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TECHNOLOGIES OF BRAIN IMAGES PROCESSING

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The purpose of present research was to analyze modern methods of processing biological images implemented before storage in databases for biotechnological purposes. The databases further were incorporated into web-based digital systems. Examples of such information systems were described in the work for two levels of biological material organization; databases for storing data of histological analysis and of whole brain were described. Methods of neuroimaging processing for electronic brain atlas were considered. It was shown that certain pathological features can be revealed in histological image processing. Several medical diagnostic techniques (for certain brain pathologies, etc.) as well as a few biotechnological methods are based on such effects. Algorithms of image processing were suggested. Electronic brain atlas was conveniently for professionals in different fields described in details. Approaches of brain atlas elaboration, "composite" scheme for large deformations as well as several methods of mathematic images processing were described as well.

Key words: mathematical methods, image, image processing methods, information and computer technologies, software, databases.

Image analysis and processing is significantly important for biotechnology [1]. Techniques of image processing are among the most powerful contemporary methods and experimental data processing [1–4]. Description of image processing methods can be found in [5–23] as well as in author's previous publications [24–30]. Several modern methods for image processing [5–23] are briefly considered below in combination with other mathematical methods [1–4, 31–98]. Bioinformatics widely uses images to elaborate the electronic information systems [1–29, 42, 45, 47, 53, 55, 79, 81–85, 87, 92–98]. Image pre-processing is necessary for purposes of bioinformatics and ordering images in digital databases of information systems (IS) [48, 49, 51, 97], for analytic work or to develop electronic brain atlases [54, 66, 88–91]. Studying the possibility of brain image transformations in interactive mode we will try to make recommendations for the subsequent design of electronic brain atlases.

Digital systems for image processing in biotechnology. These systems were designed for image processing which is common in medicine, for example, in x-ray analysis, ultrasound diagnostics [1], etc. Even working with one patient accumulates a lot of images, thus storing them in databases presents a problem. Let us consider the possibility of using image databases for the purpose of diagnosing cerebral pathologies and tissue changes based on well-known *RGB*- color scheme. A few digital systems for image processing are described below.

Medical network-based system NORMA was designed in Genoa (Italy) for radiological purposes [68]. It was elaborated jointly by teams of physicists to develop best schemes for radiotherapy treatment. The system is based on image databases. Along with the standard patient data for all medical IS there are numerous images of tumors and body parts at risk of tumor occurrence. NORMA provides new interesting possibilities to store data and visualize a large number of images for cancer diagnosis and risk areas, and it allows timely collaboration between radiologists and colleagues. NORMA has client-server architecture and it is platform-independent. Emerging Internet technologies made it easy to use without special computer knowledge.

The system is subdivided into interfaces for client and server based on Java software applications. Apart from TCP/IP, the project also includes an optimization protocol that organizes data exchange and control messages. Images for diagnoses are stored and removed from the appropriate databases (DB), DB of DICOM (Digital Images and Communications in Medicine), and PACS database via DICOM-WWW connection, which allows to connect to Internet browsers used by NORMA and DICOM software by HTTP protocol. The browser queries are sent from Web server via CGI (Common Gateway Interface). DICOM software converts queries to DICOM message and organizes the connection to the remote site of DICOM Application system.

Systems for image processing. A high-tech modern approach to brain studies is described in [18]. Authors used the iGrid 2005 system to operate a biological experiment based on globally widespread visualization, storage, computing data (including images) and network resources. Experimental brain microscopy was carried out with modern software and hardware: broadband protocols for optical networks, distributed virtual computer, scalable adaptive graphics environment, etc. These modern approaches allowed concerted multiscalar microscopic experiments, in which biologists can work with images from 20X to 5000X. This technique allowed to study images of brain regions at different levels, from complex systems such as rat cerebellum to individual dendrites. Using prepared images, researchers scanned brain sections at different levels to better study the biological structures. In their work, authors integrated several techniques: achievements of television sciences, high resolution displays, HDTV video streams, OptIPuter system software and computer resources such as graphic clusters for expanding possibilities of bioscience and computer sciences. Thus they demonstrated possibility of simultaneous work with images of a specific brain sample without changing (or randomly changing) magnification of each image. This was made possible using HDTV video streams from remote tools and from experimenters that work in other parts of the network. During such experiments, scientists could work at the same time with large data sets and databases of images from microscopes, for example, UHVEM (Ultra-High Voltage Electron Microscope), including a tool such as 3 MeV UHVEM (Osaka, Japan). Here is a block of one of technical systems for image processing (Fig. 1) [15].

Algorithm of primary image processing. A few examples of digital image-processing systems are described for two levels of biological matter organization: tissues (histological analysis) and organs (whole brain atlas). Let us start from the lower level of tissues, based on histological analysis [19, 21–23]. Fig. 2 shows a number of histological images at different stages of processing. Certain pathological features can be revealed at that time. Several methods of diagnostics and of distinguishing objects in biotechnology are based on this. Such images should be processed as fuzzy images. A processing algorithm [12] is given below:

- An image is made using web-camera.
- Colored images are transformed into binary ones with gradual black and white colors.
- Fragments of interest are selected on micro photos with additional image processing (image segmentation and distinguishing boundaries).
- Data are transformed into a matrix of numbers to enhance the image quality.
- The image is binarized and coded. Image binarization means the transformation of image in gradation of one color into binary code.
- The color of transformed pixels is considered “0” or “1”. Pixels denoted as “0” are called “background”, and pixels denoted as “1” are called “foreground”.

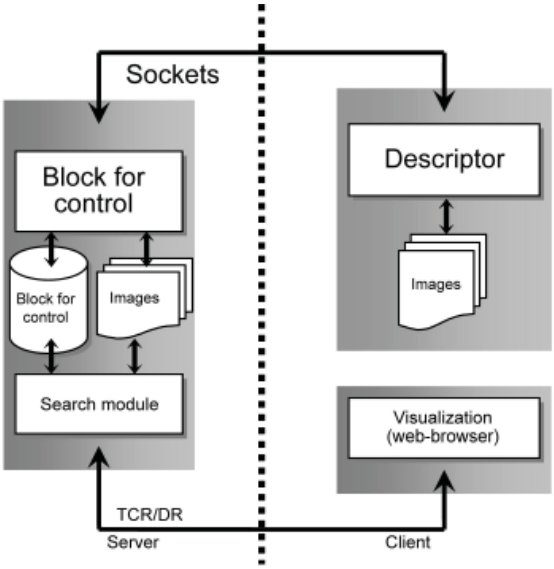

Fig. 1. **Subsystems of information system MedISeek for image processing:** necessary information can be obtained directly from each image, data integrity is supported on-line. Experimental results demonstrated that authorized MedISeek users can describe, store, and transmit biological and medical images, as well as the relevant diagnostic data [15]

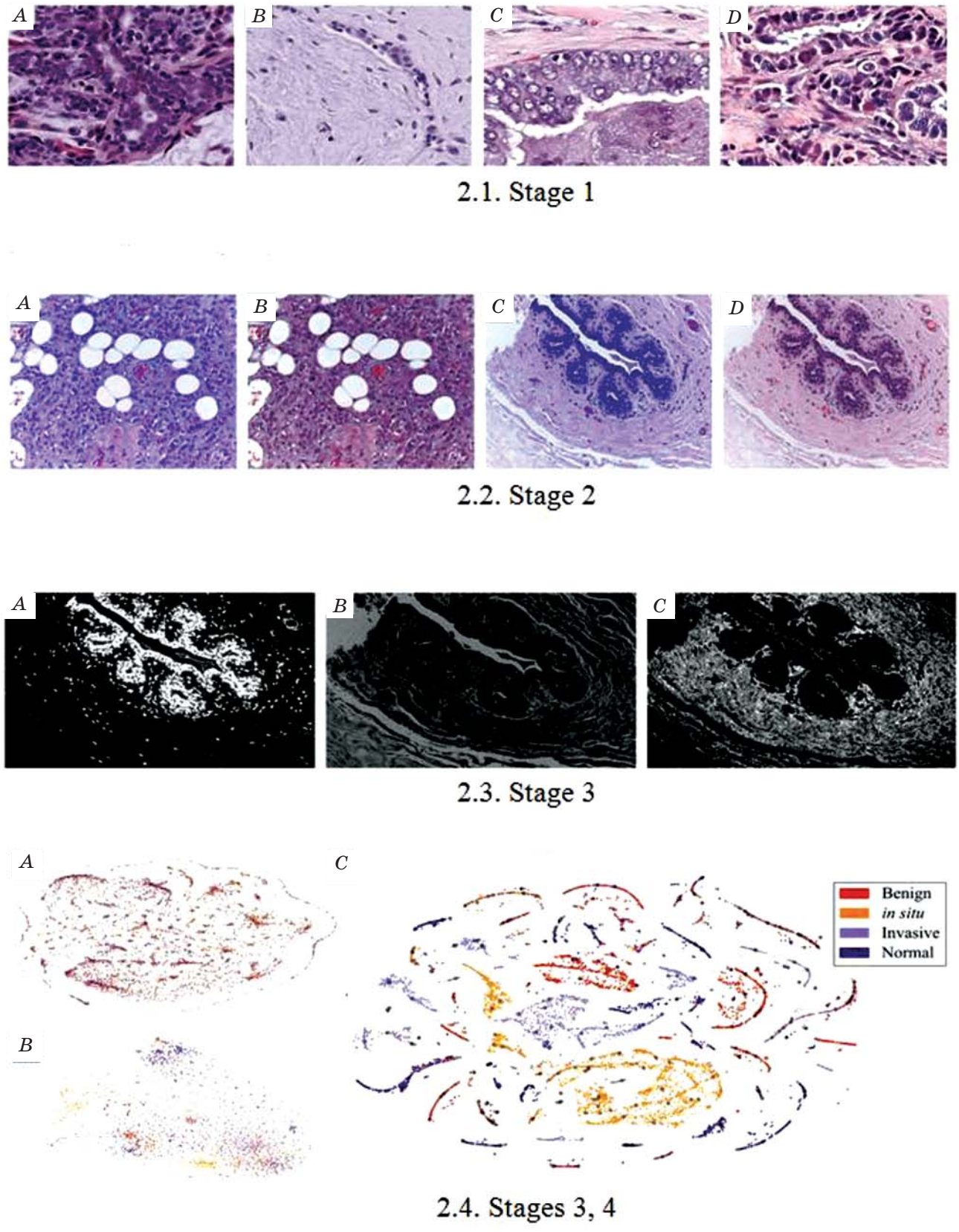

Fig. 2. **Algorithm of histological image processing for further separation of normal and pathological areas using ANN method; sequence of images groups demonstrates stages of processing [12]**

A lot of useful computer inventions are based on obtained and processed images. One such invention is electronic brain atlas which is very convenient for professionals in different fields of biotechnology. Its construction and some methods of mathematical processing are described in [54, 66, 88–91].

Images of brain elements for digital databases at information systems. The level of organs is higher than a cellular level of biological organization. Let us review a number of publications and methods of whole brain atlas construction [54, 66, 88–91]. The main purpose of elaborating digital versions of printed anatomical or stereotactic atlases is to help doctors and neurophysiologists use them for navigating elements of virtual brain. Certainly, such electronic atlas is a very convenient tool for biotechnologists. Different examples of 3-dimensional (3D) brain atlas obtained using magnetic resonance method [10, 20] were suggested for this purpose. Such atlas would be accepted as a standard if there are datasets of images obtained from a real healthy patient. The method of magnetic resonance requires transformating sets of images that "connect" the coordinate space of the patient's brain to the coordinate space of the general model. Due to individual brain differences, real results may considerably vary. Since the value of a stereotactic image-based system is directly related to the simplicity and speed of use, an individual atlas with simple and quick setup and advanced registration technologies are really valuable for professionals in the field of neurosciences.

"*Multiformal" atlas of the human brain*. At organ level of the hierarchy, research targets an image database of sections of the entire brain rather than individual cells. With the appropriate processing of database contents, a whole brain can be reconstructed, navigated, and turned into a "brain atlas" [1]. Because the brain atlases have spatial localization as the basic idea, they will guide navigating and visualizing a lot of data in neurosciences. Associated with relevant databases, the atlases can access information about what is currently known about the brain with its corresponding analysis. Since paper versions of brain atlases are yet unable to solve such problems, efforts are aimed at creating electronic atlases of the brain [1, 54, 66, 88–91].

Brain atlases can serve several purposes if they have following features [1, 19]. First, they must accurately reproduce the 3D brain structure, reflecting its individual variability and changes in the developmental process. Secondly, the databases should be coordinated within the same species and also individuals of different organism types. Thirdly, methods of obtaining, selecting and rendering data must be powerful and flexible. Fourthly, high-speed Internet and well-designed friendly interfaces are needed for universal access and simplicity. Today there is progress in all these areas of atlas development, although none of them today fully satisfy all four criteria.

Atlases can also model brain structures with various imaging and visualization methods. Many recently elaborated similar atlases are based on images of structures obtained by magnetic resonance [10, 20], which provides a good resolving ability across all three spatial axes. Some atlases are based on data from a single brain. Others present averaged data from many individuals, registered for the same stereotactic positions. For the atlas of cerebral cortex, the strategy of creating images on strongly curved surface of this cortex is chosen.

Each of these approaches has limitations that can be minimized in a "multiformat" atlas. It would contain data from an individual brain and a statistically averaged brain in which data are recorded at the same spatial points as in the individual brain. It also would contain volumetric data of the whole brain plus a superficial reconstruction of both cerebral hemispheres and cerebella cortex completely for the individual brain. The surfaces must be shown in natural configuration as a spherical map, after smoothing main curves. In each configuration, cerebral frontal lobes and cerebellum lobes must be colored differently, the pillars in the cortex shaded with darker colors. When using the software suitable for visualization (such as "Caret" for surfaces and "AFNI" for volumes), the volume-to-surface relationship can be detected interactively.

General patterns of image processing in brain atlases designs. Distinguishing differences between brain parts (and, accordingly, their images) by comparing them (in other words, classifying [1, 19] which is often used in morphological or functional studies of human brain) is a method developed at the beginning of XX century. Brodman identified 52 regions or zones in the brain based on microscopic and cytoarchitectonic images [1]. Although the resolution capacity in magnetic resonance scans is much lower than in a microscopic study [10, 20], some of these areas can also be thus identified since they are limited to visible gyrus or bulges. Numerous interactive and automatic methods for

recording general and individual data are developed on different algorithms. They can be subdivided into nine categories. Three most used categories of methods for developing digital brain atlases are based on magnetic resonance images of individual brains.

Algorithms of images processing for brain atlases. Using the concept of compressed strain field and intensity registration techniques, smoothing algorithm using a decline gradient similarity criterion, doubles and uniform Gaussian smoothing were proposed for regularization [1, 30]. Gaussian smoothing works under the transformations as a filter for low frequencies. Because it is stationary, it has the same scale σ everywhere in space. In this way, it either smoothes the transformation too much in the high-variable parts of the image or leaves noise in their more stable parts. This is a fast algorithm, and the computation time can be reduced further with paralleling methods (or parallel execution of algorithms). This approach was used by other researchers as well. Computation time for each iteration will be reduced if the gradient of the similarity criterion is not calculated at points where the gradient had low values during the previous iteration. Early works towards creating the atlas of brain sections attempted to restore intensity of parametric transformation between two images before assigning similarity criterion based on intensity. Other researchers [1, 19] found a link between similarity and regularity. It was recorded as a differential equation and more sophisticated criteria for the case of multi-modal registration were added, such as mutual information and the correlation coefficient. In order to deal with heterogeneous transformations, it was necessary to regularize transformation using the concept of anisotropic diffusion, based on the intensity values of local images.

Other authors studied spatial transformation with dimensions of lower orders using B-spline grids to simulate arbitrary shape deformation and register magnetic resonance images during mammography. This algorithm also uses intensity-based registration method. However, time constraints usually also limit the degrees of freedom of this model, and thus reduce its spatial resolution. In order to dynamically select the appropriate number of degrees of freedom that describe transformation, some authors used multi-resolutions approaches. It was proposed to use a locally affine model on each block of spatially adaptive spatial decomposition [19, 30]. These authors estimated the transformation roughly taking into account the false information linked with voxels, and used multigrid scheme of improvement to avoid complex calculations in poorly known image parts (usually located on the edges of the image). Thus the calculation time can be reduced to approximately one hour. Already a report was published about image processing reduced to 3 hours for typical images and the final grid (size $17\times17\times15$). However, this time can be further reduced by using parallel processing.

One of the currently best electronic brain atlases was constructed digitally by Talairach and Tournoux [9, 20]. However, more and more samples of electronic atlases are created for the solution of local problems in different hospitals in the world [16, 19, 20]. Based on the atlas of Talairach and Tournoux, other researchers [1, 9] employed a method based on the characteristic features of conformational evaluation in the model of free deformation. The main advantage of that system was that transformations were determined only in areas interpolated into brain model and were important in clinical practice (cortex, ventricles, commissures and tumors). The methodology we propose later in the article combines some of the achievements and approaches mentioned above into a new scheme. First, they tried to apply a density transformation algorithm to consider complete information contained in images and their small details. The authors attempted to confirm that the described transformations could not be inverted to avoid potential topological problems when applying the method to segmentation (for example, in atlas tags and surface contours). Secondly, they tried adapting the registration process to the nature of imaged objects, since the optimal level of transformation laws was not constant. Since the registration process requires certain computer time, it also solved the time consumption problem. The executed algorithm should be sufficiently fast (a few minutes). That is why it was necessary to include the algorithm in a queue of more complex processing, which made possible even more complicated interaction between the algorithm and the user. This problem was addressed by parallel implementation on computer clusters connected to the network. This type of parallel computing platform has already been used to solve problems in other industries. Today this approach of computer network is also proposed to be applied in research either at the level of local networks or on-line.

The method on which the algorithm of image processing for virtual brain transformation is based [16, 19]. Since images are discrete, the representation of non-rigid transformations is the displacement of each voxel in a final image, that is, the vector displacement of the field U(p), for which T(p) = p+U(p). Then the point p with intensity I(p) in the final image corresponds to the point T(p) with intensity J(p+U(p)) in the source image. To simplify the notation, the transformation of the original image was marked as $(J\circ U)(p)\triangleq J(p+U(p))1$.

In the applied algorithm, there are criteria for maximizing similarity and regularities. Similarity is maximized due to the gradient of decline. In this algorithm, you can apply various similarity criteria, such as the least squared distance or local correlation coefficient.

The step of the decline gradient can be described as follows: given the current value of the deformation U, a small additive correction u must be found minimizing the chosen similarity criterion [16, 19]. The Taylor's expansion of the first order gives the following:

$$SSD(IJ\circ(U\circ u)) = SSD(IJ'\circ(o+u)) \approx SSD(IJ') + \int 2\left[(J')(p) - I(p)\right]\left[\nabla(J')\right](p)^T \times u(p)dp \approx SSD(IJ\circ U) + \int 2\left[(J\circ U)(p) - I(p)\right]\left[\nabla(J\circ U)\right](p)^T u(p)dp$$

Since the definition $\int f(p)u(p)\,dp$ is not a point product of the vector of functions f and u, let us carry out the identification:

$$\nabla SSD = 2\left[(J\circ U)(p) - I(p)\right]\left[(\nabla J)\circ U\right](p).$$

With Taylor's extension, the criterion is minimized if the current offset of the U^n field is updated as iteration n, adding a small fraction ε of the gradient $u^n = -\varepsilon\bullet\nabla SSD$ in order to get $U^{n+1}=U^n+u^n$. This decline gradient of the first order is the usual equation of evolution, used in several methods. The daemon algorithm corresponds to a slightly more complex decline gradient scheme of the second order, where the gradient is renormalized.

The scheme [16, 19] is quite successful but a few comments must be added:

• The add-on correction scheme mentioned above does not re-compute the gradient of initial image at each optimization step. It performs its own summation. Thus the additive scheme is not suitable for large local rotations; it can lead to the impossibility of non-inverse transformations. Hence, the next step was the emergence of "composite scheme", which justifies all types of displacements and, accordingly, provides the inverted ability of the restored transformations.

• In many real cases, deformations are highly non-homogeneous in certain areas but exhibit greater spatial coherence in others. It can be shown that regularization with a homogeneous Gaussian is not adapted to restore such deformations, and elastic models are very expensive for digital implementation. Consequently, it is necessary to propose a faster method of regularization, which corresponds to non-homogeneous deformations and requires a short computation time.

• In such algorithms, all voxels are considered equally. Based on publications that show that some of the areas in the images contain more meaningful information than others, methods were developed to weight the local influence of correction field when registering *a priori* information about the local validity of the similarity criterion for each voxel.

"Compositional" scheme for large deformations [16, 19]. An additional Taylor expansion formulation makes it possible to reduce to the fact that the gradient recession direction is proportional to the resample gradient of the initial image ∇J, without changing its direction. In real cases, when the deformation contains large local rotations, the gradient direction for the criterion will become parallel to the contours of the impeded images J∘U, corresponding to a decrease in its efficiency at each iteration. If the correcting application is replaced and fields Un+1 = Un+un are offset using the composition of the corresponding transformations and if Id is a transformation of identity, then it corresponds to the equation:

$d+Un)\circ(Id+u^n)=Id+U^n\circ(Id+u^n)+u^n$.

So, denoting $(U\circ u)(p)=U(p+u(p))+u(p)$, the result of the composition transformation on the displacement fields, we obtain the equation $U^{n+1}=U^n\circ u^n$. It should be noted that the first-order Taylor expansion $(U\circ u)$ gives:

$$(U\circ u)(p)=U(p+u(p))+u(p)=U(p)+\nabla U(p)^{\mathrm{T}}u(p)+u(p)+O(\|u^2\|).$$

Thus, the two circuits are equivalent if the displacement field is locally constant ($\nabla U\approx 0$), which corresponds to local translation. Now the field of correction u must be found, minimizing the value of SSD which corresponds to $(I,J\circ(U\circ u))$. Taking $J'=J\circ U$ (Euler's formulation), we return to the

additive (Lagrange) formulation with $U'=0$ when $(0 \circ u) = u$:

$$SSD(I,J\circ(U\circ u))=SSD(I,J'\circ(o+u))\approx SSD(I,J')+\int 2\left[(J')(p)-I(p)\right]\left[\nabla(J')\right]\text{x}$$
$$\text{x}(p)^T u(p)dp\approx SSD(I,J\circ U)+\int 2\left[(J\circ U)(p)-I(p)\right]\left[\nabla(J\circ U)\right](p)^T u(p)dp$$

Hence, the main difference with the additive scheme is that the gradient of resampled image $\nabla(J \circ U)$ is taken instead of the resampled gradient from the original image $(\nabla J) \circ U$. Summing, we note that the usual additive circuit is to calculate SSD gradient in the current offset field U^n, and then in the offset updating, applying the gradient fraction:

$$U^{n+1} = U^n - \in 2\left[J \circ U^n - I\right]\left[(\nabla J) \circ U^n\right]$$

An equivalent compositional scheme is:

$$U^{n+1} = U^n \circ \left(- \in 2\left[J \circ U^n - I\right]\left[\nabla\left(J \circ U^n\right)\right]\right)$$

The gradient of ε fraction taken at each optimization step is the algorithm parameter. Large local rotation similar to the described here is common, especially in multi-subject registration, and it is difficult to recover by applying a field of additive correction.

Certain problems with processing anatomical images. A number of problems associated with image deformation arise when atlases containing images of brain sections organized in the database are developed further.

Certain methods have been proposed to solve these problems [1, 30]. As we already noted, in atlases of different brain parts real deformations in image transformations are often very non-homogeneous. This means that in some places there are zones with plenty of small details, and in some areas there is virtually no significant information (for example, at image edges). When such images are regularized by stationary Gaussian filtering, the value of the regularization is given by the standard filter deviation. This value is either too large, preventing the development of fine details, or too small, which leads to registering noise in the deformation field in smoothed areas. One of implemented solutions is to *a priori* use information about the differences in various structures on the images for local correction of the level of regularization.

One of the models that specify the local degree of regularity is elasticity. However, this model is complex and it must only be implemented digitally. Moreover, in the multi-subject scenario, the deformation linking objects on two images has no physical confirmation due to its flexibility. Another model has a heuristic motivation. If two points in the image belong to the same object, then their displacement is more correlated than if they belonged to different objects. The closer at image are two points, the more correlated is their displacement. The idea is to use a locally constant Gauss model inside each object. This has the advantage of allowing different objects to move freely within the image space. Inside each object, the choice in favor of Gaussian has a triple rationale.

1) Gaussian smoothing is similar to the elastic bias modeling; it can be simulated with a clear approximation [30].

2) The potency of rules stated by regularities is described using the local Gaussian width. By adjusting the local standard deviation of the Gaussian it is possible to regularize non-homogeneous deformations that allow to consider different image areas, such as practically "smoothed" and not very informative, and those highly informative and high-variable [30].

3) The local constant of the Gaussian model is quickly solved digitally and is easily applied in a parallel system [1, 30].

In the last model [30], non-stationary Gaussian was used in regularization with a non-stationary diffusion filter on each of the components of $U\alpha$ $(\alpha \in \{x,y,z\})$ of the displacement field:

$$\frac{\partial U_\alpha}{\partial t} = div\left(D\,\nabla U_\alpha\right)$$

where **D** is a diffusion tensor.

If the diffusion tensor is *constant and isotropic*, it can be described by *scalar value d* $(\mathbf{D} = d\,\mathbf{I}_3)$, where $\mathbf{I}_3$ is an identity matrix. In this case, the equation describes a linear diffusion filter. The largest value of d is diffusion in the most important case. In order to reconcile large deformations in some domains and small deformations in other domains, it is sufficient to make d the scalar field and to convey its large values in an area where we expect small deformations and small values in an area with large deformations. In this case, anatomical information (concerning deformations in tissues) is coded in d. Today d is determined by region-based segmentation algorithms [30]. Since d expresses the local stiffness of the initial image J, it is only necessary to make image segmentation in computer form. Unlike the registration based on characteristics and requiring precise

segmentation of chosen structures, only fuzzy segmentation is needed for the proposed algorithm.

Correlation of the deformation have to be related to the direction (or "directing"*)*. This means that the displacement of a point is in some cases more correlated with its neighbor if it occurs in a particular direction. For example, when visualising the brain surface it is very important that the deformation takes place freely, perpendicular to the surface, whereas during regularization along the tangent plane there is a constant continuity of surface. In this case, the tensor **D** in the above equation is not isotropic, and this anisotropic case is potentially more powerful.

Problems of image processing in scientific laboratories attract world-wide attention [Fig. 2], as well as new methods of image processing [1, 5–23, 56, 77, 84].

In the present article we reviewed a number of modern methods for processing biological images before ordering them in databases for purposes of biotechnology and biophysics. Proposed image databases may be incorporated into on-line technical information computer systems [1, 12–14]. Some examples of such systems used in world practice are described. Methods of processing brain images for elaboration of a digital brain atlas are analyzed. Certain pathological features can be revealed during histological image processing, which is used in a number of methods of medical diagnostics as well as object recognition methods in biotechnology. A few algorithms of image processing are also reviewed. Electronic brain atlas is described in detail, which is very convenient for professionals in different fields. Brain atlas construction, "composite" scheme for large deformations as well as some methods of mathematic images processing are described [1, 54, 66, 88–91].

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ТЕХНОЛОГІЇ ПРОЦЕСИНГУ ЗОБРАЖЕНЬ МОЗКУ

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Метою роботи був аналіз сучасних методів процесингу біологічних зображень перед їх включенням у бази даних для біотехнології. Бази даних надалі було інкорпоровано в інформаційні комп'ютерні веб-базовані цифрові системи. Приклади таких інформаційних систем було наведено в роботі для двох рівнів організації біологічного матеріалу; описано збереження даних у базах даних гістологічного аналізу та цілісного мозку. Розглянуто методи оброблення зображень для електронного атласу мозку. Показано, що під час оброблення гістологічних зображень можуть бути виявлені ознаки патології. Окремі методи медичної діагностики (для певних патологій мозку тощо), а також деякі біотехнологічні методи базуються на таких ефектах. Запропоновано алгоритми оброблення зображень. Зроблено детальний опис електронного атласу мозку, що є зручним для спеціалістів у різних галузях. Також описано методи створення електронного атласу мозку, «композиційну» схему для великих деформацій, а також деякі методи математичної обробки зображень.

Ключові слова: математичні методи, зображення, методи оброблення зображень, інформаційні та комп'ютерні технології, програмне забезпечення, бази даних.

ТЕХНОЛОГИИ ПРОЦЕССИНГА ИЗОБРАЖЕНИЙ МОЗГА

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Целью работы был анализ современных методов процессинга биологических изображений перед их внесением в базы данных для биотехнологии. Базы данных впоследствии были инкорпорированы в информационные компьютерные веб-базированные цифровые системы. Примеры таких информационных систем были приведены в работе для двух уровней организации биологического материала; описано сохранение данных в базах данных гистологического анализа и целостного мозга. Рассмотрены методы обработки изображений для электронного атласа мозга. Показано, что во время обработки гистологических изображений могут быть выявлены признаки патологии. Некоторые методы медицинской диагностики (для определенных патологий мозга и пр.), а также некоторые биотехнологические методы базируются на таких эффектах. Предложены алгоритмы обработки изображений. Выполнено детальное описание электронного атласа мозга, который удобен для специалистов в разных областях. Также описаны методы создания электронного атласа мозга, «композиционная» схема для больших деформаций, а также некоторые методы математической обработки изображений.

Ключевые слова: математические методы, изображения, методы обработки изображений, информационные и компьютерные технологии, программное обеспечение, базы данных.