Information support of the processes of diagnosis and surgical treatment of chronic subdural hematoma of the brain

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Abstract – **The study relates to the field of automation and information support of the processes of diagnostics and surgical treatment in neurosurgery. On the basis of complex software (BCS), computing and information systems of local corporate information networks of neurosurgical clinics are used, the initial data of standardized diagnostic protocols for clinical and instrumental studies of the brain of neurosurgical patients are formed. The data necessary for modeling are obtained after performing computed tomography (CT) and / or Magnetic Resonance Imaging (MRI), converting an image of the DICOM-PACS (Digital Imaging and Communications in Medicine) format on the network or from standard media (CD-R, CD-RW , USB flash drives, etc.) to build a real-time 3D model of the current state of the operated chronic subdural hematoma of the brain(CSDH), directly during its surgical treatment, based on the current 3D model of the real object of treatment**

Keywords— information technologies in medicine, 3D models, animation, control algorithms, real-time 3D hematoma model, subdural brain hematoma

I. INTRODUCTION

OBJECTIVE: The 3D model of the CSDH of the human brain is a three-dimensional digital image of the target object in the surgical field, both real and for virtual analysis. Typically, the creation of 3D models takes place in the environments of special software for 3D modeling, the functionality of which may differ slightly and specifically.

There are already programs focused on the design of 3D engineering models, there is software designed for modeling internal organic objects, as well as popular software applications for 3D visualization and animation. There is no strict classification of software for 3D modeling in this medical field, but most practical applications contain certain special functions aimed at performing specific local tasks in Neurosurgery

3D modeling is the process of creating a three-dimensional digital image of the required research object. Depending on the specific goals, the requirements for 3D modeling may also vary. So, for example, in the development of computer games, the well-known, which have already become standard, laws for

constructing 3D models are used, which, however, may not be useful when creating 3D models for subsequent 3D printing.

MATERIAL AND METODS :We note here that from the point of view of mathematics, the surface of a 3D model is a set of geometric shapes - triangles or rectangles, the combination of which forms the necessary object.To build a model, a separate subroutine is created that will process already marked images selected from a CT scan of the patient's brain. Its task is to generate a 3D model of an object in vtk (Visualization Toolkit) format so that you can work with it later.

II. READING DATA TO CREATE A 3D BRAIN HEMATOMA MODEL BASED ON CT AND/OR MRI IMAGES

It is necessary to create an algorithm and a program to determine, based on the initial data, Fig.1, the labeled part of the CT image, Fig.2. For this operation, the Python library cv2 is used. OpenCV is an open source library of computer vision, image processing and general purpose numerical algorithms.

This library allows you to define the contours of the marked part and represent them as a polygon. The logic is that all unlabeled parts are removed and the **Python algorithm** contour finding is applied.
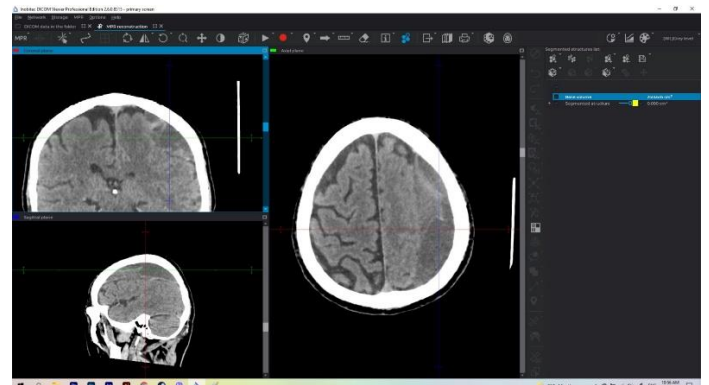

Fig.1. Primary image of a CSDH of the human brain obtained using standard medical technology based on a 256-slice CT

It is necessary to create an algorithm and a program to determine, based on the initial data, Fig.1, the labeled part of the CT image, Fig.2. For this operation, the Python library cv2 is used. OpenCV is an open source library of computer vision, image processing and general purpose numerical algorithms.

Figure 2b shows the CT image after removing the unlabeled part of the original CT image. The image is programmatically desaturated, which is required by the algorithm for finding contours. Figure 2c shows a graph drawn using the matplotlib library. The graph is an open contour of the hematoma (in the form of points, not a solid line!). Initially, it appears upside down - this is a side effect of the algorithm, which is eliminated later
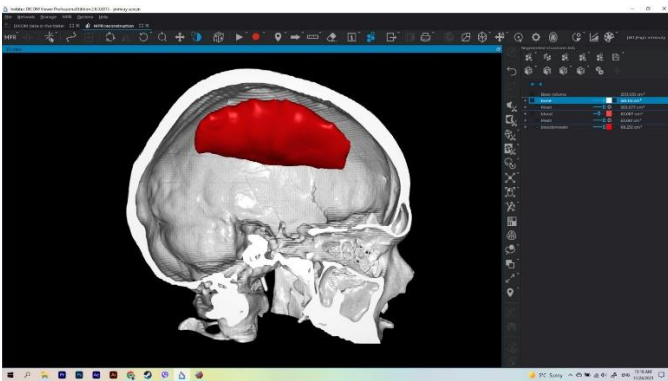

Fig.2.a. Representation of a labeled CSDH of the human brain in sagittal section (lateral view)
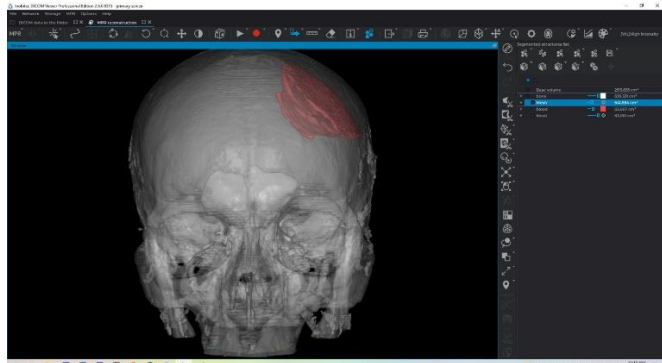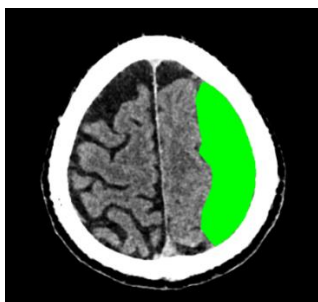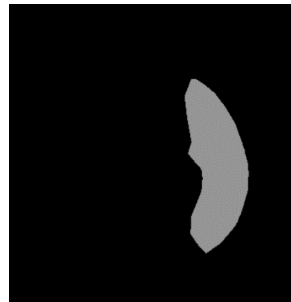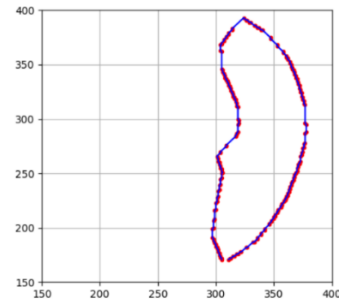

Fig.2.b. Representation of a labeled CSDH of the human brain in the frontal plane (front view)

(a)Original image
CSDH of the human brain
(coronal section)

(b)PC image,
obtained after cleaning

(c) polygon plot

Fig.3.a.b.c. Stages of obtaining contours of a hematoma (marked part)

Figure 3.b shows the CT image after removing the unlabeled part of the original CT image. The image is programmatically desaturated, which is required by the algorithm for finding contours. Figure 3.c shows a graph drawn using the matplotlib library. The graph is an open contour of the hematoma (in the form of points, not a solid line!). Initially, it appears upside down - this is a side effect of the algorithm, which is eliminated later. The vertices of the polygon are shown in red, and the sides in blue.

The polygon is stored as an array of vertex coordinates, and in the same form is used in the next stage of data transformation. These operations are carried out with all CT images marked at the previous stage.
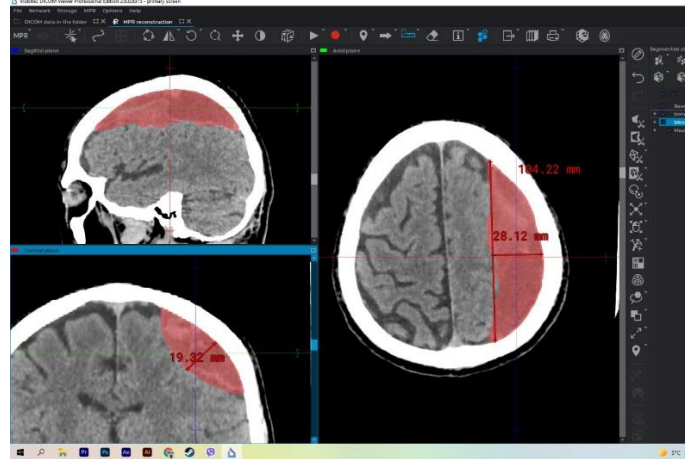

Fig.4. Image of chronic subdural hematoma in 3 planes (highlighted with a computer program)

II. Construction of a preliminary (rough) 3D model of a CSDH

Having a set of vertices that describe the shape of a hematoma, you can start creating its 3D model. To do this, it is necessary to connect the vertices of the contours located on adjacent layers of CT images. This can be done in a simple way, fig.5.a.b.c.d.
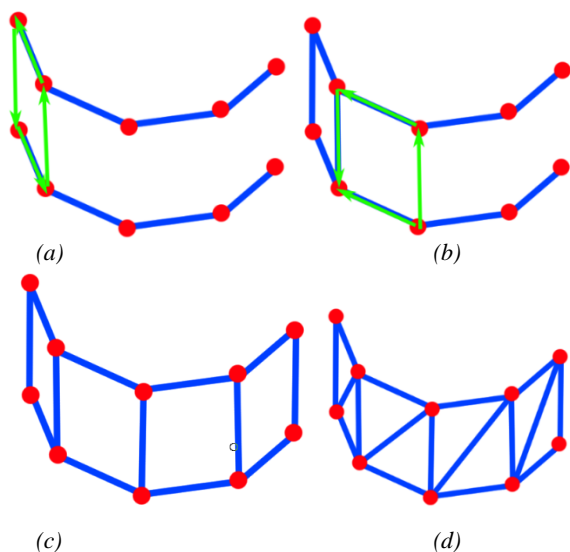
(a)   *(b)*

(c)   *(d)*

Figure 5. Steps for joining the vertices of neighboring image layers in a 3D model: (a) a demonstration of how two polygons of adjacent layers will be connected; (b) a stage in which two vertices are already connected; (c) stage with completed connectionvertices of polygons; (d) triangulated view of the resulting two-layer model.

Fig. 5 graphically shows the algorithm of how a 3D hematoma model is assembled from the contours of individual images (layers). In this case, each step is achieved by connecting 4 vertices that define one quadrangular polygon. When connecting, it is necessary to take into account the sequence, as shown in Fig. 3,(a and b) with green vertical arrows. After carrying out a series of such steps, we obtain figure 3, c, which we can already work with. But to work with programming tools, it is necessary to bring the model to a triangulated form, that is, to divide each quadrangular polygon into two triangular polygons, Fig. 3 c.

However, already at step (a) a problem arises: it is possible that it will not be possible to connect all the vertices of the polygons, since each polygon has a different number of vertices. To solve this problem, you can add to each polygon such a number of vertices that all polygons have an equal number of them. This can be done using the following algorithm:

1. The polygon with the largest number of vertices is determined.

2. For each polygon, a vertex is added to the area between the outermost vertices until their number equals the number of vertices in the largest polygon.

Now, having polygons with equal vertex counts, you can connect their respective vertices.
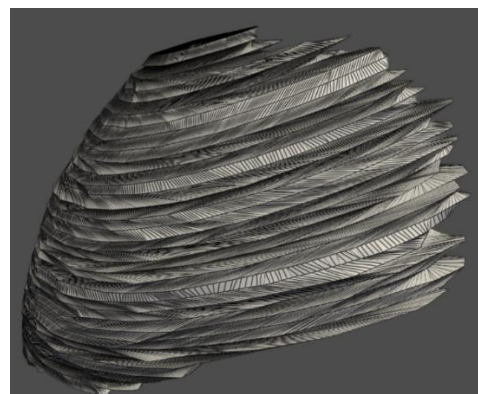
a) front view;

(b) rear view;

(c) approximate (enlarged) section of the model

Fig. 6. a.b.c. Received 3D model

On Fig. 6 shows the resulting hematoma model. It can be seen that the surface of the model has a rather chaotic relief, which is far from ideal. The main reason lies in the lack of the algorithm itself, which has just been described. Although the polygons of each layer of the 3D model received the missing vertices, the pointer to the "first" vertex of the polygon has shifted. Because of this, you can observe the texture of the object shown in Fig. 3, (c). It seems that the vertices of the polygons are not connected

in the most successful way. Additional smoothing algorithms are needed to improve the quality of the model.

III. SMOOTHING THE 3D HEMATOMA MODEL

Above, a hematoma model was obtained, but its quality does not allow any useful actions to be carried out with it. The model needs to be smoothed. Looking at the image shown in Figure 3, (b) you can see that if you move the pointers to the vertices of one polygon, it will be more successful to connect it to another polygon. Then the shift algorithm will look like this:

1. Calculate the arithmetic mean of the slopes of each line formed by connecting the corresponding two vertices from the next and previous layers of the polygon arrangement.

2. Move the pointers left and right up to a certain amount until the arithmetic mean of the slopes of the lines between the current and next polygon is as close as possible to the slope calculated in step 1.

3. Again apply the algorithm from the previous paragraph and build a model.
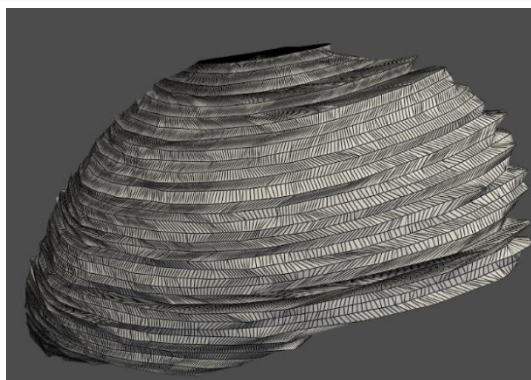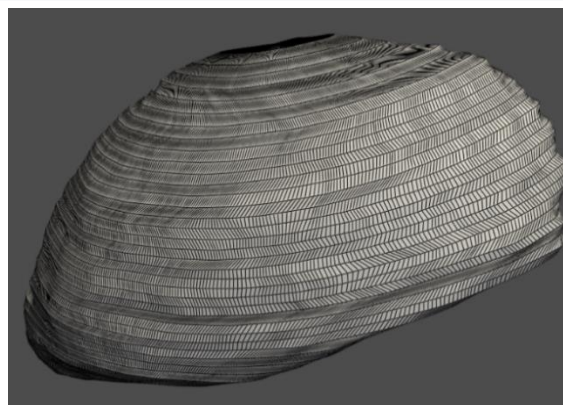

(a)   front view
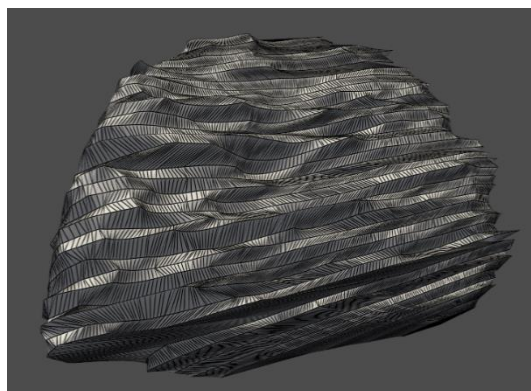
(b)   back view

Fig. 7. The resulting 3D model after vertex shifts

Fig. 7 shows a model of a hematoma after shifts of the vertices. It can be seen that it is already better suited for analysis, but some problem areas still remain. It is quite difficult to solve such a problem by means of ordinary mathematics, so it is necessary to use a combination of algorithms to smooth these Fig. 7 shows a model of a hematoma after shifts of the vertices.

It can be seen that it is already better suited for analysis, but some problem areas still remain. It is quite difficult to solve such a problem by means of ordinary mathematics, so it is necessary to use a combination of algorithms to smooth these areas.

At this stage, you can use the pyvista library. PyVista (formerly vtki) is a Visualization Toolkit (VTK) helper module that uses a method other than the VTK interface via NumPy and direct array access. This package provides a well-documented Pythonic interface that can render a powerful VTK render server to facilitate rapid prototyping, analysis, and visualization integration of spatial reference datasets.

(a)   front view
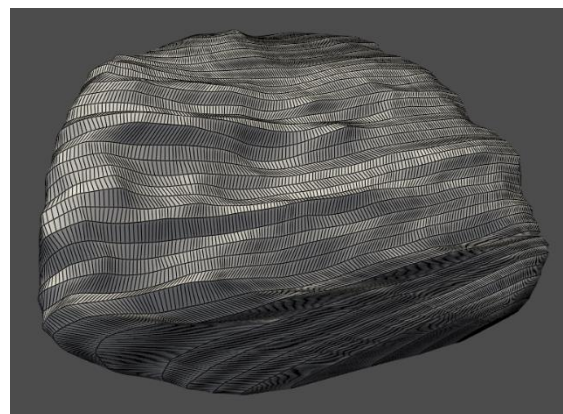
(b)   back view

Fig. 8. The resulting 3D model, after shifts and application Laplace smoothing algorithm

ou can use the pyvista library function - smooth. This function implements the Laplace smoothing algorithm. This iterative algorithm can help solve the current problem, but with a large number of iterations, the model will be smoothed with unacceptable distortion, tending to become spherical and losing useful information about the model. For our problem, it was decided to perform 150 iterations by the trial method.

After applying the smoothing algorithm, we obtain the model shown in Fig. 5. As you can see, the model turned out with a smoother relief. Theoretically, this model is already suitable for analysis, but two problems arise. First, such a model may still contain problem areas, the presence of which does not guarantee
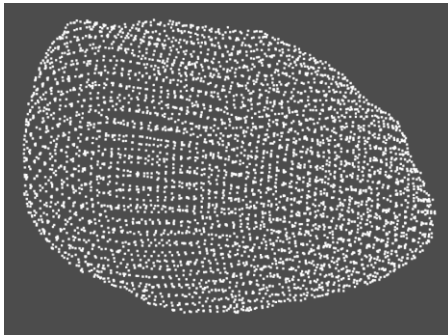
the correct analysis of the object. The second problem is the huge number of vertices, which makes the analysis process long, measured in hours. In some areas, such as the upper and lower poles of the model, the vertex density can be thinned out, thereby reducing the analysis time.
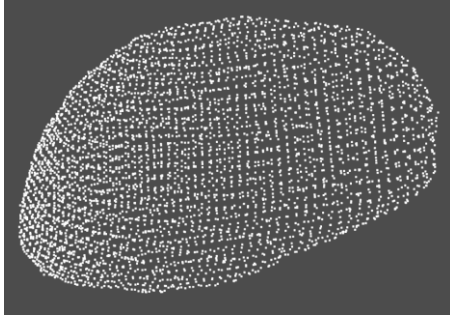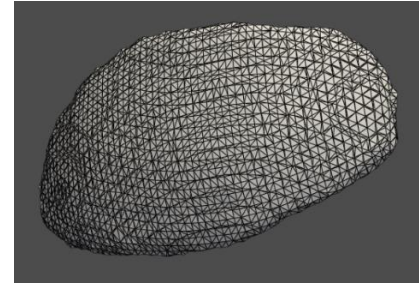

(a)   front view

back view

*(b)*

Fig.9. Model represented as a point cloud

Another method for processing image data of a hematoma model is surface reconstruction of the model. In computer graphics and computer vision, 3D reconstruction is the process of obtaining the shape and appearance of real objects. The process can be performed by passive or active methods. If the shape of the model can change over time, one speaks of a non-rigid or spatio-temporal reconstruction.

The algorithm that is used here is called the "ball rotation" or alpha spheres algorithm. This algorithm is implemented using the create_from_point_ cloud_alpha_shape function of the open3d library. To use the function, you first need to generate a point cloud, which can be obtained using the sample_points_poisson_disk function, passing data about the model shown in Fig. 10. To simplify the analysis, a tenth of the points of the primary model was taken. The points are taken uniformly according to their density in space.

(a) front view

Fig. 10a. Reconstructed model using the "ball rotation" algorithm
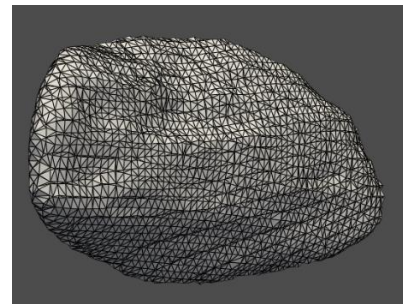
(b) back view

Fig. 10b. Reconstructed model using the "ball rotation" algorithm

As a result, we get the HSDG model shown in Fig. 11. As expected, the polygons are evenly distributed over the surface of the model.
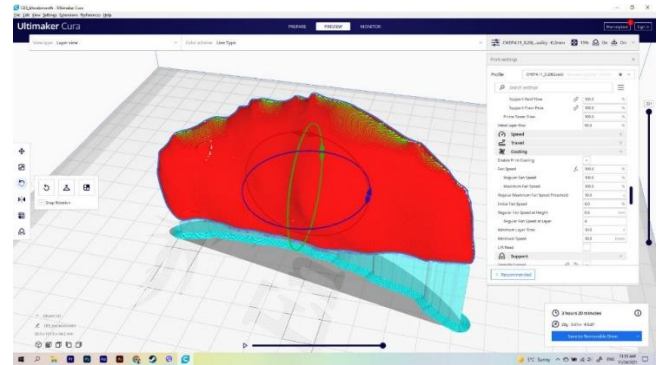

Fig.11. The final view of the rotating 3D model of the HSDG

However, like any anti-aliasing algorithm, the algorithm used neglects some of the useful information that described the more detailed topography of the model. This is not very critical, as the analysis will use the spherical part of the hematoma model surface, which is adjacent to the dura mater. This side effect can be reduced by choosing better parameters for the above functions, but this may require more effort. The resulting model is most likely suitable for analysis, which has shown its practical use in the practice of neurosurgery, which the authors will talk about in their next articles and communications.

RESULTS: The originality of the method proposed by the authors lies in the systemic, multi-stage programmed visual information that is promptly received by the surgeon at a convenient time and at the right time, according to his desire, to support and ensure the reliability and safety of processes in the surgical treatment of CSDH, Fig. 10 and Fig. 11.
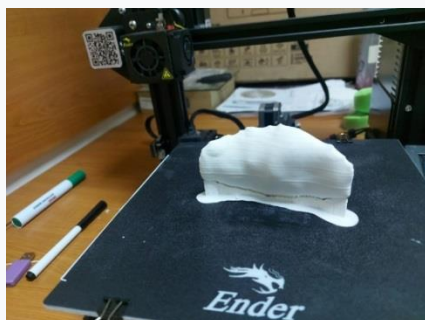

Fig. 10

Conclusions: The results of the practical use of the developed 3D model during brain surgery are very positive. An analysis of the current practice in neurosurgery and the results of scientific research indicate the need for differentiated approaches to the choice of management tactics for patients with chronic subdural hematomas, taking into account the clinical phase of the disease.

Information support in the development of pathogenetically substantiated methods of surgical and conservative treatment of hematomas, taking into account the data of a comprehensive study, will make it possible to substantiate the timing, volume and nature of the surgical intervention - the number, nature and location of inlets in emergency conditions in neurotraumatology using 3D models in real time.

Information support of Fig.10 and Fig.11 based on the original software for the formation of a 3D model facilitates a comprehensive diagnostic system, improves the safety of surgical treatment and improves the prevention of intracranial complications in patients with traumatic subtentorial chronic subdural hematomas using therapeutic and diagnostic neuroendocscopy and effective methods of rational drainage and sanitation of the postoperative cavity.

Visualization, up to 3D printing of the SHSG model, provides reliable spatial information in the form of virtual and/or spatial models. The possibilities of diagnosing chronic subdural hematomas have significantly expanded with the introduction into neurosurgical practice of such highly informative and non-invasive examination methods as computed tomography and magnetic resonance imaging, transcranial Doppler ultrasound.

Their use opens up new possibilities and perspectives in the study of chronic subdural hematomas.

(Корниенко В.Н., Васин Н.Я., Кузьменко В.А., 1987; Туркин А.М., Эль-Кади ХА., Корниенко В.Н., Becker D.P., Miller J.D., Young H.F., 1982;) and, as a continuation of this path, the technology of neurosurgical operations on the brain described in this article.

The mini invasive neurosurgical interventioncombined with information support and 3D reconstruction and printing offers a better medico-financial balance.

The use of the algorithm of measures for information support developed by the authors in the diagnosis and surgical treatment, prevention and treatment of intracranial complications in patients with traumatic CSH, depending on the nature and location of the compressive factor, favorably and expediently affects the nature of operations and the psychological climate in the medical environment.

Fig.11

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