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Program & Abstract

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プログラム・抄録集

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Segmentation of stereo endoscopic video images using super-pixel and disparity map in laparoscopic surgery

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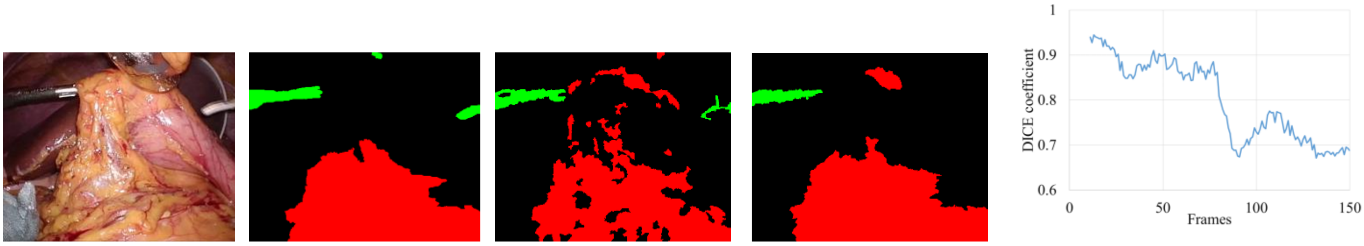
Abstract

Gastrectomy with lymph node dissection is a standard of laparoscopic surgery and improves the survival rate of gastric cancer patients. During lymph node dissection, surgeons remove the fat that contains the lymph nodes. Since the pancreas is covered with the fat and also image features of the fat and pancreas are similar, estimating their boundary from visual cues is difficult for novice surgeons. On the other hand, in recent years stereo endoscopes, which allow binocular disparity, have become widespread. In this paper, we propose a method for automatic tracking of multiple organs in the stereo endoscopic images using image and depth features. Masoud et al [1] estimated three-dimensional shape of non-rigidly deforming organs in endoscopic images using image features and a CT image. The method first estimates the likelihood of each pixel being inside a specific organ, then three dimensional reconstruction is performed. Bodenstedt et al [2] also used random forest for structure classification in laparoscopic surgery, but they employed the super-pixel algorithm as a preprocessing to improve classification accuracy.

In this paper, we improve Bodenstedt's method by adding the depth feature derived from the stereo endoscope and graph cut algorithm as in Yang et al [3]. In experiments, three-class classifications (surgical instruments, pancreas and background) were performed on real surgery videos by the previously method [2] and the proposed method. Two video sequences (150 frames in length), close-up and zoom-out views, extracted from a lymph node dissection surgery were used. The random forest was trained with the first 10 frames and tested with the remaining 140 frames. An example of experimental results is shown in Fig 1. Following the experiments in [2], we employed DICE coefficient as a performance metric. As a result, the average DICE coefficient of the two sequences using the previous and proposed method was 0.725 and 0.777, respectively. Our future work includes improving the feature vector and increasing the number of patients in the training dataset which may eliminate the need for the patient-specific training by searching a similar sequences from the large database.



(a) Input Image (b) Ground truth (c) Previous method (d) Proposed method (e) DICE coefficient

Fig 1. Example segmentation results (green: surgical instruments, red: pancreas). (a) Input image, (b) ground truth segmentation provided by an expert surgeon. The segmentation result by the previous method (c), and the proposed method (d), (e) DICE coefficient of proposed method as a function of time.

Keywords: Stereo endoscopic image segmentation, super-pixel classification, disparity map, laparoscopic surgery

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Super pixels based deformation recognition for endoscopic images

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Abstract

Deformation recognition of intra-operative organs, which means that each region of the organ can be tracked during the surgery even the organ is deformed, is especially necessary for locating tumor positions and planning resection maps in a surgery. Many researchers realized deformation recognition using 3D models deduced from pre-operative Computed tomography volume Data. For example, Nakao and Minato utilized pre-operative 3D model to locate tumor positions [1]. However, for organs such as the lungs, which are inflated before surgery but deflated during surgery, it is difficult to provide precise information by only using the pre-operative data. To improve this kind of 3D models, our research focuses on tracking each small region of the lung surface from intra-operative endoscopic images.

In recent year, super pixels are widely used in medical image processing since it can divide the whole image into small region in which all pixels are nearly homogeneous [2]. The boundary of each super pixel represents the dividing line between two different groups of homogeneous pixels. When deformation of the organ happens, its appearance and shape are changed. Thus, tracking techniques such as SIFT, SURF, Mean-shift fails in such a situation. By contrast, the boundaries of super pixels are more robust against deformation because the local contrast around the dividing line still exists even the organ is deformed. If we can track the boundary of each super pixel, the small region tracking of the organ can be achieved. This presentation will mainly introduce how to calculate the boundary of each super pixel, and how to track these boundaries using local contrast. Figure 1 shows an example of the super pixel boundary tracking. As the red arrows show, the super pixel is tracked even it is deformed.

Keywords: Deformation, Lung, Super pixel

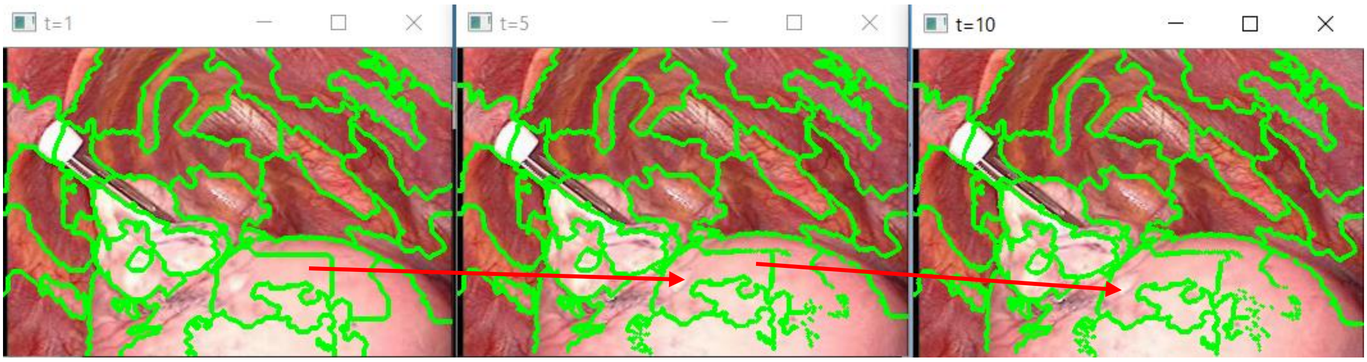

Fig. 1 An example of the super pixel boundary tracking

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The utilization of multidetector computed tomography (MDCT) for Simulation-based training program for minimally invasive cardiac surgery (MICS)

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Abstract

Minimally invasive cardiac surgery has been widely adopted recently. However, it takes an enormous amount of time to acquire this skill because of its difficulty and the limited number of the operation. The marked progress of medical devices like MDCT is so tremendous that we can visualize stereoscopic human anatomy in detail. As a result, we could make patient-specific replicas. We have introduced the simulation-based training program for MICS to assure its skill effectively. In this presentation, we will introduce our new surgical simulator using a fusion of the Patient-specific model and technology of AR (Augmented Reality). We have ever made the silicon replica models manufactured by a 3D printer from the images obtained by MDCT. Segmentation was performed by CT workstation (Vincent, Fuji Film). We could successfully perform MICS with no events by this simulator. It ultimately led to a complete planning of the operation because we could try various techniques, and to optimize procedural details regarding the direction of suture traction, exposure approaches, the order of stitches, coordination, and arrangement of the procedures. Moreover, had the opportunity to train the use of knot pusher in the limited operative field. But the problem of using patient-specific model is the cost of making the model. So we created and output quite a new simulation model using AR engine (Unity, Unity and Vuforia, PTC) to solve these problems. It reflects the body type's difference to output the skin and thoracic cage data. Our simulation-based training is useful to contribute to the safety and smoothness of the operations. Various technologies can help standardize the operative technique about MICS through visualization and simulation.

Figure 1.our new surgical simulator using a fusion of

the Patient-specific model and technology of AR (Augmented Reality)

Keywords: Simulation-based training, minimally invasive cardiac surgery (MICS),

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Viscoelastic simulation based on facial motion measurement

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Abstract

Facial expression is caused by facial skin deformation. Therefore, one's expression can be affected by the characteristics of facial skin. Because the characteristic changes are caused by a variety of reasons, such as aging and plastic surgery, it is important to consider the effect of characteristics for facial expression. While a lot of facial physical models have been proposed, the prediction of personal facial expression with facial skin characteristic changes is difficult due to the necessity of the personal facial modeling.

In this research, we propose expression reconstruction using facial shape deformation simulation based on facial skin viscoelasticity and facial motion measurement to consider use's facial skin characteristic changes. The proposed reconstruction method combines user's facial motion data and physical simulation of facial skin deformation. In our method, the facial motion is determined based on motion measurement without considering mimic muscle model. The user's facial motion is measured with a commodity depth sensor. The motion data are used to determine the displacement of a part of the nodes of the facial model as driven nodes which are chosen based on mimic muscle alignment and preliminary experiment. Viscoelastic finite element model is used to simulate the facial shape deformation because facial skin is considered as a viscoelastic material in the proposed method.

In the experiment, 3D facial shape, facial motion, and viscoelastic parameters of a participant were obtained to construct personalized facial model. The facial motion was measured with commodity depth sensor and five types of facial motions (instructed smiling, natural smile, lip purse, mouth opening, and cheek puff) were measured. The facial motions were expressed as a time series of displacement of the nodes of 3D facial shape consisting of over 1,000 nodes. We used a part of the nodes of the time series data to determine facial motion. The viscoelastic parameters of 68 points on the subject's face were measured with cutometer. We determined the nodes that are moved based on motion data by comparing the reconstructed result and motion measurement in various conditions.

Keywords: facial expression, feature tracking, viscoelasticity, finite element method.

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Structure of soft biological tissues based on viscoelastic propeties (物性から考察する生体軟組織の構造)

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Abstract

Understanding the properties of soft biological tissue is a key issue for mechanical systems used in the health care field. We found from the experiments that soft biological tissues have specific and complex viscoelastic properties and propose a simple model to identify the viscoelastic properties. I would like to share some of our work in mechanical model of soft biological tissues and the relationship between properties and structure [1]. The result also suggests that liver tissue has a complex fractal structure where the liver tissue is mechanically equivalent to a cubed fractal structure (fractal of a fractal of a fractal) whose basic elements are elastic and viscous elements.

Keywords: mechanical properties, viscoelastic properties, fractal structure, scale free

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Development of Feature Extraction Method based on Stacked Convolutional Neural Networks for Cancer Pathological Images

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Abstract

Recent development of computational image recognition based on deep neural network allows us to recognize and classify wide range of complex images automatically. Convolutional neural networks are one of the promising approaches for analysis of complex images because of its powerful potential for image analysis without using predefined features. In this study, we present two applications of the neural networks; a classifier that distinguishes transcriptome subtypes of lung adenocarcinoma from slices of pathological images, and a predictor of pathological images between different staining methods. In order to recognize the types of tumors, we need not only to detail features of cells, but also incorporate statistical distribution of the different types of cells within the tumor tissue. We constructed a model of deep neural network for feature extraction from pathological images of lung adenocarcinoma, which compromise three gene expression subtypes previously defined by the Cancer Genome Atlas (TCGA). Since the tumor tissues are composed of heterogeneous cell populations, recognition of tumor transcriptome subtypes requires more information than local pattern of cells but statistical distribution of cell patterns. Thus we used multiple reduction stages to integrate information from larger area of pathological images. We demonstrate that this network successfully recognized morphological features of lung adenocarcinoma, and classified them into three transcriptome subtypes with 99.6% accuracy. Moreover, we also applied this model to predict multi staining pathological images of pancreas cancer. By training two stages of autoencoder and predictor for immono staining images, which represents cell replication activity were predicted from images of HE staining of the contact slices. Those models will be applied for evaluation and prediction of other types of multiple staining methods.

Keywords: biomedical imaging, machine learning, deep convolutional neural networks, cancer pathological images.

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Clustering Biomedical Information by Deep Learning

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Abstract

Deep learning is a well-known method for feature extraction, classifier, and clustering. We examined if the method is of use to understand the unknown implicit feature in the given labeled data to biomedical information. In this research, we address two topics: DNA analysis and cell phenotype analysis.

[DNA analysis] DNA sequences has often been categorized using SNP (single nucleotide polymorphism). The SNP explains the temporal changes of genome sequences. Although we easily understand genome mutations through the SNPs, there is no proofs that essential features can be enveloped by SNP-based phylogenetic tree. We addressed letting a stacked auto-encoder learn DNA sequences and confirmed that the reduced dimensions show clusters. The results indicate the deep learning auto-encoder can provide natural categories.

[Cell phenotype analysis] Small-molecule compounds into cells often bring out cell morphology. In the morphing, the cell appearance diverges, e.g. enlarged nucleus; increased mitochondria; warped membrane shapes. In drug discovery, phenotypic screenings have been proposed to discover compounds serving as drugs. Phenotypes are derived from cell morphological image features. In this study we apply deep learning to phenotypic profiling. We tried to determine whether the cell phenotype changes certain compounds when added to cells by using the Convolutional Neural Network (CNN), which is a deep learning architecture specified to visual analysis. In experiment, we learned 1854 CNNs for 1854 compounds. In the results, although cell images are not clearly distinguishable by the authors (Fig. 1), the CNN achieved high recognition accuracy for some compounds. The CNN output can be assumed as a feature value representing a cell phenotype and we used the CNN output values for compound clustering.

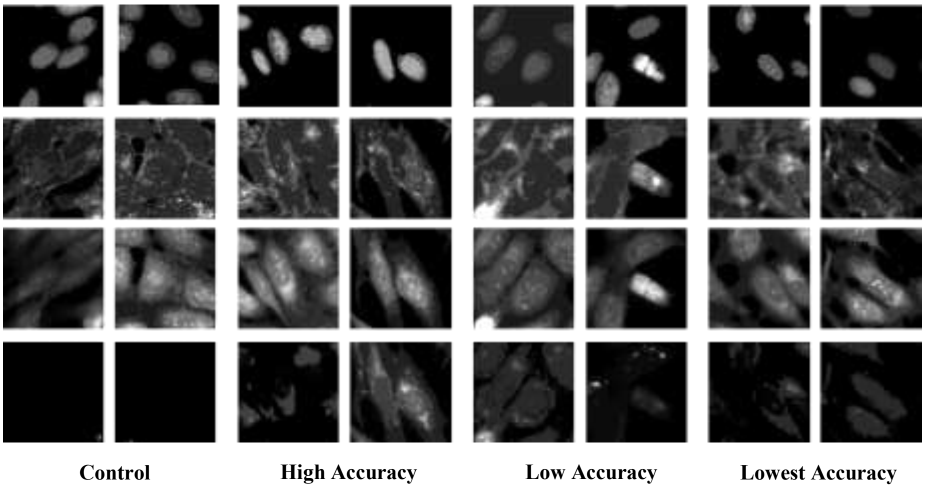

Figure 1. Fluorescence images of cells (each row shows different organelle) with high, low, and lowest recognition accuracy by CNNs.

Keywords: clustering, deep learning, biomedical imaging, DNA analysis, cell phenotype.

Remark

The research has been done by the collaborative group with Mitsubishi Tanabe Pharma Corporation.
- Osaka University: Shuya Yamamoto, Kanako Sugiyama, Satoshi Asatani, Hirohiko Niioka, and the authors
- Mitsubishi Tanabe Pharma Corporation: Ryuta Saitou, Hirokazu Nishimura, Kentaro Matsumoto, and Ken Ohno

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Progress on Deep Learning in Computer Vision and its connection with Medical Image Computing

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Abstract

Deep Learning, deeply layered neural networks, has been focused on in many research fields and has been reported its succeful result. In this talk, we introduce the progress on deep learning in computer vision and its connection between computer vision and medical image computing.

Keywords: Medical image processing, Computer Vision, Deep Learning

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Soft Computing in Medical Image Processing

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Abstract

Soft computing approaches include fuzzy logic, neural networks, deep learning, support vector machines, evolutional computation, probabilistic approaches, and chaos theory. They have been introduced into medical image processing because it is an effective approach to handle uncertainties in acquired image data. This talk introduces a fuzzy object model (FOM) to represent the knowledge of anatomical organ shape, and fuzzy connected image segmentation method using FOM. To present the performance of the proposed method, it has been applied to neonatal brain segmentation in MR images.

Keywords: Soft computing, Fuzzy logic, Fuzzy object model, fuzzy connectedness, neonatal brain image segmentation.

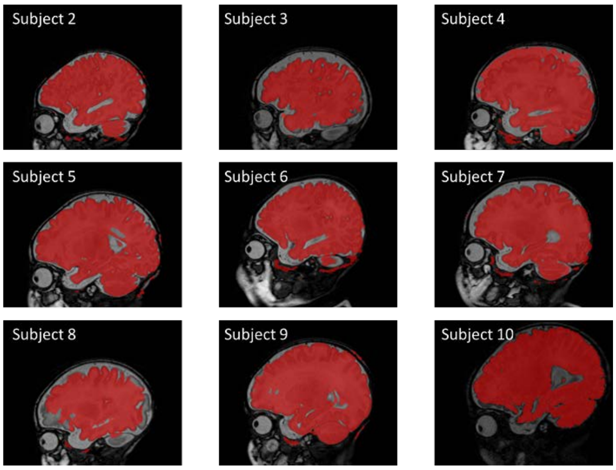

Fig 1. Experimental results with LOOCV.

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Medical-Engineering collaboration and Biomedical imaging research

Tatsuhiko Arafune[1], Yuki Nakano[1], Shinji Chiba[2], Takashi Suzuki[3], Toshikatsu Washio[4], Tomoyuki Yano[5]

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2 Microsoft Japan co. ltd, Tokyo, Japan
3 Institute of Advanced BioMedical Engineering and Science, Tokyo Women's Medical University, Tokyo, Japan
4 National Institute of Advanced Industrial Science and Technology, Ibaraki, Japan
5 Plastic Surgery, Gent University, Belgium

Abstract

We will introduce that our approach for medical-engineering collaboration with plastic and reconstructive sutrgeon and image processing based breast reconstruction plastic surgery assist system on behalf of the M-E collaboration. The breast reconstruction surgery assist system is constructed by 3D capture sensor (Kinect V2, Microsoft co. ltd), image processing software and projection-mapping system.

Keywords: biomedical imaging, breast reconstruction, plastic surgery, 3D imaging

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Evaluation of machine learning classifier for glaucomatous optic nerve head structure using optical coherence tomography images

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Abstract

The English abstract is presented here. Minimum length is 50 words; maximum length is 350 words.

Glaucoma is a multifactorial eye disease resulting in damage to optic nerve. It is supposed that Nicolela's classification of optic nerve head based on its structure, including four types, seems to be useful to know glaucomatous factors, and select proper treatments for patients with open-angle glaucoma (OAG). However, it depends entirely on subjective judgments acquired from color fundus photographs. This study aimed to develop a machine learning classification model to identify optic nerve head structure objectively. This study enrolled 113 eyes of 113 OAG patients. Fifty five parameters were applied in total, including the demographic data, and a variety of quantified ocular parameters from swept-source optical coherence tomography images: circumpapillary retinal nerve fiber layer thickness (cpRNFLT) and optic nerve head structure. Data was reviewed and graded by three glaucoma specialists. From all the eyes, 76 eyes were randomly selected as training group data, to build a classification model, while the remaining 37 eyes were used as test group data to validate the performance of the built model. Three machine learning classifiers were used and compared the performances: Neural Network (NN), Support Vector Machine (SVM) and Naïve Bayes (NB). To employ the most effective features in machine learning, a hybrid feature selection method combining mRMR (minimum Redundancy Maximum Relevance) and feature selection method based on genetic algorithm. As a result, accuracy of the classification for NN, SVM, NB were 81%, 79%, and 77%, respectively. All quantified ocular parameters were ranked by their importance, calculated by the best model (NN). The 7 most important features were disc angle (horizontal), average cup depth, spherical equivalent, horizontal Cup/Disc Ratio, Disc Height Difference, age, and average superior nasal clock-hour cpRNFLT. The proposed method makes it possible to objectively classify the glaucomatous optic nerve head based on its morphology with good accuracy, without using color fundus photos. Furthermore, the confidence score of predicting optic nerve head shape, calculated by the classification model, was supposed to be valid, in the case of having multiple factors simultaneously.

Keywords: machine learning, open-angle glaucoma, optical coherence tomography, optic nerve head.

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Partial region learning in CNN and majority voting for breast lesion classification in mammograms

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Abstract

In recent years, breast cancer has been increasing in Japan. Therefore, the importance of early detection, early diagnosis and early treatment of cancer has increased, and the importance of mass screening is being recognized. However, for physicians engaged in diagnosis, an increase in interpretation work in mass screening is a considerable burden. Therefore, it is necessary to develop a computer-aided diagnosis (CAD) system in which a doctor uses the result quantitatively analyzed by a computer as a "second opinion".

In this study, learning and evaluation experiments were carried out with the aim of achieving benign-malignant discrimination of mammograms using computer with deep learning. As a method of deep learning, a convolution neural network (CNN) which is learning method targeting general image recognition was used. In fact, machine learning requires a large amount of data, but it is difficult to obtain a large amount of data due to problems such as protection of personal information. Therefore, we extracted multiple small regions from one image, prepared a large amount of learning data with diversity, and carried out partial region learning. In our method, first, small regions are extracted from a single region of interest (ROI) of lesion with randomized locations and sizes. Then, the small regions are scaled to fit the size of the CNN input. Finally, based on multiple CNN outputs for the small regions, final decision of classification for the lesion is made by majority voting. In our preliminary studies, approximately 84% of correct classification rate was achieved by using 11-fold cross validation with the open database of MIAS and DDSM.

In summary, our method based on CNN with partial region learning and majority voting is feasible for breast cancer classification.

Keywords: breast lesion classification, deep learning, partial region learning, majority voting

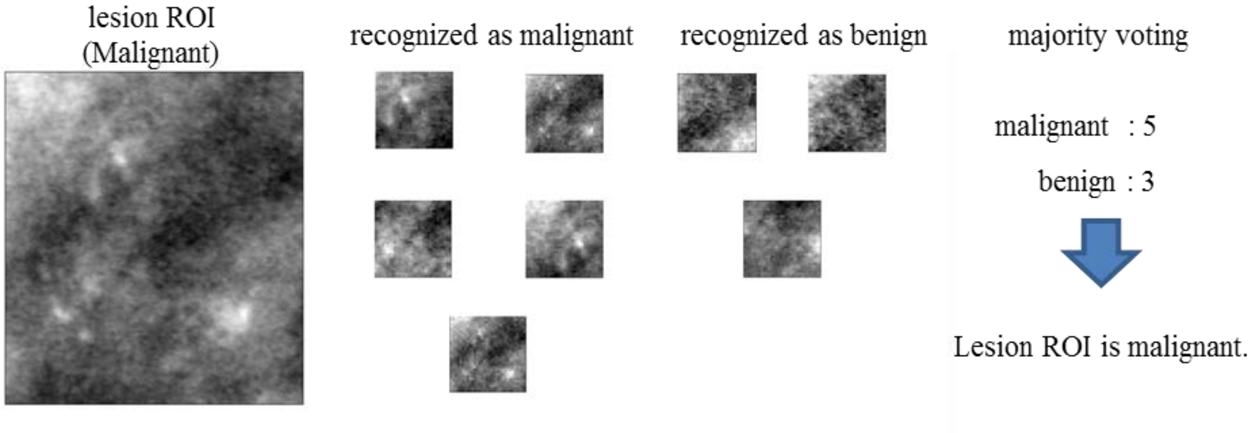

Figure 1. Examples of extracting small areas (8 pieces), performing differential diagnosis by majority voting

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Multi-class diagnosis for Parkinsonism with support vector machine using DaTSCAN SPECT images

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Abstract

Parkinson disease (PD) is a progressive neurological disorder and is included Parkinson syndrome (PS). PS contains some diseases: PD, dementia with Lewy body (DLB), progressive supranuclear palsy (PSP), and Alzheimer disease (AD). In clinical diagnosis, DaTSCAN SPECT imaging is conducted. The binary classification between normal (NR) and PD has been investigated [1][2], but multi-class classification for PS has not been reported. The aim of our research is a multi class classification for PS based on DaTSCAN SPECT images and other information by using machine learning. Our proposed method located a rectangle ROI around the striatal and normalized by whole brain mean count. Next, we trained all voxel values and diagnosis label by a classification algorithm, and evaluated the performance. In our previous research, we conducted the binary classification NR and PD. We trained image data (213 NR cases and 1189 PD cases) from Parkinson Progression Marker Initiative (PPMI) database by support vector machine (SVM). On this study, we evaluated learned SVM using clinical data (7 NR cases and 15 PD cases) provided from Nippon Medical School. In a result, SVM derived the accuracy of 86.4%. This performance against clinical data is effective. Therefore, we try to classify PS on the next phase. Moreover, we must consider the method to combine image data and other information, because, for instance, age is closely related to PS.

[1] Francisco P. M. Oliveira et al. , 2015, “Computer-aided diagnosis of Parkinson’s disease based on 123IFP-CIT SPECT binding potential images, using the voxel-as-features approach and support vector machines”, J. Neur. Engi., 12

[2] Shogo Watanabe et al., 2017, “Investigation of Potential Usability of Machine Learning to Diagnosis of Parkinson Disease Using SPECT DaTSCAN”, IFMIA2017

Keywords: DaTSCAN SPECT, Parkinson syndrome, machine learning.

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Stability analysis of a dynamical system describing competition for multi-valued discrete tomography

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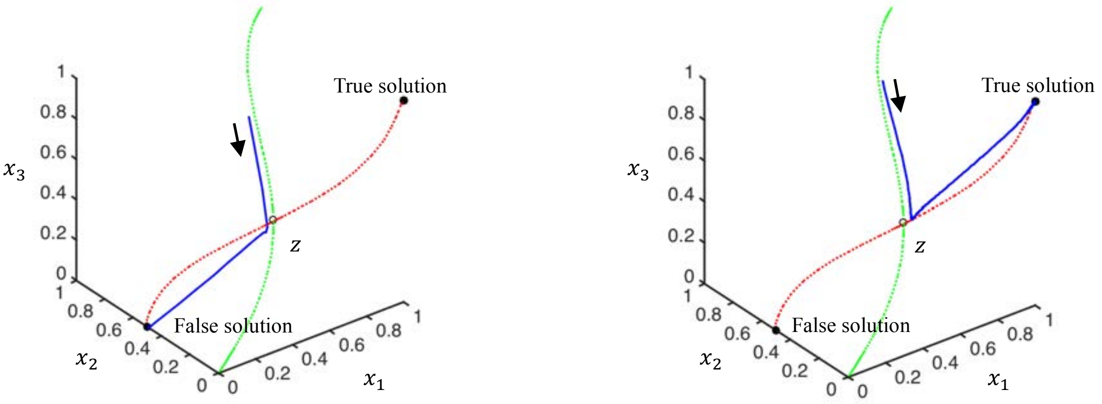
Abstract

We previously proposed a method for multi-valued discrete tomography using a dynamical system enabling an exclusive behavior of a competitive model. The dynamical system has been designed so that the solutions starting from appropriate initial values converge to the true solution corresponding to the exact image.

We have proved the coexistence of the true solution and the false solutions as stable equilibria and the existence of the saddle type equilibrium that plays an important role in the behavior of solutions. Figure 1 shows an example of the phase portraits obtained by projecting the trajectories in the eight-dimensional phase space into the three-dimensional phase space. The trajectories emanating from different initial values go towards the saddle z along the stable manifold, and then after approaching to z, they leave from z and converge to either the true solution or the false solution depending on their initial value. The results suggest that the stable manifold of z separates into the basin which converges to the true solution.

Keywords: multi-valued discrete tomography, image reconstruction, nonlinear differential equation, competitive model



(a) (b)

Figure 1: Trajectories of solutions

$x = (x_1, x_2, \dots, x_8)$ denote state variables. Blue lines represent the trajectories emanating from uniformed initial value (a) 0.7 and (b) 0.8. Closed circle represents stable equilibrium. Open circle represents saddle type equilibrium z. Green dotted line represents stable manifold of z. Red dotted line represents unstable manifold of z.

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Kinematic analysis of forearm rotation by 2D-3D registration using biplane fluoroscopy

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Abstract

In orthopedics, quantification of three-dimensional kinematics of the bones is useful for diagnosis and treatment planning. In case of forearm, 3D motion analysis of pronation and supination is important to clarify the anatomical function. Shian et al [1] focused on the motion of the radius around the ulna and analyzed the movement of 3D rotation axis between maximum pronation and maximum supination using four CT images in different postures. Kazama et al [2] used biplanar radiographies in five postures and a CT image. In order to understand the anatomical function in more detail in a clinical routine, a method which allows 3D motion analysis with high temporal resolution while keeping the radiation dose at the conventional level is essential. Our goal is to analyze the detailed mechanism of dislocation including a quick movement. For this purpose, we propose a 2D-3D registration method using a calibrated biplanar dynamic fluoroscopy and a CT image. This method follows that of Otake et al [3] in which simultaneously optimize the rigid transformation parameters of multiple bones by maximizing the similarity between the fluoroscopy and digitally reconstructed radiograph (DRR). We use CMA-ES as optimizer and gradient correlation similarity metric.

In this paper, we report a simulation experiment using a bone phantom and a real image experiment using clinical dynamic fluoroscopy (12.5 fps, 125 frame images). In the simulation experiment, we compared the effects of accuracy on different radiation dose levels. The registration accuracy was evaluated using Euclidean distance error between the marker position on the fluoroscopy and estimated marker position on DRR. The average error at low, middle and high radiation dose mode were 1.96 mm, 2.05 mm and 1.72 mm, respectively. Fig.1 shows 3D kinematics estimated from the clinical fluoroscopy images. Fig. 2 shows the angle of rotation from the neutral position. Our future work includes introducing smoothness constraint to improve robustness and accuracy in 2D-3D registration.


(a) (b) (c) (d)

Fig.1 Example 3D kinematics from the clinical fluoroscopy images. (a) LAT image, (b) AP image, (c) and (d) LAT and AP images overlay estimated 3D bone position.

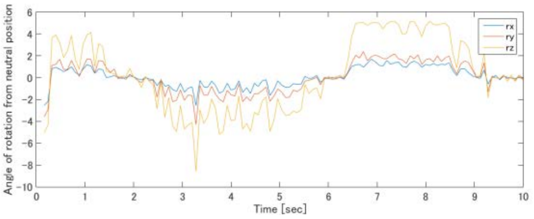

Fig.2 The angle of rotation from the neutral position.

Keywords: kinematic analysis, forearm, 2d3d registration

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Database construction of pre- and post-operative musculoskeletal structures and implants towards statistical modeling in total hip arthroplasty

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Abstract

3D surgical planning systems for total hip arthroplasty (THA) require a complicated user interaction considering the balance of various clinical evaluation criteria, and requires a lot of labor, time and skill.

We have been developing an automated surgical planning system for THA based on statistical analysis of dataset of past patients. This system produce a surgical plan automatically from the patient CT image. Although a planning considering postoperative implant position and soft-tissue tension is desirable [1], the database of our system currently consists of only preoperative data.

The goal of this study is to create a surgical plan for THA in consideration of CT images before and after surgery. In this paper, we report on the database we created. The database includes (1) the relative displacement of the bones (i.e., pelvis and femur) before and after surgery, (2) the muscle shape deformation between preoperative and postoperative CT, (3) the difference of implant position that is planned preoperatively and the actually placed location. The method to determine each element is described below.

(1) Relative displacement of the bones. (1-1) The pelvis and femur were segmented manually from CT images, (1-2) registration was performed on the pelvis before and after surgery, (1-3) the relative displacement was obtained from the registration results.

(2) Muscle shape deformation. (2-1) The gluteus medius muscle was manually segmented from CT image, (2-2) the transformation matrix obtained in (1-2) was applied to align the coordinate system, (2-3) pseudo x-ray images of the pre- and postoperative gluteus medius muscle was created.

(3) Difference of implant position. (3-1) The transformation matrix of the implant in preoperative plan was obtained from the surgical plan, (3-2) 3D-3D registration between the postoperative CT and the CAD model of the implant was performed to find the postoperative implant position.

Future work includes creating a surgical plan using this database.

Keywords: Total hip arthroplasty, Database, Automatic surgical plan

Reference

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