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Analysis of Contours of Tumor Masses in Mammograms by Higuchi's Fractal Dimension

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We have tested a new method of assessment of mammographic images for medical diagnosis to differentiate between benign masses and malignant breast tumors. 2-D image is preprocessed to form 1-D signature of the image contour and then its complexity is analyzed using the Higuchi's fractal dimension method. We prove that the Higuchi's fractal dimension, $\mathbf{D}_f$, is a good classifier enabling differentiation between malignant tumors and benign masses.

Keywords: fractal dimension, breast cancer, image analysis

1. Introduction

Mammography is a popular X-rays technique for early diagnosis of breast cancer. This technique is often used in screening for detection of tumor masses. After detecting a tumor mass in mammogram, biopsy is needed for checking the kind of the tumor, whether it is benign or malignant tumor. The tissue from biopsy is examined by a pathologist. The biopsy is an invasive and time demanding method. Recently, many studies are devoted to find quick noninvasive methods based on mammographic images for classification of breast tumors. Several methods of image analysis were tested [1÷7]. The techniques based on fractal analysis are among them [8÷15].

Fractal analysis can be a very useful method for quantitative assessment and classification of many kinds of medical images [16÷17]. R. M. Rangayyan and T. M. Nguyen tested some fractal analysis methods on images of breast tumor masses to differentiate between malignant and benign tumors. They computed fractal

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dimension of contours of breast masses obtained from mammographic images either directly from the 2-D contour or from the 1-D ‘signature’ derived from the contour; they applied either the 1-D ruler method or the box counting method [8]. Again, we propose to use the Higuchi’s method for analysis of ‘*signatures’* – the method is simpler than the other fractal methods and leads to comparable results.

2. Methods

The Higuchi’s fractal dimension ($\boldsymbol{D_f}$) is calculated directly from the data series, without embedding the data in a phase space [18]. It is, in fact, fractal dimension of the curve representing the series, and so it is always between 1 and 2, since a simple curve has, dimension equal 1 and a plane has dimension equal 2. The fractional part of $\boldsymbol{D_f}$ is a measure of the series complexity. It should not be misled with fractal dimension of an attractor in the system’s phase space.

There are few ways to obtain signatures from image contour. In presented study we used the following methods. The contour of an image is specified in any rectangular coordinate system, i.e. by the set of pairs $(x_i\ , y_i\ )$ such that pairs $i-1$, i, $i+1$ correspond to consecutive points on the contour for any $i = 1, \dots , N$; the first point $i = 1$ may be chosen arbitrary and the point $i = N + 1$ coincides with the point $i = 1$ i.e. the contour is a closed planar curve.

We calculate arithmetic averages, x_0 and y_0, of coordinates of all contour points and transform rectangular coordinates into polar ones; it is enough to calculate r-coordinate:

$$r_i = \sqrt{\left(x_i - x_0\right)^2 + \left(y_i - y_0\right)^2}. \tag{1}$$

The series r_i is a 1-D ‘signature’ of the 2-D contour and we analyze the signatures of breast masses contours using the Higuchi’s method.

We tested the Higuchi’s fractal dimension, $\boldsymbol{D_f}$, as a classifier for breast masses to benign or malignant tumors categories. We checked effectiveness of $\boldsymbol{D_f}$ for distinguishing benign masses from malignant tumors by analyzing a ROC curve [19÷21] (Receiver Operating Characteristic; plot *Sensitivity* against 1-*Specificity*). We calculate the Higuchi’s fractal dimensions, $\boldsymbol{D_f}$, from the whole signature.

3. Data

Two main data sets of contours of breast masses were used in this study both supplied to us by Prof. R.M.Rangayyan (University of Calgary, Alberta, Canada). The diagnostic classification of the masses was based upon biopsy. The contour of each mass was manually drawn by an expert radiologist specialized in mammography and verified independently by another radiologist.

Most of the benign masses in the data set 1 (DS1) are well-circumscribed (circumscribed benign or CB) (Fig. 1a), whereas most of the malignant tumors are spiculated (spiculated malignant or SM) (Fig. 1b), as typically encountered in mammographic images. The data set DS1 contains the contours of the 57 masses.

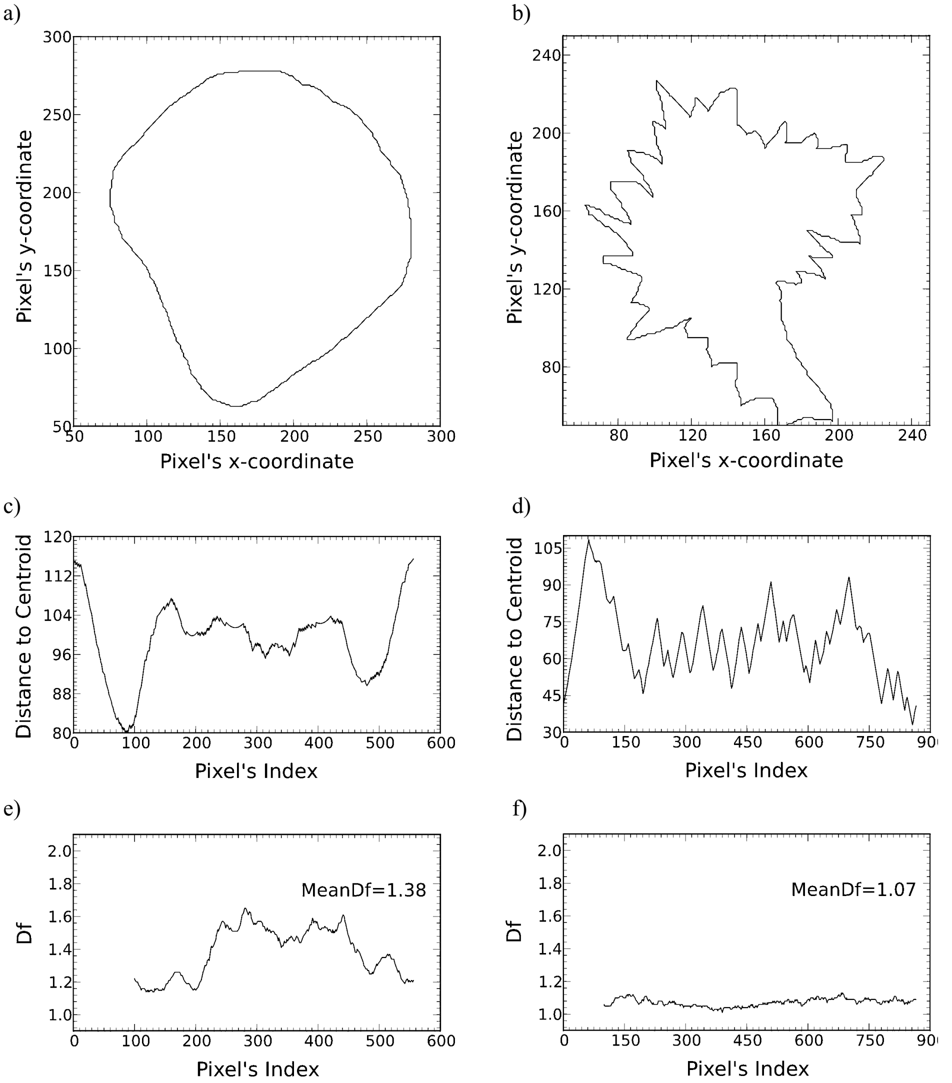

Fig. 1. Contours of a circumscribed benign (CB) mass (a) and of a spiculated malignant (SM) breast tumor (b) their signatures (c and d respectively; cf. Eq. (1)) and the signatures' Higuchi's fractal dimension (e and f respectively). Signature of malignant tumors shows lower fractal dimension (f) than that of a benign mass (e)

The data set 2 (DS2) includes circumscribed and spiculated cases in both the benign and malignant categories. SB (spiculated benign) masses and CM (circumscribed malignant) tumors are unusual, and tend to cause difficulties in pattern classification studies. The data set DS2 contains the contours of the 54 masses.

It is created a third data set, for global statistic. The combined data set (CDS) was prepared by combining all cases in the first and the second data sets.

The results obtained are presented for the three data sets (first and second data sets separately and combined) to demonstrate the strengths and weaknesses of the Higuchi fractal dimension method when used in characterizing of the breast masses and the tumors of various types. More information about the data contains paper of R. M. Rangayyan and T. M. Nguyen [8].

4. Results and Discussion

We calculated the average Higuchi's fractal dimension for the data sets DS1 and DS2. In the data set DS1 37 benign masses had average $\boldsymbol{D_f}$ equal 1.3 ± 0.14. (mean ± standard deviation). The remaining 20 masses were malignant tumors with the average Higuchi's $\boldsymbol{D_f}$ was equal 1.07 ± 0.05. In the data set DS2, the average $\boldsymbol{D_f}$ of 28 benign masses was equal 1.13 ± 0.11 and average $\boldsymbol{D_f}$ of 26 malignant tumors was 1.05 ± 0.3.

While contour of a circumscribed benign breast mass (Fig. 1a) seems to be more regular than contour of a spiculated malignant breast tumor (Fig. 1b), fractal dimension of the malignant breast tumors is lower than fractal dimension of the benign breast masses. If the contours were magnified one observed that these of the benign masses showed much more small irregularities than those of the malignant tumors. That is why signature of benign mass shows many small 'fluctuations' while that of malignant tumor does not (cf. Fig. 1a and Fig. 1b, respectively), so leading to differences in their fractal dimension. Problem of calculation of the length of coast-line considered by Mandelbrot [22] is quite analogous. In fact, fractal dimension turned out to be the best characteristics that actually gives possibility to compare properties of different coast-lines .

For assessment performance of the Highuchi's fractal dimension for differentiation of benign from malignant tumor analysis of Receiver Operating Characteristic curve (ROC) [19÷21] was used. In a ROC graph true positive rate (TPR, Sensitivity), is plotted *vs.* false positive rate (FPR, 1 – Specificity) for different cut-off points. Definitions of TPR, FPR, Sensitivity, and Specificity are as follows:

TPR = *true positive results of test/all positive results of test*
FPR = *false positive results/all negative results of test*
Sensitivity = TPR
Specificity = *true negative results/all negative results of test*

Each point of the ROC curve represents a sensitivity/specificity pair corresponding to a particular decision threshold. The better test's performance is for curve closer to the upper left corner of the graph. So, performance obtained for the data set DS1 was much better than for the data set DS2 (Fig. 2). Table 1 contains cut-off points for the best sensitivity and specificity calculated for all studied data sets.

The area under the ROC curve (AUC - Area Under Curve) is a general indicator of quality of the test. Summarized results of AUC are contained in Table 2.

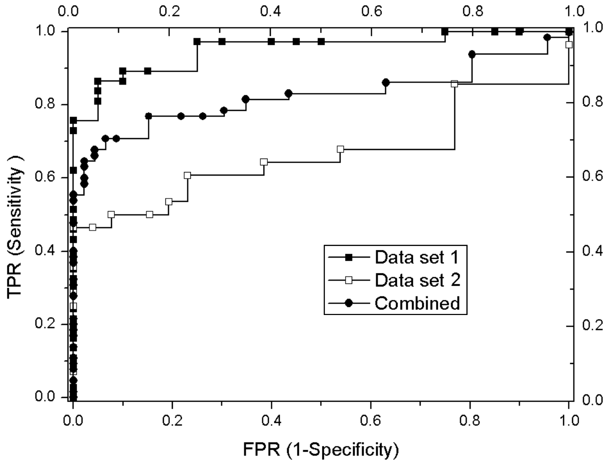

Fig. 2. ROC curves indicating the classification performance of Higuchi's fractal dimension for Data Set 1 (DS1), Data Set 2 (DS2), Combined Data Set (CDS). The area under ROC curve, AUC, for these data sets DS1, DS2 and CDS are 0.96, 0.7, and 0.84, respectively (Table 2)

Table 1. The optimal cut-off points for best performance of the test

Data set	Cut-off point for the best sensitivity and specificity
DS1	1.14
DS2	1.11
CDS	1.11
Circumscribed masses (subset of data set 2)	1.11
Spiculated masses (subset of data set 2)	1.03

Table 2. The results of quality of the test by area under ROC curve, AUC

Data set	AUC – area under ROC curve	Standard error of AUC	95% confidence interval	*Z* statistic	Significant level *P* *p*-value
DS1	0.96	0.03	0.872 to 0.994	18.715	0.0001
DS2	0.70	0.07	0.562 to 0.819	2.846	0.0044
CDS	0.84	0.04	0.759 to 0.903	9.228	0.0001
Circumscribed masses (subset of data set 2)	0.92	0.07	0.722 to 0.990	7.025	0.0001
Spiculated masses (subset of data set 2)	0.58	0.11	0.393 to 0.757	0.793	0.428

The *p*-value (Table 2) showed ability of $\boldsymbol{D_f}$ to distinguish between benign and malignant masses. If *p* is significantly smaller then 0.05 then AUC is significantly different from 0.5 and therefore there is an evidence that the fractal dimension can distinguish the malignant masses from the benign masses. For the data set DS1 the test based on $\boldsymbol{D_f}$ was excellent; for the combined data set, CDS, the test was good. But for DS2 the test was only fair, because this set contained unusual cases; if we subdivide DS2 into two subsets with the first subset containing circumscribed masses and the second subset containing spiculated masses then we can see why the test is only fair. The average $\boldsymbol{D_f}$ of the circumscribed benign masses was equal 1.2 ± 0.09 and $\boldsymbol{D_f}$ of the malignant tumors was equal 1.07 ± 0.03 so the result was similar to values obtained for data set 1. The area under the ROC curve AUC = 0.92. These results are better than for CDS and close to the results obtained for DS1.

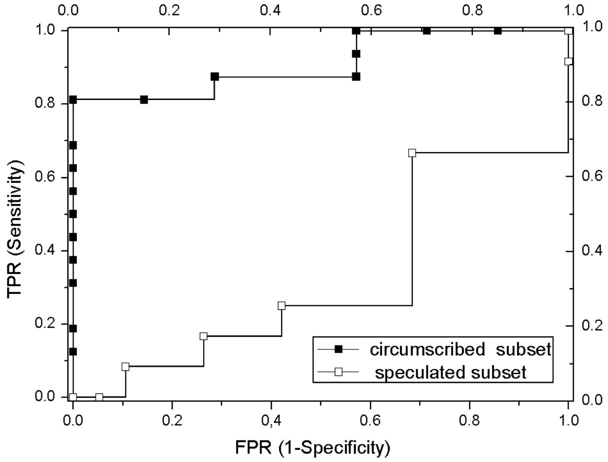

Fig. 3. ROC curves indicating the classification performance of Higuchi's fractal dimension for circumscribed and speculated subsets of Data Set 2. AUC for speculated masses is not statistically greater than 0.5 so it is not possible to distinguish benign from malignant tumor by values of $\boldsymbol{D_f}$

The result of analysis of AUC (Table 2) showed that $\boldsymbol{D_f}$ classifier did not differentiate benign masses from malignant tumors for the subset of spiculated masses (last row in Table 2). The average values of $\boldsymbol{D_f}$ were the same for the benign and for the malignant tumors – for the spiculated masses were equal 1.03. When we took cut-off value for CDS, equal 1.11 (Table 1), all spiculated cases were indicated as the malignant tumors. AUC for the spiculated masses were not statistically greater then 0.5 so it was not possible to distinguish the spiculated benign from the spiculated malignant tumor by values of $\boldsymbol{D_f}$. The performance of clinical test for the spiculated cases failed. We found that in DS2 all false negative results were for the spiculated masses.

The Higuchi's fractal dimension shows accuracy comparable to the fractal dimension estimated with the 1D ruler method [8]. Furthermore, $\boldsymbol{D_f}$ is more accurate classifier for circumscribed masses; however it is poor in classification of atypical SB masses. The classification performance for masses of $\boldsymbol{D_f}$ is comparable to the other shape feature such as compactness [6], fractional concavity [7], spiculation index [5] and Fourier factor [6], which were compared with FD by R. M. Rangayyan and T. M. Nguyen [8].

5. Conclusions

The Higuchi's fractal dimension, $\boldsymbol{D_f}$, is a good classifier of malignant tumors and benign tumors for circumscribed masses, while $\boldsymbol{D_f}$ shows poor classification performance for spiculated masses. The tests for spiculated shape of masses are usually false positives. The Highuchi's fractal dimension well classifies circumscribed masses while the 1D ruler method well classifies speculated masses. So, these two methods combined well classifies all tumor masses.

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