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A Software Tool Design for Cerebral Infarction of MR Images

Kyoung-Jong Park, Woong-Gi Jeon, Hee-Cheol Kim, Dong-Eog Kim, and Heung-Kook Choi

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***Abstract*—** The brain MR imaging-based clinical research and analysis system were specifically built and the development for a large-scale data was targeted. We used the general clinical data available for building large-scale data. Registration period for the selection of the lesion ROI and the region growing algorithm was used and the Mesh-warp algorithm for matching was implemented. The accuracy of the matching errors was modified individually. Also, the large ROI research data can accumulate by our developed compression method. In this way, the correctly decision criteria to the research result was suggested. The experimental groups were age, sex, MR type, patient ID and smoking which can easily be queries. The result data was visualized of the overlapped images by a color table. Its data was calculated by the statistical package. The evaluation for the utilization of this system in the chronic ischemic damage in the area has done from patients with the acute cerebral infarction. This is the cause of neurologic disability index location in the center portion of the lateral ventricle facing. The corona radiate was found in the position. Finally, the system reliability was measured both inter-user and intra-user registering correlation.

***Keywords*—** Software tool design, Cerebral infarction, Brain MR image, Registration

I. Introduction

THE cerebrovascular disease, heart disease and cancer are the main fatal factor in Korea [1]. General neuron scientists use the advanced medical image technologies e.g., CT, MRI, PET etc. Furthermore, they have researching in-vivo obtained image analyses which are an important part until now. The conventional research method of neuron scientist is as follows:

1) Image acquisition of CT and MR
2) Visual inspection the selected ROI
3) Image registering of the subjective visual inspector
4) Accumulation the subjective visual images

However, the visual inspected registration cannot correctly map the size and shape to the standardized coordinate space. These conventional research methods have just yielded the qualitative result data which was occurred the high incidence errors of the difficult analysis. Also, in spite of the same experiment conditions, the results were frequently occurred the difference result according to the subjective researcher decision.

For the problem solution, the neuron scientists instituted the statistical brain atlas concept. The stochastic probability brain atlas converts from the qualitative brain clinical trial results to the numerical data based clinical trial results [2]-[6]. This concept was implemented using a registering algorithm by the standard brain template mapping [7]-[10] with a mathematical algorithm for the ROI of a neurologist. The diverse software with the applying statistic probability brain atlas concepts has been developed to improve the reliability and accuracy of brain disease research. However, the existed software could not be easily available to the outpatient data for the treatment. The conventional software needed the full 3D brain images (about 300 slides). In spite of the lesion suspected region scanned, the existed software needed the full 3D brain images. A whole 3D brain image can be scanned to research objective and it is limited the numbers. Also, for the research objective scanning needed 10 times data and consumed 10 times the image acquisition time and cost. As a result, the neurologist could not use a mount data to experiment. Therefore the experiment reliability should be reduced. The large brain images of a patient could be process to the treatment. We explained the general clinical patient images for a possibility of the amount image processing. Consequently, we present the image analyzer system to the diverse analyses through the image overlapping.

II. The Related Background

The representative software of the relative brain disease researches is the SPM(Statistical Parametric Mapping) [11] and MRIcroN [12]. In addition, the software tools are presented the Brain Voyager, 3D Slicer(MIT Artificial Intelligence Lab and the Surgical Planning Lab at Brigham and Women's Hospital) and ITK(Insight Segmentation and Registration Toolkit). SPM has developed to analyze the brain imaging data sequences. SPM handles the functional neuron images which are fMRI(functional-MRI), PET(Positron Emission Tomography), SPECT(Single photon emission computed tomography), ECG(Electrocardiography) and MEG(Magnetoencephalogra-phy). SPM yields the statistical numerical data and fMRI visualization of the brain activity region. And SPM registers in each other image sequence for the different modalities or the same modalities. SPM cannot

K. J. Park is with the School of Computer Engineering, Inje University, Gim-Hae, Gyeong-Nam, Rep. of Korea (phone: +82-55-320-3643; fax: +82-55-322-3107; e-mail: kevinpark1981@ gmail.com).
W. G. Jeon is with the School of Computer Engineering, Inje University, Gim-Hae, Gyeong-Nam, Rep. of Korea (phone: +82-55-320-3643; fax: +82-55-322-3107; e-mail: wjsdndrl0814@ gmail.com).
H. C. Kim is with the School of Computer Engineering, Inje University, Gim-Hae, Gyeong-Nam, Rep. of Korea (phone: +82-55-320-3720; fax: +82-55-322-3107; e-mail: heeki@ inje.ac.kr).
D. E. Kim is with the Department of Neurology, Ilsan Hospital, Dongguk University, Goyang, Rep. of Korea (phone: +82-31-961-7200; fax: +82-31-961-7212; e-mail: dxtxok@ gmail.com).
H. K. Choi is with the School of Computer Engineering, Inje University, Gim-Hae, Gyeong-Nam, Rep. of Korea (phone: +82-55-320-3437; fax: +82-55-322-3107; e-mail: cschk@ inje.ac.kr).

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execute for itself. That can use to install MATLAB [13] with the supplemental Library. However, MRIcroN can execute alone software differently than SPM. MRIcroN which is not functional registering can obtain more useful result if it uses with SPM. MRIcorN can support the ROI extraction functionalities and if necessary, researcher can directly add any ROI. Additionally, MRIcroN is widely used to the brain disease researches because of the compatible to the other Analyzer Format software.

TABLE I
FUNCTIONAL COMPARISON TO THE CONVENTIONAL SOFTWARE

Item	SPM	MRIcroN	RASM
Data Type	3D Data (Analyzer, NIfTI)	3D Data (Analyzer, NIfTI)	2D Data (DICOM)
Interface	Required Study	User Friendly	User Friendly
ROI	X	O	O
Registration	O	X	O
Massive Data	X	X	O
Support Query from Researchers	X	X	O
Statistical Probabilistic Map of Brain	X	X	O

Table I has shown the comparison our developed software to the conventional brain image processing software. SPM is widely used to international research fields but it ought to the prior learning firstly and it slowly access because of MATLAB based production. There is impossible to query access about the error correction of registering, amount of data processing and researcher requirement of some patient group. MRIcroN is also impossible to registering and the variable statistic processing. The two software are limited the 3D data format supporting (Analyzer, NifTI [14]). Consequently, as the introduction mention, the general patient data to treatment objective cannot accumulate a large data.

III. Brain Software Tool

A. Objective

Our research objective selects the lesion which is ROI of the clinical brain disease patient and develops a registering system analyzer for the standard brain template effectively. The developed research system is built to process and to save a large clinical experiment data. The developed system could be enhanced a reliability because of creating of the several thousand experimental results by the data accumulation.

B. System Structure

Fig. 1 showed a schematization for the whole system construction which consisted of two parts i.e., register and analyzer. The register supports a ROI selection to the neurologiist through a reading DICOM image of a stroke patient. After registering, the wrong part of the results could be confirmed that the user can individually modify by the providing tools. Analyzer yields some results by the data processing of the created register. A lot of data determined an experimental group through of a query and filtering process. It will be shown the final result with the similar color mapping of the filtered data overlapping. Thus, the result data can be useful by the Excel data saving to the various statistical package i.e., SAS, SPSS or BMDP.

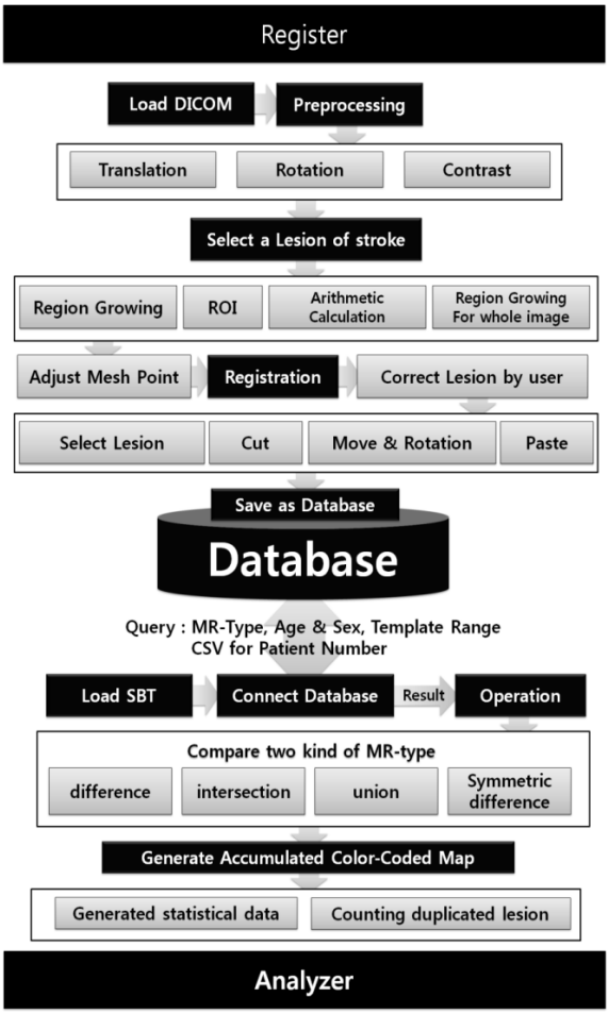


Fig. 1 Working flowchart

IV. Implementation Methods

A. Register

1) Implementation methods

DICOM-based image registering when loading the image data makes the normalization. DICOM images of the 12 bits or 16 bits gray level images contain some information. Our DICOM image case is 16 bits which value -32,768~32,767. But the monitor visualization shows the RGB color space (0~255). DICOM images which have the different values according to the scanning machine ought to scale the value 0~255 concerning to MIN and MAX value of DICOM header. Eq. 1 shows a formula to mapping (0~255) the MIN and MAX value

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of DICOM header. In formula x is the real pixel value of DICOM image. A rigid body transformation requires an image correction to the patient movement under the image scanning.

2) Lesion Selection

The register selects a lesion by the region extraction and region growing algorithm. Fig. 2 has shown the Diffusion and T2 weighted MRI lesion gradationally. Firstly, the weight was controlled after ROI setting and some lesion selection. If the region of interest is set, the weighted by the selection does not select a region of interest even if that extends out. The two types of MRI images show a little bit differences to select lesions. The Diffusion MRI images, the ventricle part is black and lesion part is white. The brain ventricle and lesion shows same intensity of T2 MRI. Therefore the whole brain ventricle shows if the simple region growing algorithm selected a lesion. The lesion selection needs using region growing algorithm if only selecting ROI. The lesion selection needs only the region growing algorithm.

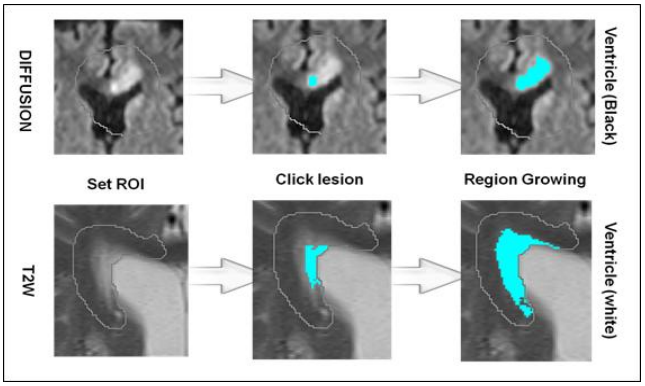


Fig. 2 Lesion selection

3) Mesh-Warp Registration

The registration algorithm uses a Mesh-warp [15]-[18]. The Mesh-warp algorithm used a 15 x 15 size Mesh grid and the Mesh-point can edit into an individual position. The algorithm interpolates [19]-[25] a Mesh-point as X-axis and Y-axis respectively and accurately adjusts the two distortion images.

The registration process is as follows:

1) Centralized the Mesh-point of two images
2) Adjust the end-points which are up, down, right and left of the two images
3) Registering of the linear interpolation
4) Individually modify the Mesh-point of the internal distortion part after the result confirmed
5) Re-registering

Mostly, the internal distortion part is not correctly registered. Their case can adjust to individually modify the Mesh-point. Fig. 3 shows the registering process after the Mesh-point setting.

B. Analyzer

Analyzer through a registration matching loaded with accumulated data is calculated as the statistical results. Finally, patients who would like to involve an experimental group can be selected.

Process of the Analyzer:

1) Read the standard brain template image
2) Filtering the accumulated data through the brain image number
3) Filtering by the queried condition of the user selection
4) Visualization a pseudo-color mapping on where overlapped the filtered result
5) The yielded result stores the numerical MS Excel format

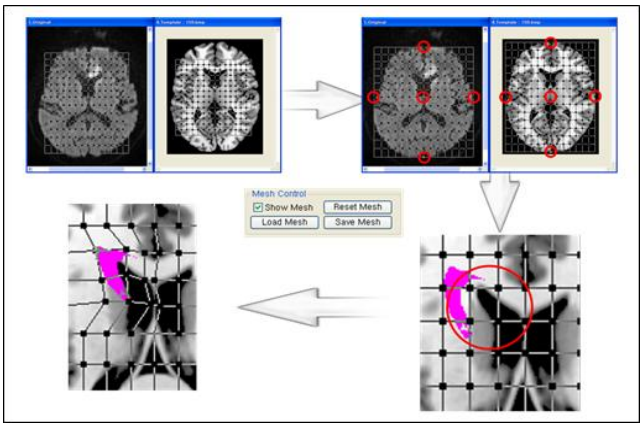


Fig. 3 Mesh-Warp registration

1) Filtering of the Patient Group

Filtering process is divided into the following five steps.

1) MR Type
2) Age & Sex
3) Template Range
4) Patient ID Number
5) Operation between the different MR-sequences

The register filtered out the other MR type without the desired type of 4 MR types. Next, the register filtered out a patient group of the age and sex to applying demographic variables. The filtered data are determined to including or excluding to compare the standard brain image number. Also, analyzer can choose the desired patient group of the any patient number setting. This is designed to using the existed neurological stroke patient database.

All of Korea stroke patient data has been stored to the neuroscience database. Therefore analyzer supports the first filtering functionality using a patient number from the patient group of neuroscience database. And, analyzer also supports a filtering functionality to the right and left of a brain image. The analyzer gets rid of the right or left brain region from the patient ID-number inputting into the result image. The reason of this process is due to afterimage sometimes of T2 image appeared that is the simultaneous scanning to the several MR types.

The template range which is the standard brain imaging can be selected in the range of numbers. This function is developed to include the experiment result of similar regions because ten slide differences can define a similar region of the whole brain region. Fig. 4 shows a filtering process of the template range as schematically.

The analyzer set TRA(Template Range) from the inputting TNO(Template Nember). Next, the analyzer brings an

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ED(Experimental data) and compares to bring one more data at ED if TNO does not included TRA. If the data is included in the TRA, the data of the PNO (Patient Number) and FDT (Filtered Data Table) compared with the PNO does not exist, FDT allows the insertion. If the data contained in the FDT of the PNO, the analyzer compares each TNO and PNO close to 171 is replaced by selecting the data. This process is done for all the ED, and ultimately is stored the FDT.

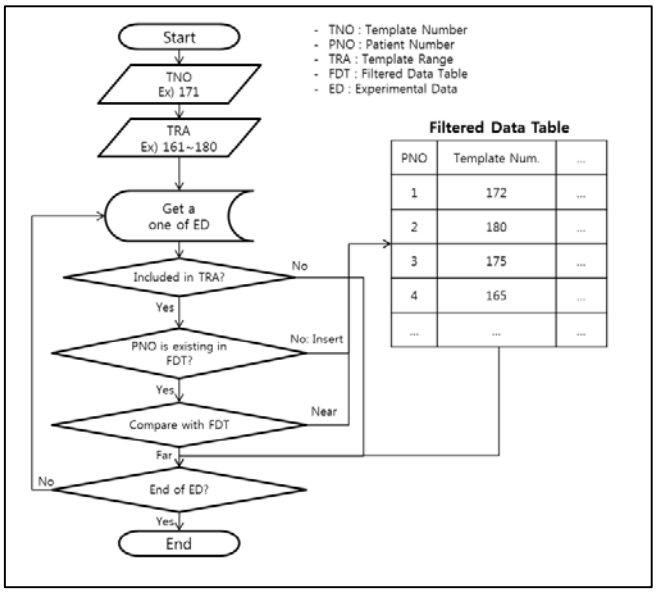


Fig. 4 Mapping Filtering process of the Template Range

2) Threshold

Analyzer under the same conditions on the resulting data for a comparative analysis thresholding function is applied. The result of the threshold function is possible to the change the Min and Max values. The pseudo-color of analyzer used a general Lookup table which can make increasing from RGB(0,0,255) to RGB(255,0,0) step by step. The left image of Fig. 5 consists of the threshold value with the original result Min and Max value. The overlapped maxima region shows red color. The right image of Fig. 5 is a result image of the threshold range 1~50. Changing the Max value to 50, the red color region converts to Green. The visualization could be possible to comparing the diverse experimental result to unify Min and Max value.

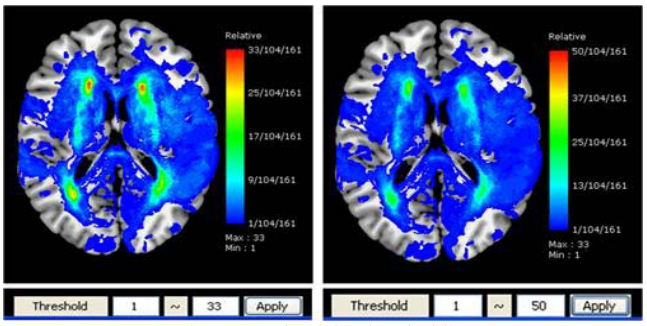


Fig. 5 Result of the thresholding

C. Compression of ROI

The newly developed system has stored the registered result to text file format. Before the registered result was stored the registered result by a image format. The method stored the rest region as well as the registered result. But the registered result enough visualized 1 bit per pixel according to the lesion or normal region. However, the image format storage method needs 25 bits which are not necessary space. To solve these problems, the text format was used a compressed storage scheme. The coordinate information stores for the text storage and the results of the specifying registration range can be compressed the data. Fig. 6 shows a compression concept of the text file. In the figure the white part need not register but the black part ought to be register. The text format repository is stored the X and Y axis coordinate system as the numerical data of the right of the Fig. 6.

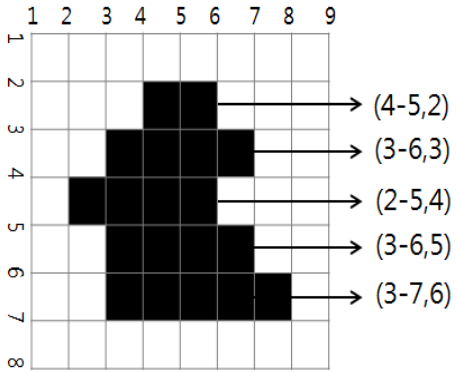


Fig. 6 Compression of ROI

The text expression shows a coordinate value ”3-6, 3” because of X-axis compressed. The region that is X-axis coordinate space 3-6 and Y-axis coordinate space 3 shows the registering result. When the result of Fig. 6 stores the specific type stored as “4-5,2; 3-6,3; 2-5,4; 3-6,5; 3-7,6”. The storage space requires 9x8x24 bits (1,728bits) for the Fig. 6 image. However, our compression method requires the space 30x8 bits (240bits). When we use our compression method the storage space saves about 7.2 times. The real registering result of the standard brain image size is 301x370 bits the registering result data using image compression method is 301x370x24 bits (2,672,880 bits) about 2.6 MB. However, if our image compression method uses the data size is 50x2x6x8 bits (4,800 bits).

The compression method with the Y-axis line number and the numbers of lesions are affected without any region size of lesion. Therefore, if the real data size has the vertical 50th line and 2 lesions, that calculate as above. 6 what is the meaning of the number one line of display data is being consumed by 6 characters. When we see this place can be reduced to 556.85 times the storage space absolutely reduce the conclusion. The reduction is not the only repository space. The result production of analyzer can be calculated pixel-value existing through all coordinate space circulating. Therefore, the calculating an image processes 301x370 operations. If we have 300 patients the 4 type MR operations calculate 133,644,000

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(301x370x300x4) operations.

On the other hand, the text format compression method is set 1 to the indicated text region. The lesion size is Y-axis 50 and usually 2 lesions takes 50x2x4 = 400 processing time. As the result, the processing can be reduced about 334,110 times. Of course, text analysis time takes a little but it is a few. Table II summarized the improved result above.

TABLE II
COMPARISION METHODS WITH THE RESULTS

Item	Image	Text	Result
Space	2,672,880 bits	4,800 bits	557
Processing	133,644,000	400	334,110

V. System Specifications

A. Hardware specifications

The used system environment was HP Workstation Z400 (Inter Xeon W3520 2.66, 3GB RAM, Windows XP 32Bit). The register required Intel Pentium4 CPU or more than 128MB. The tools for the software development used Microsoft Visual Studio 2005 Standard Edition. The computer program language was Visual C++ and the libraries were GDI+2.0 [26] and DCMTK (DICOM Toolkit) [27]. The developed software has completed the driving test in Window XP, Window Visita and Window7 operating systems.

B. Software specifications

1) Standard Brain Template

Our research used a standard brain template for a brain image standardization of the individual deviation. Our system read the "ch2better" to conjugating MRIcroN Z-axis value was stored from bottom by 2 step increasing. In this way, the obtained slides are 139 and the image identity number is the z-axis value.

2) Experimental Data

The experimental data are gleaned the cerebral infarction and the brain transient ischemia attack patients who were more than 300 patients from Department of Neurology at Dongguk university hospital in Korea. MR data was 4 types to the Gradient Echo, T2 weighted image, Fluid Attenuated Inversion Recovery (FLAIR) and Diffusion weighted Magnetic Resonance Image. The developed system was created a result data using 300 patients (about 7,500 slides) which are the real clinical patient data.

VI. Results

A. Interface of the System

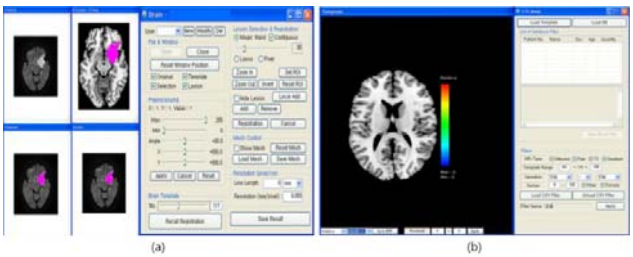


Fig. 7 Interface of RASM : (a) Register, (b) Analyzer

The register is separated a main window and 4 sub-windows as Fig. 7. The main window consists of an interface to the control the diverse functions concerning to the registration. The analyzer consists of two windows. This parted a control window and a check result window. The control window is inputted the patient group assignment, filtering conditions and checking window result.

B. Evaluation of Software Usability

The feasibility study of our developed software was carried out using the computation functionalities. Firstly, 101 patients who have occurred within 1 week of the acute cerebral infarction take FLAIR MRI and diffusion MRI scanner (Fig. 8 (a-b)). Through this analysis, we could see an acute cerebral infarct occurrence of the chronic ischemic brain damage part.

Furthermore the index location of neurologic disable causality located at corona radiate which nearly contacted center portion of lateral ventricle (in Fig. 8(c)). Thus, if FLAIR MRI taken before onset phase chronic ischemic damage in the central portion of the lateral ventricle facing the corona radiata in the region began to happen, we are drawn to the hypothesis that clinical awareness are likely to have.

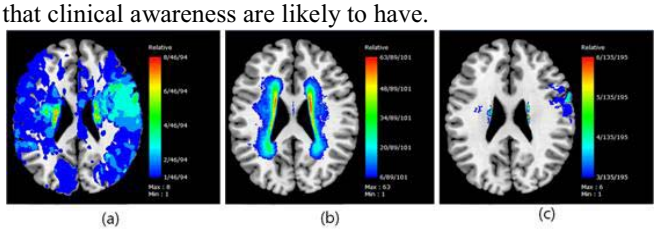


Fig. 8 Evaluation of the software usability

C. System Reliability Test

To verify the reliability of the system tests was conducted. Two research assistants observed in the diffusion weighted MR imaging of the acute ischemic brain lesions performed the task of matching the standard edition and it was reviewed by a neurologist. Between inter-users i.e., research assistant and neurology residents and the intra-users i.e., neurology residents were measured the matching consistency.

The center of gravity of the randomly selected 18 lesions from the 9 randomized patients has been verified to see that a linear relationship. In order to determine intra observer agreement using the matching by comparing the original and distortion if user feels that user can change the position, magnification, reduction, etc. to perform fine-tune a semi-automatic calibration device is inherent. The consistency was obtained between inter-users and intra-users of verifying its registration.

Through future clinical research studies in order to be utilized more rapidly in the automatic selection and registration seems to be supported. And the improved registration algorithms are needed for the study. The Mesh-warp base is currently being used to further enhance the registration method to the analysis of the distorted parts of the brain and the Mesh-point and an algorithm to automatically generate will be developed.

The system of a single medical institution as well as the several medical institutions the number of data can be used

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jointly. Therefore, the information environment by establishing an expanded statistical analysis and effective to enable a free search will have to gradually improve the system.

VII. Conclusions

In this study, a brain MRI stoke image analysis system based on a large-scale clinical data was constructed. The conventional software has been difficult on the individual modifications of the error and a large-scale data processing. In particular, we could be constructed a large amount stroke brain images as the 2D image data. The additional experimental cost could be reduced by exploiting of the general clinical patient data. By introducing the concept of two-dimensional large scale matching of data to accumulate, and by introducing the concept of statistical probability an anatomical brain mapping was established and standardized the image data. Using standardized data used in another study by cerebrovascular disease contribute to the improvement of the results were reliable.

Study and use of our system through the continuous feedback from medical doctor a more user-friendly interface was developed. More than tens of thousands of people to aggregate data from patients with cerebrovascular disease is effective in the clinical practice that can help to validate and verify the results. Furthermore, for a brain-related disorders can contribute to writing standards was a high possibility.

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