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DNA Modeling in Biomedical Image Matching

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Abstract

Medical image matching (MIM) is the application of image processing techniques to clinical diagnosis. In this work a novel method for the alignment of different MRI images is evaluated. This method called as The Quarter Code Algorithm. The method is based on the linear mapping and the one-to-one correspondences between point features extracted from the images and on calculating similarities in pixel values. This correspondence is determined by comparing two strings constructed from pixel values of the images. The method uses a table called the Quarter Code table, which is the set of characters and numbers. In this table every number between 0 and 255 is translated into a unique string of four letter alphabet. Letters A, C, G, T are chosen, since they are the same as used in DNA sequences. In this way it possible to utilize tools originally programmed to DNA sequences analysis. When all pixel values of MRI images are converted to virtual DNA sequences, one can show the differences between two virtual DNA sequences. The comparison between two virtual DNA sequences is done by Chi-squared test, Markov Chain and glm plot.

Keywords: MRI images; Genetic code; Sequence alignment; Markov chain model; Glm

Introduction

Image matching is an important area of research in the field of inverse engineering, artificial intelligence, pattern matching, machine vision and biomedical image analysis. These techniques are able to detect image variations in different images. In biomedical aspect the ability to match an anatomical atlas, which illustrate the structure of the human brain, to individual patient images provides the basis for solving several important problems in medical image interpretation. During years a large amount of research has been carried out on medical image matching methods. The methods may be categorized into several broad classes depending on how the images are analyzed? One of the earliest records of image matching technique is the method proposed by Tanimoto [1].

He claimed that many biomedical images share the property that their objects and subject properties are highly predictable. He has examined some ways for generating and testing correspondences between "observed" entities and objects of the model that may be useful for diagnosis [1].

Letter in 1988 Yamada [2] are applied a model-based dynamic programming matching method to extract the optimally fitting shape from each static frame in a sequence of echocardiograms, while allowing for a certain amount of change of length of each side of a model polygon [2]. This model was employed for dynamic imaging. Simultaneously a knowledge-based approach to retrieve medical images by feature and content with spatial and temporal constructs is developed by Chu [3]. In this method feature and content are extracted by type abstraction hierarchy (TAH) and the high-level nodes models for providing features and contents. Features and content are stored in a database [3].

Type abstraction hierarchy (TAH) data structure is an efficient organize framework for coupling data and knowledge for cooperative query processing [4]. The knowledge-based retrieve medical image model is proposed to present the various feature and content of image with spatial and temporal constructs. Different knowledge about image feature can provide default parameter values for specifying query conditions. Some researches like Williams, Wilson and Hancock have formulated the image matching problem under a Bayesian framework and believe that Bayesian methodology facilitates a principled approach to the development of a matching model [5]. Kumar A and colleagues are also presented a retrieval system for dual-modality PET/CT images by proposing the use of graph-based methods to spatially represent the structural relationships within these images [6].

They have used attributed relational graphs (ARG) with the purpose to compare different objects by means of graph matching algorithms for similarity measurements. Kumar and colleges claim that quantitative evaluation demonstrated that their dual-modal ARG enabled the content-based image retrieval systems of dual-modality PET/CT [7]. However, in critical point of graph

matching Horst [7] claims that in real world applications we can't always expect a perfect match between the input and one of the graphs in the database. Therefore, what is needed is an algorithm for error-tolerant matching, or equivalently, a method that computes a measure of similarity between two given graphs [8].

In 2011 Sikiö [8] and collogues are evaluated the role of texture analysis (TA) of magnetic resonance images in detecting subtle changes between the hemispheres in various brain structures in patients with early symptoms of parkinsonism. They have performed Co-occurrence matrix-based Texture analysis to detect changes in texture between the hemispheres and clinical interesting area in the brain. The Texture analysis results were statistically evaluated using the Mann-Whitney U test [9]. The problem in Co-occurrence Matrices methods involved understanding the nature of various types of matrices. Leydesdorff and Vaughan introduce several problems involving multiple mathematical operations [10].

Recently, in 2012 Wang [10] has purposed a new method to repair mild asymmetry using computer-aided design technique. In this method, the Medpor implants in the body are displayed using surface rendering technique after operation. The surface rending technique involves collection of data on a body in order to create a three dimensional image of that body. The postoperative evaluation of method is performed using matching technique [10].

In this research study numerous point correspondence medical image matching methods have been evaluated in this field, each exhibiting its own characteristics, strengths, and weaknesses. The main problem and disadvantages of the above approaches are sensitivity to loss of data which are useless for medical applications and Neuroimaging aspect as well. In order to overcome these problems, we have presented a novel medical image matching. The technique is based on DNA Modelization of digital images and their statistical analysis.

Methods and Materials

The technique is based on DNA Modelization of digital images and their statistical analysis. The main objective of this study is to test if Chi-Squared test is applicable to image analysis. DNA Modelization of a digital image is an arrangement for allowing numbers of pixels values and pixel maps to be presented as a sequence of characters. In this system every pixel value is coded by four characters. The first step in the method proposed by the author of this research is to carry out the direct coding of the digital image, with the four letters A, G, C, and T. Alphabet {A, C, G, T} is chosen, because it is the same as in real DNA sequences.

The novel idea is that analysis tools for DNA sequences may be applicable to image processing. The next stage implements statistical inference methods to detect similarities in virtual DNA sequences. This method is executed by Chi-Squared test. Chi-Squared test is a statistical test method commonly used to compare observed data with data we would expect. For improving the results we will execute Chi-Squared test in Markov chain model, because the first order Markov model provides a mathematically tractable solution. After statistical tests, the distribution of the data is evaluated using a glm plot techniques. The glm plots provide a useful way to visualize the data being compared.

Experiment Results

DNA modeling and statistical conclusions on two hippocampus images

We performed the experiments two real hippocampus (brain) images. These were taken on the same subject of on different time position in order to allow an assessment of progression of the disease. In this experiment we selected two different frame images from the same position. It means that the angle and trans axial of images is the same. The time interval between two these images is 2 years and our intent is to determine changes happened during this time interval. The experiment starts with the DNA modeling of the MRI images. The first image is called Slice1 and the second image is called Slice 2, see Figure 1.

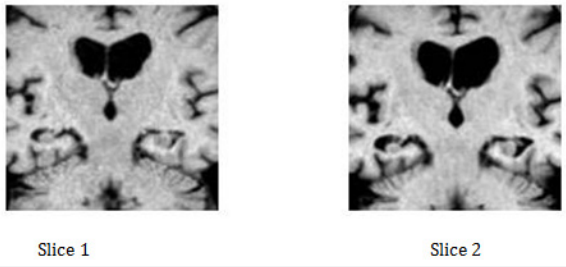

Figure 1: Serial MRI, Adding the time dimension, time-interval between slice 1 and slice 2 is 2 years.

Results from practical experiments with two different images are presented in this section to demonstrate our approach. The table for pixel values based on X and Y coordinates in Slice 1 and Slice 2 are determined. In the second stage of DNA modelization process we will replace all pixel values with the Quarter Codes based on Table 1.

Table 1:

[0]= AAAA, [1] = AAAC, [2] = AAAG, [3] = AAAT, [4] = AACA, [5] = AACC, [6] = AACG, [7] = AACT, [8] ...

Statistical conclusion of images comparison

Statistical conclusions are divided into three parts: medical image matching based on Chi-square test, Markov model and glm plot.

Medical image-matching based on chi-squared statistics

Chi-squared test is a statistical experiment commonly used to compare observed data. To show our comparison approach, we use the Slice 1.dna and Slice 2.dna sequences obtain from previous work. First we will count the number of nucleotides 'A', 'C', 'G' and 'T' in two sequences (Table 2 & 3).

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Table 2: Results of Chi-Squared test for the two sequences Slice 1 and Slice 2.

X-Squared	Df	P-Value
707.53	11	< 2.2e-16

Table 3: Results of Chi-Squared test for the two first order Markov chains, for Sequences Slice 1 and Slice 2

	Df	Deviance	Resid. Df	Resid. Dev	P(>|Chi|)
NULL			31	13914.9	
current	3	2524.6	28	11390.3	0.0
MRI	1	0.1	27	11390.2	0.7
current: following	12	10091.7	15	1298.4	0.0
current: MRI	3	672.5	12	625.9	1.913e-145
current: following: MRI	12	625.9	0	-3.637e-12	3.079e-126

Slice 1:

a c g t

22626 17320 26200 22405

Slice 2:

a c g t

25654 18163 21518 23370

For counting of the frequency of two nucleotides we used the R program.

The frequencies of nucleotides for two sequences are:

Slice 1

a c g t

0.2555138 0.1955935 0.2958747 0.2530180

Slice 2

a c g t

0.2892058 0.2047573 0.2425793 0.2634575

Execution Chi-Squared test for Slice1 and Slice2 (used R).

Conclusion

X-squares are 707.53. Therefore there is evidence that the sequences cannot be the same. So the images must be different.

Optimization of the result

For optimizing the results we can test the Chi-Squared for two first order Markov chains and glm plot, too.

Medical Image-Matching Based on Comparison of Two First Order Markov Chain. We next execute the Chi-Squared test for two first order Markov chains with the frequency of two nucleotide words in the first order Markov chain. (Used R) *P-value is 3.079e-126*, it means there is an evidence that dependence in Markov chain models is different in MRI Slice 1 and Slice 2 (Figure 2).

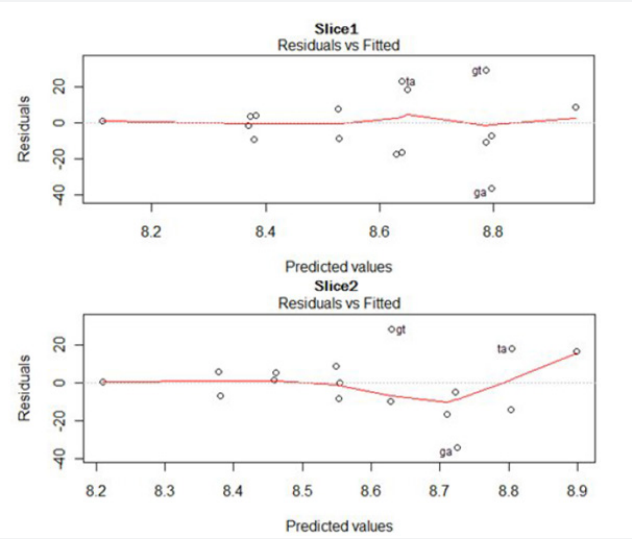

Figure 2: glm plot for two first order markov chains.

Medical image-matching based on general linear models (glm)

Generalized liner models (glm) have been incorporated into the R statistical language in order to implement their enhancement of glm. We use glm plot for observing distribution of two first order Markov chains in Slice 1 and Slice 2. The graph shows that two plots are different. It means that two sequences are different.

Conclusion

We proposed the Chi-Squared test method for the comparison of two biomedical images. Chi-Squared statistics was used to compare the distribution of frequency counts across different populations. This comparison is based on distribution of frequency counts. If the X-squared test score equal to 0 and p value equal to 1, the two sequences are similar. This is however always not true because in some cases frequency counts are distributed identically across different populations. In this case the distributions are identical, but distribution of first order Markov chains of sequences may be different. Therefore for referring the results and obtaining the desirable results we execute the Chi-Squared test in Markov chain model because the first order Markov model provides better fit to a DNA sequence. But in some cases it is possible that two sequences are still different unless the test that p-value for Chi-Squared test from two first order Markov chains is equal to 1. In this situation glm plots provide a useful way to visualize the sequences being compared. In this case the set of letters A, C, G and T are defined as y coordinates and the set of virtual DNA string is defined as x coordinates.

The desirable matching ratio for two images is obtained by execute Chi-Squared test in two stages:

1. Run Chi-Squared test to obtain X-squared and p-value between two virtual dna format sequences

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2. Run Chi-Squared test to obtain p-value between two "first order Markov chain" of two virtual dna format sequences

For visualization of the variation between two images we use glm plot. The glm plot is the best method if the Chi-Squared testes are indicates no differences between images. It means that glm plot is the best comparison method in this process.

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