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Detection of small changes in medical and random-dot images comparing self-organizing map performance to human detection

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ABSTRACT

Radiologists use time-series of medical images to monitor the progression of a patient's conditions. They compare information gleaned from sequences of images to gain insight on progression or remission of the lesions, thus evaluating the progress of a patient's condition or response to therapy. Visual methods of determining differences between one series of images to another can be subjective or fail to detect very small differences. We propose the use of quantization errors obtained from self-organizing maps (SOM) for image content analysis. We tested this technique with MRI images to which we progressively added synthetic lesions. We have used a global approach that considers changes on the entire image as opposed to changes in segmented lesion regions only. We claim that this approach does not suffer from the limitations imposed by segmentation, which may compromise the results. Results show quantization errors increased with the increase in lesions on the images. The results are also consistent with previous studies using alternative approaches. We then compared the detectability ability of our method to that of human novice observers having to detect very small local differences in random-dot images. The quantization errors of the SOM outputs compared with correct positive rates, after subtraction of false positive rates ("guess rates"), increased noticeably and consistently with small increases in local dot size that were not detectable by humans. We conclude that our method detects very small changes in complex images and suggest that it could be implemented to assist human operators in image-based decision making.

1. Introduction

Radiologists have to detect the progression of patients' conditions on the basis of, often hardly detectable, local changes in medical images. The images are captured through various imaging techniques, such as magnetic resonance imaging (MRI), computerized tomography (CT) and positron emission tomography (PET). These images provide the radiologist with visual information about the state or progression of a given condition, and help determine the course of treatment. Traditional methods for handling such images involve direct visual inspection, which is by its nature subjective. Image science has proposed methods for the automated processing of medical images, which involves various different image processing techniques to identify specific diagnostic regions of interest and features, such as lesions. [1,2] proposed a computational framework to enable comparison of MRI volumes based on gray-scale normalization to determine quantitative tumor growth between successive time intervals. They proposed three tumor growth indices, namely, volume, maximum radius and spherical radius. The approach, however, requires an initial manual segmentation of images, which can be a time-consuming task. [3], first, semi-automatically segmented a tumor in an initial patient scan and then aligned the successive scans using a hierarchical registration scheme to measure growth or shrinkage from the images. This method relies on accurate segmentation and requires manual supervision, in order to detect changes of up to a few voxels in the pathology. [4] describe a procedure aimed for difficult-to-detect brain tumor changes. The approach combines input from a medical expert with a computational technique. In this paper, we propose a new technique based on self-organized mapping that considers the whole medical image, as opposed to an image segment, as region of interest. This excludes manual benchmarking tasks designed to eliminate inclusion of structures with similarity to tumor pathology. The basic principle behind direct image analysis is that there exists an intrinsic relationship between medical images and their clinical measurements, which can be exploited to eliminate intermediate procedures in image analysis. Compared to traditional methods, direct methods have more clinical significance by targeting the final outcome. Thus, direct methods not only reduce high computational costs, but also avoid

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errors induced by any intermediate operations. Direct methods also serve as a bridge between emerging machine learning algorithms and clinical image measurements. Finally, to show how the output variable called “quantization error” of image analysis by SOM may be exploited as an indicator for the presence of potentially critical local changes in image contents, we compared the quantization errors of SOM outputs from analyses of random-dot images with very small progressive increases in the local size of a single dot to the capacity of human observers to detect these changes.

2. Materials and methods

2.1. Self-organizing maps

A self-organizing map (SOM) is an unsupervised neural network learning technique that does not need target outputs required in error correction supervised learning. SOM, [5] are used to produce a lower-dimension representation of the input space. Thus, for each input vector, so called, competitive learning is carried out to produce a lower-dimension visualization of the input data. SOM are typically applied as feature classifiers of input data. From an initial randomization of a map, input data is iteratively applied to optimize the map into stable regions. Where the node weights match the input vector, that area of the lattice is selectively optimized to more closely resemble the data for the class the input vector is a member of. From an initial distribution of random weights and over multiple iterations the SOM eventually settles into a map of stable zones. Each region of the map becomes a feature class of the input space. Each zone is effectively a feature classifier, and the graphical output is a type of feature map of the input space.

The central idea behind the principles and mathematics of SOM is that every input data item shall be matched to the closest fitting region of the map, called the winner (as denoted by M_c in Fig. 1), and such subsets of regions shall be modified for optimal matching of the entire data set, [6]. On the other hand, since the spatial neighborhood around the winner in the map is modified at a time, a degree of local and differential ordering of the map occurs to provide a smoothing action. The local ordering actions will gradually be propagated over the entire SOM. The parameters of the SOM models are variable and are adjusted by learning algorithms such that the maps finally approximate or represent the similarity of the input data. While studies have mainly concentrated on the performance of various SOM on a given dataset, we set to unveil the behavior of various datasets on a single SOM. Given related sets of medical image series and a constant SOM, can we detect a significant trend in the images? Is the trend of any clinical significance?

2.2. The quantization error in SOM outputs

The task of finding a suitable subset that describes and represents a larger set of data vectors is called vector quantization (VQ), [7]. VQ aims at reducing the number of sample vectors or at substituting them with representative centroids. The resulting centroids do not necessarily have to be from the set of samples but can also be an approximation of the vectors assigned to them, for example their average. VQ is closely related to clustering, and SOM performs VQ since the sample vectors are mapped to a (smaller) number of prototype vectors, [8]. The prototype vectors are called the best matching units (BMU) in SOM. As a property of SOM, the quantization error (QE) is used to evaluate the quality of SOM. The QE belongs to a type of measures that have been used to benchmark a series of SOMs trained from the same dataset. In our work, we have used QE to do a somewhat opposite measure: to benchmark a series of datasets using SOM trained with the same parameters. In other words, we use the same SOM, same map size, feature size, learning rate and neighborhood radius to analyze series of image datasets with clinical significance, or random-dot images, as shown later herein. The QE is derived after subjecting an image to a self-organizing map algorithm analysis and by calculating the squared distance (usually, the standard Euclidean distance) between an input data, x, and its corresponding centroid, the so-called “best matching unit”, or BMU. This gives the average distance between each data vector (X) and its BMU and thus measures map resolution:

$$QE = 1/N \sum_{i=1}^{N} \|X_i - (\mathrm{BMU}_{(i)})\| \quad (1)$$

where N is the number of sample vectors x in the image.

This measure completely disregards map topology and alignment, as noted by [8], making it applicable for different kinds and shapes of SOM maps. Besides, the calculation does not rely on any user parameters as seen in (1) above. A 16 by 16 SOM with an initial neighborhood radius of 5 and learning rate of 0.2 was set up for the extraction of data from images. These initial values were arrived at after testing several sizes of the SOM to check that the cluster structures were shown with sufficient resolution and statistical accuracy, [6]. The learning process was started with vectors picked randomly from the image array as the initial values of the model vectors. For each of the following three experiments, the SOM parameters were kept constant.

In this study, we started by applying SOM to time series of original imaging data from a patient's knee before and after blunt force traumatic injury. Then, we added artificial lesion growth to these images and ran SOM analyses on the modified images. [4] modified original images by adding synthetically evolving pathological content of 1%, 5% and 22% volume growth prior to further analyses. They did not use SOM analysis but conducted visual and computational recognition experiments with these images to test the detection of the artificial "pathologies".

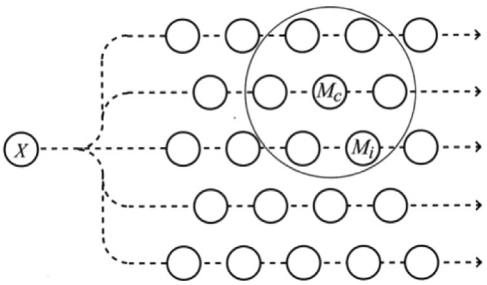

Fig. 1. Schematic illustration of a self-organizing map. An input data item X is broadcast to a set of models M_i, of which M_c matches best with X. All models that lie in the neighborhood (larger circle) of M_c in the grid match better with X than with the rest, from [6].

3. Results from SOM analyses

3.1. Original medical images

We used two sets of images from a patient with a sprained knee, courtesy of Hopital de Hautepierre, Strasbourg, France. The same acquisition parameters (machine, sequence, coil, etc) were used to acquire each set which consisted of 20 MRI images. Table 1 shows the QE values obtained from each set of images, taken on two consecutive clinical visits, almost two months apart. Fig. 2 is a graphical display of the data.

The QEs shown in Table 1 were submitted to one-way analysis of variance (ANOVA). The difference between image series is statistically significant (t (1, 38)=3336; $p < .01$).

3.2. Medical images with artificially added "lesion" contents

On the first set of images, we added a synthetic lesion to each image