Visualization of Three Dimensional Brain Atlases for Image Guided Neurosurgery

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ABSTRACT

In this paper, a novel and reliable approach is proposed to visualize three dimensional (3D) brain atlases for image-guided neurosurgery. Since the existing atlas is either in 2D or a 3D atlas, we firstly apply nonlinear interpolation on digitized 2D TT atlas [3], and pre-registered it into a referenced MRI data with defined AC-PC coordinate. Meanwhile, we apply a Fast Marching and Morphological Reconstruction segmentation to the same referenced MRI data to create a 3D atlas. Hence the two atlases are mediately registered together. Then, the dissect names of the ROIs are labeled according to the gray values of the atlases. Finally, the 3D visualization of the atlases is implemented and it is integrated into the neurosurgical operating system. The system is tested by a neurosurgon to be useful for clinical application.

Keywords: Surgery Navigation; Brain Atlas; Regions of Interest; 3D Visualization

1. INTRODUCTION

No two brains are the same in all aspects including their shapes, their sizes and the ways they are organized, which makes it difficult to know whether normal or not. Is that piece of tissue a doctor sees on a scan an aberration or just a normal variation? Brain researchers are often frustrated by differences which confound their attempts to compare data from several subjects. And for surgeons, the risk is always there that they may unwittingly slip into dangerous territory. Unable to actually view the critical areas in a patient's brain, neurosurgeons must plot their course via functional magnetic resonance scans on each individual patient. Furthermore, the development of computer science and current imaging technology allow the challenge of the visualization of 3D atlas of the human brain. Furthermore, improvements in the quality of images have made possible the use of 3D segmentation and 3D visualization techniques to develop a true 3D atlas of the human brain [8, 9].

Accordingly, there is now a great deal of interest, by a number of independent investigations, in developing a 3D atlas of the human brain. Several groups have been working to generate the 3D atlas of human brain. The most representational groups are the Talairach Tournoux（TT）[3], the Whole Brain atlas (American),VOXEL-MAN Brain atlas (German)[4],

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http://se.sjtu.edu.cn/igst)

Brainweb Brain atlas (Canadian)[5,6], etc. However, as the data of domestic and foreign digital brain atlas are mainly in 2D atlas or from the fault data or foreigners' body sections, and the research of our Chinese own digital brain atlas is very limited, developing a Chinese own brain atlas become imperative. We know that 3D atlas will not only bring a great help to medical research, but also be very far-reaching significant for the future teaching.

The primary goal of our system is to assist user to choose any structure from the atlas, to find the corresponding anatomical name from our atlas database, to show the space relationship and visualize, and to manipulate in real-time. The novel features of our system include: it is based on Chinese brain data; it can be visualized, manipulated and quantifid 3D anatomical structures; any new data can be added to the system and labeled; and low cost.

The paper is organized as follows. In section 2, we provide the methods to generate 3D brain atlas, to register the atlas to referenced AC-PC coordinate and then we introduce how to label the ROIs and 3D visualization. Some results of this experiment are shown in section 3. Finally, we will come to our future work and conclusion in section 4.

2. RECONSTRUCTION OF A HYBRID ATLAS

This section describes the method in which the 3D brain atlas was generated from the MR images and how to label the ROIs. The detail of the user-interface generated in this system is also demostrated.

2.1 Methods

2.1.1 Fast Marching and Morphological Reconstruction Hybrid segmentation

Mathematical morphology provides us with many powerful transformations for image analysis. It can efficiently classify articular shapes in an image and reconstruct defined regions via appropriate Structuring Elements (SE).

A supervised segmentation of MR images is performed to define distinct tissue classes. We reduce the connectivity between ROIs and the neighboring tissues by recursively eroding operation first. Then, a pixel is selected as the seed; and the fast marching method is employed to quickly propagate the user-defined seed to a position close to the boundary. [1]

The Fast Marching (FM) algorithm is the level-set segmentation method under special case. While the sign of the speed function in general in level-set approaches can be both positive and negative, which does not change in the FM. This restriction makes the FM much more rapid. However, sometimes the traditional FM method leads to overflow of the evolving front into neighboring regions, which is connected with the ROI. To prevent the front propagation from overflowing, we employ the improved FM described in [10] which introduced global information.

Below, to take the output of the previous step as the initial seed, morphological reconstruction was used to refine the initial contour. Morphological reconstruction (MR) is a typical approach to extract seeded regions, and is defined as:

$$\begin{cases} s_{i+1}=(s_i \oplus k) \cap |m| & (i=0,1,2,\cdots) \quad s_i - s_{i-1} > \delta \\ stop & s_i - s_{i-1} \le \delta \end{cases} \tag{1}$$

Where ⊕ represents a dilation operation, and |m| represents the mask reflecting the edge information in ROI, which is defined via a threshold operation using a histogram analysis. The mask is used to restrict the propagation within the ROI. S denotes the seed when k is the kernel size of dilation operation. δ is the deviation threshold value between |m| and Si. δ and k are both user defined. Since MR operates on individual pixels, it is sufficiently accurate to recover the ROI.

At last, we recover the lost data elements from first step via recursive dilation method, where the number of iterations is the same as the times of recursive eroding operation in first step. When an anatomical ROI was extracted, all of its pixels were marked with a unique integer. After labeling each ROI with different grey value, a pseudo-grey-scale dataset was obtained. Also, in order to distinguish different structures by different colors (Fig.2), a lookup table mapping from grey scale to RGB space was created.

We apply this segmentation method to the sbrain atlas to create a 3D atlas. Below is the result of this segmentation.

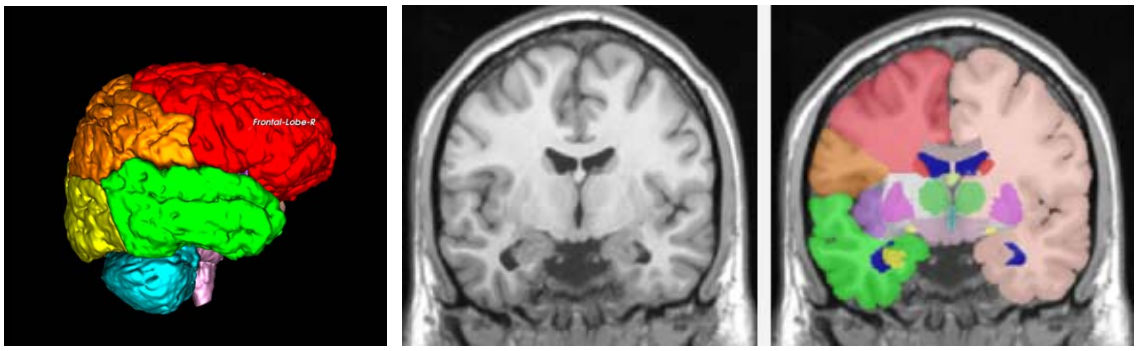


Fig.2. the segmentation result

Left: 3D visualization model; Middle: the original image before segmentation; Right: 2D show

2.1.2 Nonlinear interpolation

As the low spatial resolution and larger gap between each slice of the data the system will use, the first step is using nonlinear interpolation to pre-processing.[2] This algorithm is using the convolution based non-linear interpolation technology, and the impact nuclear function is adapted the basic function: Cardinal spline

$$h_{s_n(x)} = \sum_{k=-x}^{\infty} (b^n)^{-1}(k)\beta^n(x-k) \tag{2}$$

Where n is 3, $(b^n)^{-1}$ represents B-Spline filter.

We apply this algorithm on digitized the standard TT atlas and so get a new 2D atlas. This 2D atlas can avoid the display difficulty which is caused by the big gap between each slice. And it also makes the 3D visualization be stronger.

*sbrain: see http://www.bic.mni.mcgill.ca/brainweb/

2.1.3 Nonlinear registration

No two brains are the same during the surgery for the problems caused by real-time registration, such as respiratory. In order to avoid the repeat operations in the process of real-time registration for various types of brain atlas, and then make the system more humane, we apply the 3D nonlinear registration to register TT atlas to sbrain's AC-PC coordinate. Then we apply this method to register the 3D atlas we have created before to sbrain's AC-PC coordinate. Hence TT atlas and 3D atlas are mediately registered together. (See Fig.4) Next is the framework of registration (See Fig.3), the basic components of the registration framework are two input images, a transform, a metric, an interpolator and an optimizer.

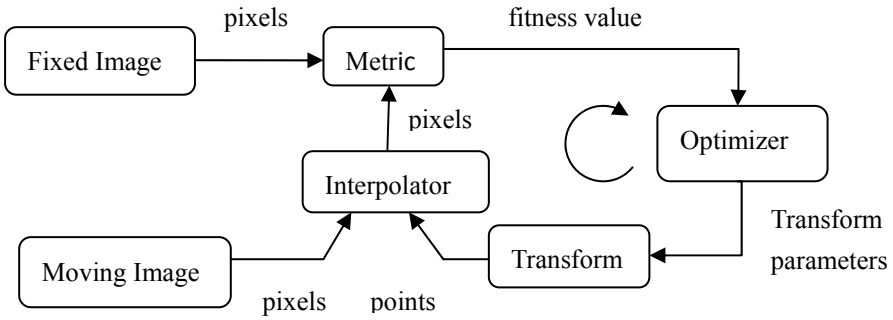


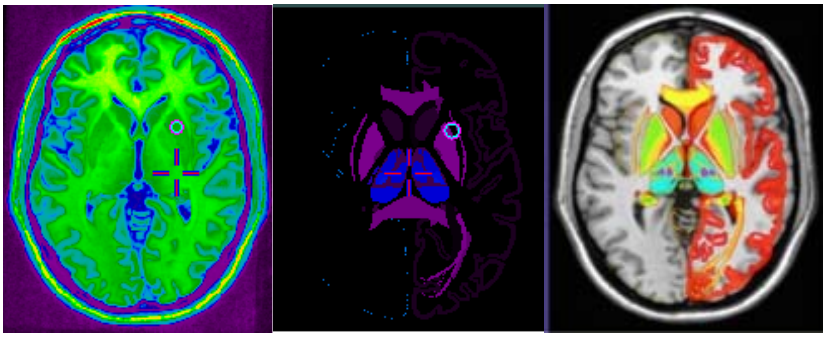
Fig.3. Registration Framework

We apply Nonrigid Registration Based on Normal Vector Information [7]:

$$S(T,R,g)=\frac{1}{|V|}\sum_{X\in V}\left|\cos\theta\left(N(X'),N(X)\right)\right|^2 \tag{3}$$

V is the volume of test image that overlaps with the reference image;
N(X) denotes the transformed NV value in the location X of the test image;
N(X')=N' is the NV of the corresponding position X' in the reference image;
X'=F(X) is the position of the reference image mapped from the pixel X of the test image by the transformation F.
θ represents the included angle between the two vectors.

By using this method, the doctors in surgical processing would not have to repeat registration, and so reduce of the operation time of the surgery and alleviate the patient's suffering.



(a) (b) (c)

Fig.4. Nonlinear registration: image a and b are the original atlases, the color atlas of image c is the new atlas created by nonlinear registration the first two atlas, TT and MRI images.

2.2 Our approach

We use the methods which are introduced before to construct a 3D visualization atlas. A flow chart of our multistage method is shown in Fig. 1.

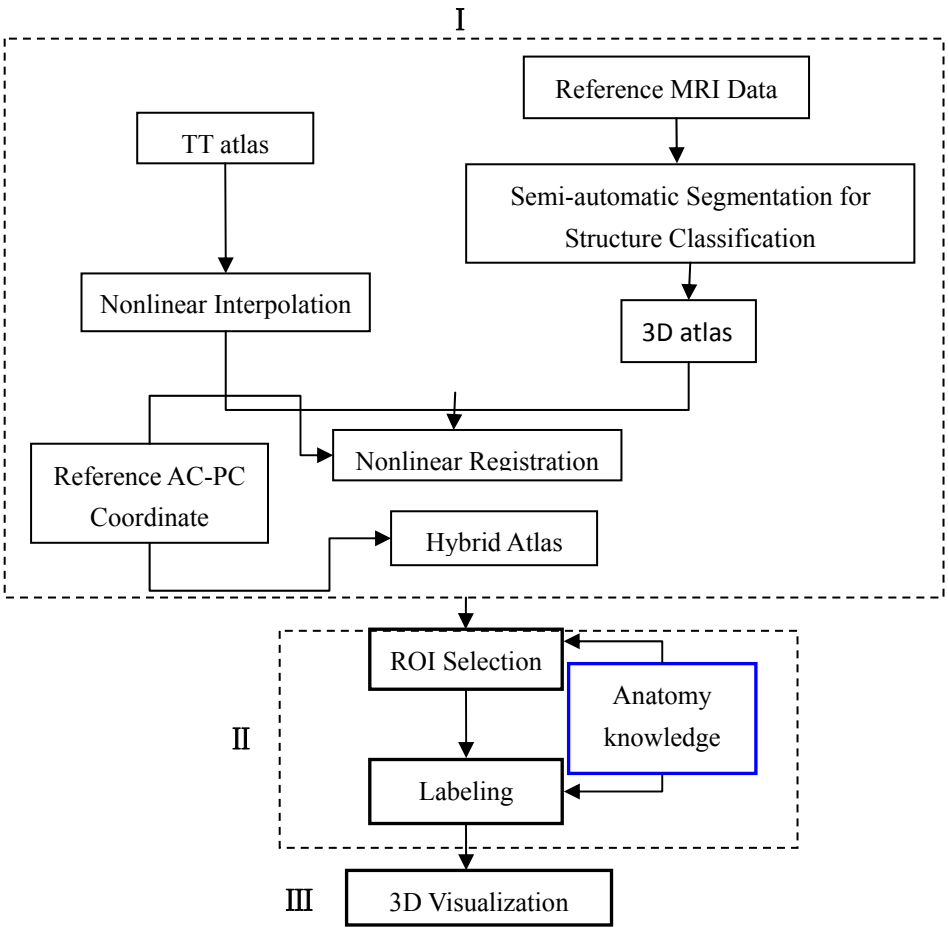


Fig.1. The framework: step Ⅰ is using Fast Marching and Morphological Reconstruction Hybrid segmentation method to create atlases, using nonlinear interpolation method to pre-processing and last using nonlinear registration method to pre-registration patient data and the atlases we have created. Step Ⅱ is to select ROIs according to anatomy knowledge and then label these structures. StepⅢ is to develop the 3D interface of our system.

2.2.1 Labeling ROIs

The primary goal of labeling ROIs is to quantify of organization's size, and then to demonstrate it in 3D space which is very useful to the instruction for surgery and treatment, such as to tumor monitor. Moreover, it also works a lot for medical teaching.

By linking labels to a set of ROIs, we are able to display many specific neuroanatomical structures. This labeling system also incorporates a hierarchical organization, so that neuroanatomical structures can be grouped according to specified

relations among structures. A complete description of the landmarks has been made available to the reader upon request. (See Table 2) Individual areas such as temporal lobe, prefrontal cortex and basal ganglia are defined in detail in previous publications. Briefly, the regions delineated include: sulci/fissures, basal ganglia, white matter, ventricular system, limbic, diencephalon, midbrain, cranial nerves and so on. Several white matter tracts, including the corticospinal tract and the optic radiations were also delineated and reconstructed in 3D. Altogether, there are currently over 60 labels in our atlas data set.

According to the character of the atlases, the labeling of ROIs is based on the gray value of the atlases. Because each different structure has different gray value, we can note each ROI's gray value and its corresponding anatomical name. For the definition of anatomical ROI's it was necessary to use operator driven interactive editing, based on the results of the initial segmentation. For instance, there is no contrast mechanism available to separate the superior frontal gyrus from the middle frontal gyrus. Both would be classified as gray matter in the initial segmentation. To edit the label maps (i.e., ROI definitions) we develope an interactive editing tool, allowing the user to review the original cross-sectional data, with a colored overlay of the label maps, read the gray of ROIs and label the structure name for it.

2.2.2 Hierarchical browser

Anatomy is organized hierarchically. For instance, the superior frontal gyrus is part of the frontal lobe which is part of the neocortex, which is part of the brain, etc. Since the atlas contains the finest level of detail, the organizational information regarding the hierarchy was stored as a script text. This file can be easily modified whenever new structures are going to be added in. The navigator had a hierarchical browser of all tissues included in the atlas, which is completely based on this script file. Each structure was assigned a color based on its gray value. The viewer can browse through the hierarchical representation and expand or collapse the level of detail displayed. (See Fig.5)

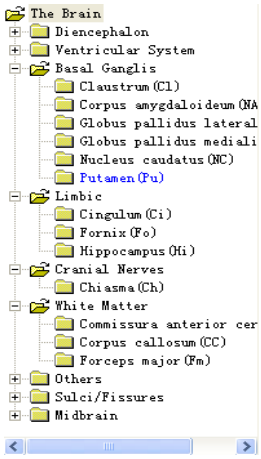


Fig.5. Tree Structures

3. EXPERIMENT RESULTS

3.1 Software and source data

Our system environment is implemented in Python, extensive used the visualization toolkit (VTK) and is run on a 2.80 GHz Pentium IV PC with 1.0GMb DDR2 memory, a nVidia GeForce 6800 graphics card, and Windows-XP PC. And we

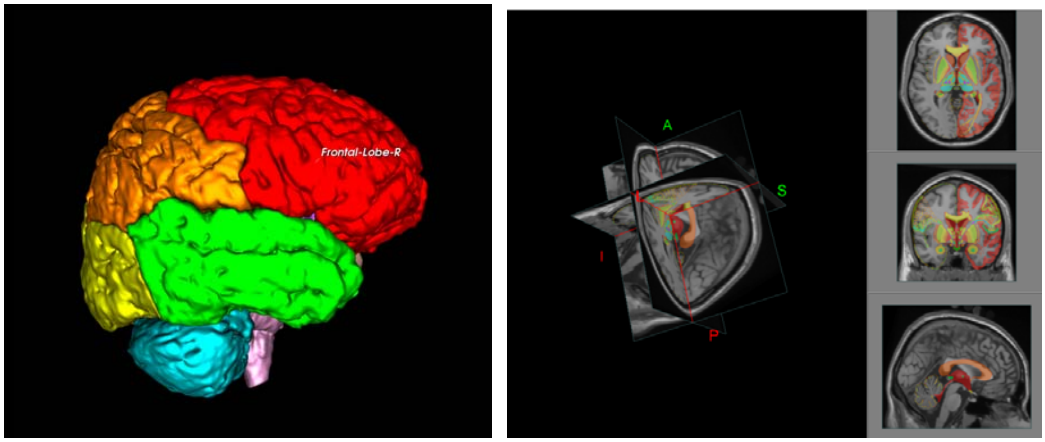
use C++ and OpenGL to segment the MR images.

The MR data set of brain, which is in high-resolution (1mm isotropic voxels) and low-noise ratio, is from Shanghai Ren Ji hospital. It is created by registering 27 scans of a normal individual in stereotaxic space where they were sub-sampled and intensity averaged. The volume contains $181 \times 217 \times 181$ voxels and covers the brain completely, extending from the top of scalp to the base of foramen magnum.

3.2 3D visualization

The user interface for navigation of the brain atlas is developed by wxPython and VTK. And it provides a user-friendly interface for user interaction and manipulation. Currently supported interactions are classified into two categories: 3D visualization, manipulation and labeling (See Fig.6.(a)); 2D image browsing with labeling information. (See Fig.6.(b))

The interface is mainly composed of four view ports (See Fig.6.(b)) and a tree list window (See Fig.5). The amount of information to be displayed is huge: MRI axial, coronal, sagittal slices; the Talairaeh-Tournoux axial, coronal, sagittal sections; the Schaltenbrand-Wahren axial, coronal, sagittal microseries sections; triplanar; 3D image; anatomical index, etc. The TT atlas has both high resolution and low resolution images and the user can manipulate or labeling on this two kind images. The user is provided with all these data on the screen, and is able to continuously navigate through the data such as that any structure from the anatomical index can be traced continuously in space both for the patient and the atlas data. Continuous navigation (see Fig. 1) includes continuous resizing of axial, coronal, sagittal, and triplanar views; brain atlases (Fig. 4); continuous triplanar – 3D image blending. The user is provided with all these data on the screen, and is able to continuously navigate through the data such as that any structure from the anatomical index can be traced continuously in space both for the patient and the atlas data. Furthermore, the opacity of the slices, as well as the window/level can be adjusted independently.



(a) (b)

Fig.6. 3D Visualization Interface: it is clearly indicate the dependencies, relationships, and positions of cortical and subcortical regions in the atlas, other elements as well. There are two types of models, triangular mesh models (a) and surface models (b). The names of these structures can be illustrated interactively. Many methods are provided for users to interact with the atlas, so it is easily to be applied in neuroanatomy education.(b)The left view is triplanar view; the right views are: 1st is axial view, 2nd is coronal view, 3rd is sagittal view

Table 1 Dimensions and Time Rate of 3D Visualization

Type	Dimensions	Time Rate
Surface Rendering	82057 polygons	0.01s
Volume	36*237*408 voxels	0.015s

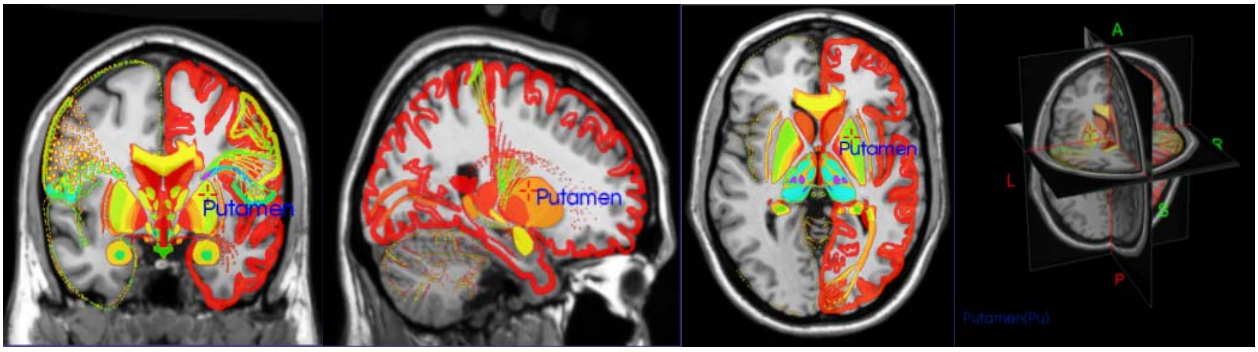
3.3 Testing

We evaluate our system in two aspects: the accuracy of the labeled result and the efficiency of the labeling procedure.

Firstly, we evaluated the accuracy of the labeling results. Fig.7. shows the accuracy of the labeling in our system. We have classified the brain structures into nine parts. (See Table 2) And in Fig.7, we can see the ROIs, Putamen, in axial, coronal, saggital view. The accuracy has been previously evaluated for cortical and subcortical structures. Typical misregistrations of well-defined structures in the subcortical areas of interest (e.g., putamen, head of the caudate nucleus) between the model brain and a patient MRI is 0.1-1.2 mm, with the larger errors generally being at sites on the periphery of the region of interest. Secondly, we tested the efficiency and for the first place we chose is to think about the efficiency, so refresh rate of our system is less than 0.01s.

Table 2 Classify Brain Structures

Diencephalon	Midbrain	Sulci/Fissures	Basal ganglia	White matter	Ventricular system	Limbic	Cranial nerves	Others
28	6	1	6	3	1	3	3	12



(A) (B) (C) (D)

Fig.7. Labeling of ROIs: (A) Coronal View; (B) Sagittal View; (C) Axial View; (D) 3D View

In order to make the software more easily and friendly for use, we provide the user with the ability to:

- ✧ View an atlas in any direction: angle, elevation, and rotation
- ✧ Scale the size of the ROIs (for visualizing small objects)
- ✧ Place labels on a ROIs to annotate parts of 3D display
- ✧ Change the font color, font type, font size of labels
- ✧ Draw lines on the Ortho-view to measure the distance between two ROIs

4. CONCLUSION

We propose a digitized human brain atlas to visualize in three dimensions for the surgical procedures. The result shows that the methods we have used are efficient and time saving. This system is not only useful for the surgical navigation, but also served as a powerful teaching tool, for spatial relationship among neuroanatomical structures can be more readily envisioned when the user is able to view and rotate the structures in 3D space which are interested in. Moreover, each element of the brain atlas is associated with a label, displayed by which structure the mouse point on.

As the future work, we plan to improve more accuracy labeling of ROIs, friendly link the ROIs with their landmarks, add the registration tool for this program in order to implement the function of model driven segmentation based on this brain atlas, and so on. Also, we are using this labeling method in the SW images.

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