ages ranging from 20 to 60 years. Their MRI scans were stored in the database of images in JPEG image formats.
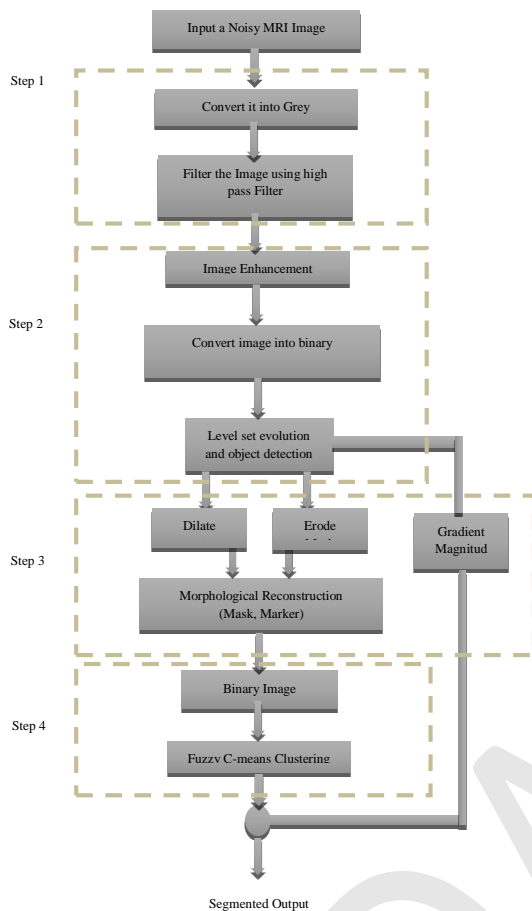
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Figure 2: Flow chart of proposed work

the Morphological Reconstructions (Mask, Marker) from which binary image is extracted. The Gradient Magnitude is stored to be added with the output of C-Means Clustering Algorithm.
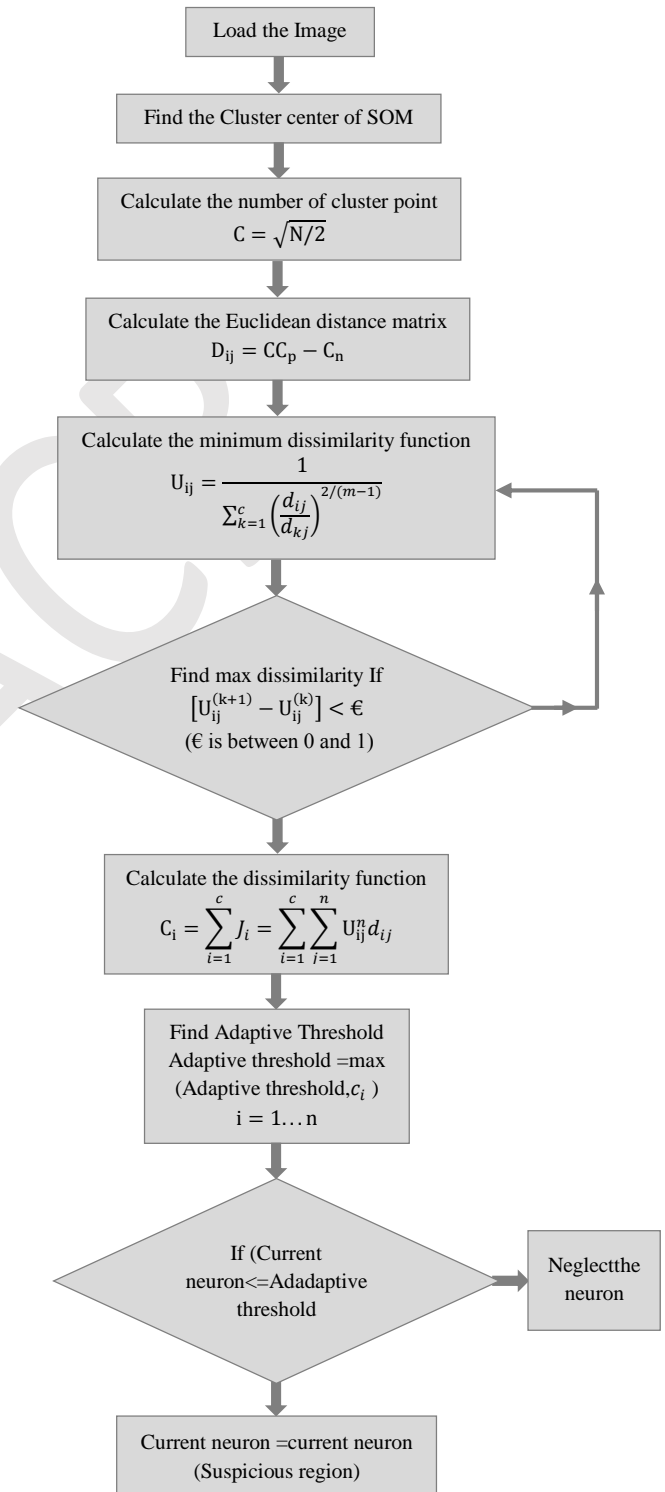

Figure 3: Flow chart of MRI data mapping using Self Organizing Map

Pre-processing

The first phase is to get the MRI image and application of pre-processing steps. There are various methods which come under this step; we will be dealing with only grey scale and filters. Basically pre-processing is done to remove noise and blurring as well as a ringing effect in order to get the enhanced and much clear image for our purpose. The filter which we have used is a high pass filter but as we are working on image samples that are required for the medical purpose. The high pass filter has to be passed with mask for better image, to achieve this we are using a sobel operator.

Level Set Function

The Level Set Function is used here to robust the image under consideration towards noise condition, aptitude in extracting curved objects with complex topology and its clean numerical framework of multidimensional implementation. With the initialization of level function we generate the initial region of image as a rectangle. Level set evolution and object detection is further divided in three categories i.e. dilate marker, erode marker and Gradient Magnitude. The first two are subjected to

Self-Organizing Maps

Self-organizing maps (SOMs) are a data visualization technique invented by Professor TeuvoKohonen which reduce the dimensions of data through the use of self-organizing neural networks. The problem that data visualization attempts to solve is that humans simply cannot visualize high dimensional data as is so techniques are created to help us understand this high dimensional data. The way SOMs go about reducing dimensions is by producing a map of usually 1 or 2 dimensions which plot the similarities of the data by grouping similar data items together. So SOMs accomplish two things, they reduce dimensions and display similarities.

As you can see in the figure 3, like colours are grouped together such as the greens are all in the upper left hand corner and the purples are all grouped around the lower right and right hand side.

Self-organizing maps are dissimilar from other artificial neural networks in the sense that they use a neighbourhood function to preserve the topological properties of the input space.

This makes SOMs valuable for imagining low-dimensional views of high-dimensional data, akin to multidimensional scaling. The model was first labelled as an artificial neural network by the Finnish professor Teuvo Kohonen, and is also known as a Kohonen map or network.

Like most artificial neural networks, SOMs operate in two modes: training and mapping. "Training" builds the map using input examples (a competitive process, also called vector quantization), while "Mapping" automatically classifies a new input vector.
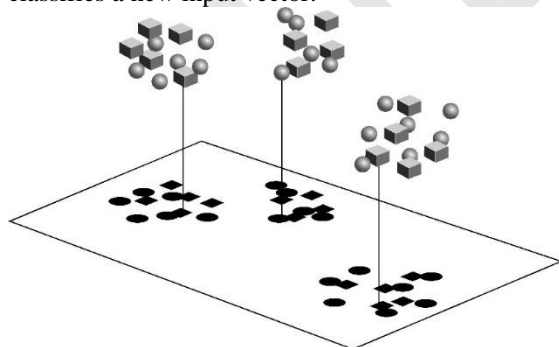

Figure 4: Self-organizing maps [11]

Algorithm: SOM
Step 1: Randomize the map's nodes weight vectors.
Step 2: Grab an input vector.
Step 3: Traverse each node in the map
Step 4: Use Euclidean distance formula to find the similarity between the input vector and the map's node's weight vector.

Step 5: Track the node that produces the smallest distance (this node is the best matching unit, BMU)
Step 6: Update the nodes in the neighbourhood of BMU by pulling them closer to the input vector.

$$Wv(t + 1) = Wv(t) + alpha(D(t) - Wv(t))$$
(1)

Increment t and repeat from 2.
$alpha-$> Monotonically decreasing learning coefficient. It is 1 for neurons close to BMU and zero for others.
$D(t)-$>Input vector
Neighbourhood function shrinks with time. At the beginning, when the neighbourhood is broad, the self-organizing takes place on a global scale. When the neighbourhood has shrunk to just a couple of neurons, the weights are converging to local estimates.

Fuzzy C-means clustering

In fuzzy clustering, each point has a degree of belonging to clusters, as in fuzzy logic, rather than belonging completely from just one cluster. Thus, points on the edge of a cluster, maybe in the cluster to a lesser degree than points in the center of cluster. An overview and comparison of different fuzzy clustering algorithms are available.

With fuzzy c-means, the centroid of a cluster is the mean of all points, weighted by their degree of belonging to the cluster:

$$c_k = \frac{\sum_x w_k(x)x}{\sum_x w_k(x)}$$
(2)

The degree of belonging,$w_k(x)$, is related inversely to the distance from x to the cluster center as calculated on the previous pass. It also depends on a parameter m that controls how much weight is given to the closest center. The fuzzy c-means algorithm is very similar to the k-means algorithm:

1. Choose a number of clusters.
2. Assign randomly to each point coefficients for being in the clusters.
3. Repeat until the algorithm has converged (that is, the coefficients' change between two iterations is no more than, the given sensitivity threshold) :
   - Compute the centroid for each cluster, using the formula above.
   - For each point, compute its coefficients of being in the clusters, using the formula above.

The algorithm minimizes intra-cluster variance as well, but has the same problems as k-means; the minimum is a local minimum, and the results depend on the initial choice of weights. Using a mixture of

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Gaussians along with the expectation-maximization algorithm is a more statistically formalized method which includes some of these ideas: partial membership in classes.
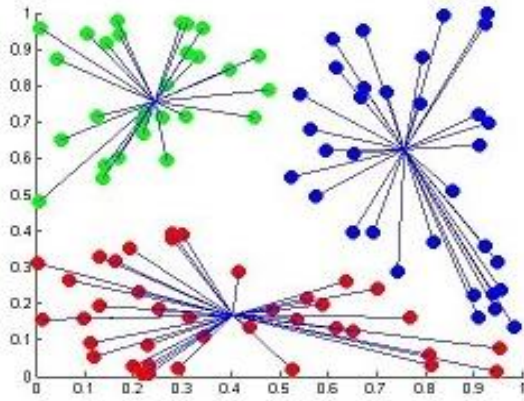

Figure 5: Fuzzy c-means clustering [12]

Algorithmic steps for Fuzzy c-means clustering:

Let $X = \{x_1, x_2, x_3 \ldots, x_n\}$ be the set of data points and $V = \{v_1, v_2, \ldots, v_c\}$ be the set of centers.

1. Randomly select 'c' cluster centers.
2. Calculate the fuzzy membership μ_{ij} using:

$$\mu_{ij} = 1/\sum_{k=1}^{c}(d_{ij}/d_{ik})^{(2/(m-1))}$$

3. Compute the fuzzy centers v_j' using:

$$v_j = \frac{\left(\sum_{i=1}^{n}\mu_{ij}{}^{m}x_i\right)}{\sum_{i=1}^{n}\mu_{ij}{}^{m}} \forall_j = 1,2, \ldots c$$

4. Repeat step (2) and (3) until the minimum 'J' value is achieved or

$$||U^{(k+1)} - U^{(k)}|| < \beta.$$

Where,
'k'= the iteration step.
'β'= the termination criterion between [0, 1].
'$U = (\mu_{ij})_{n*c}$' Is the fuzzy membership matrix.
'J' = the objective function.

IV. SIMULATION AND RESULTS

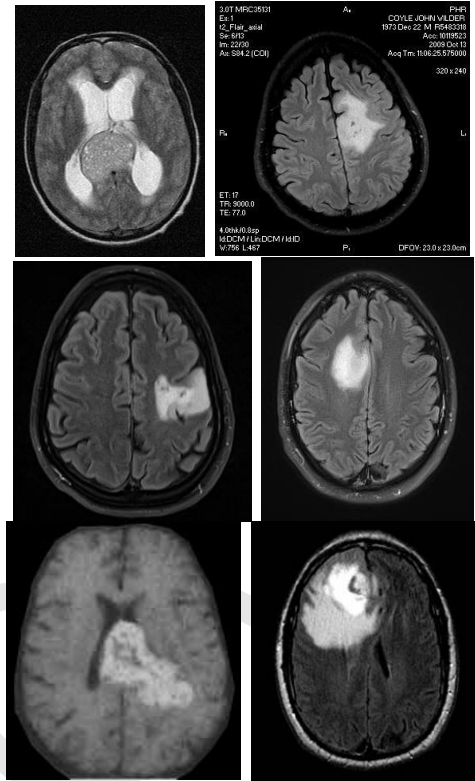The performance of proposed algorithms has been studied by means of MATLAB simulation.
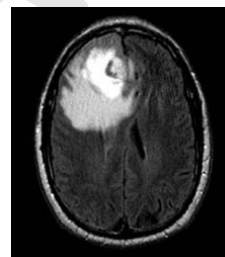

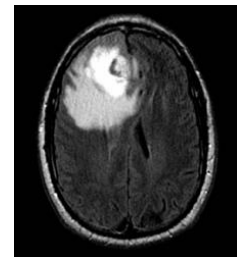Figure 6: Input images

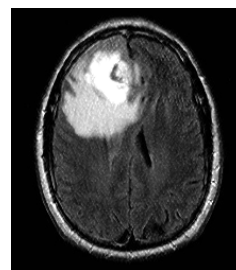Figure 7: Acquired image

Figure 8: High pass filtered image

Figure 9: Enhanced image

Figure 10: Binary image

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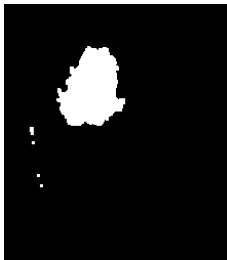

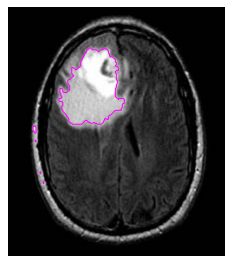Figure 11: Morphed image with detected tumor region

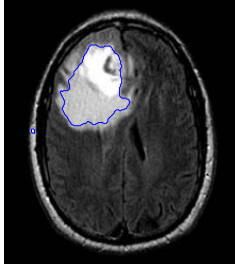
Figure 12: Original image with initial tumor region
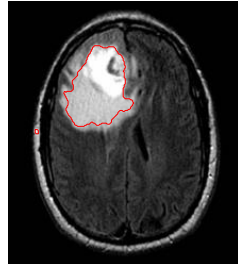

Figure 13: Iteration no. 87
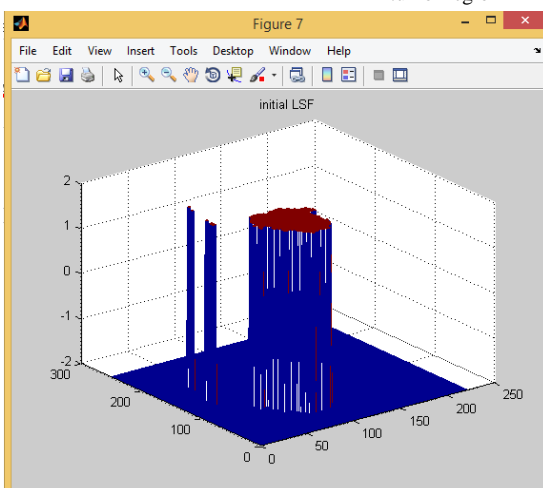

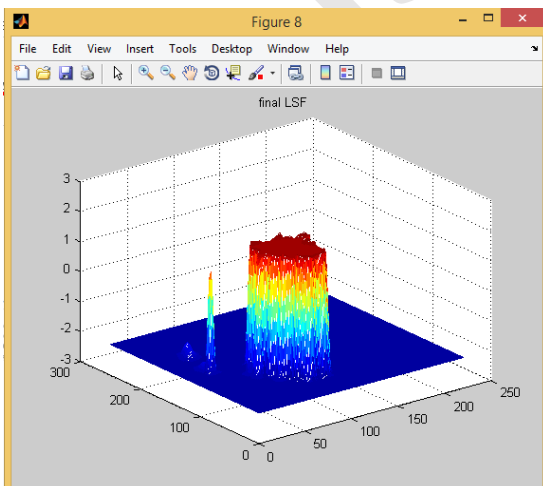Figure 14: Original image with tumor region

Figure 15: Initial LSF

Figure 16: Final LSF

V. CONCLUSION

The results show that Fuzzy Clustering Classification can successfully segment a tumor provided the parameters are set properly in MATLAB environment. Our Hybrid approach algorithm performance is better for the cases where the intensity level difference amongst the tumor and non-tumor regions is higher. It can also segment non homogenous tumors providing the non-homogeneity is within the tumor section.

This paper proves that methods aimed at general purpose segmentation tools in medical imaging can be used for automatic segmentation of brain tumors. The quality of the segmentation was similar to manual segmentation and will speed up segmentation in operative imaging.

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