A comparative study on the fractal dimension method and the time series analysis with applications in medical imaging

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Abstract: - The goal of this paper is to develop and compare two methods: the first based on fractal analysis and the second one on nonlinear time series analysis, in order to decide which one is more appropriate for discrimination between normal and modified kidney tissue. For this study, a set of 100 CT images containing normal and a malign affected renal tissue was used. The classification procedures are based on the box-counting method and computing the correlation dimension of the reconstructed attractors of the time series associated to each CT image, respectively. The paper concludes, by means of statistical analysis, that, when considering CT images, the results of the first method are less satisfactory than of the second one. The argumentation for this fact and related results are also provided.

Key-Words: - fractal analysis, nonlinear time series analysis, CT image

1 Introduction
Fractal analysis and nonlinear time series analysis, both in close connection to chaos theory, generally provide useful methods for clinical sciences [1], [2], [3], [4], [5].

Typically, fractal analysis refers to a collection of methods for the description and quantization of geometric features of irregular forms and patterns. It was largely applied for the study of biological systems and subsystems at microscopic and macroscopic scale ([6]) because of their fractal-like structure. Its most known tool is the fractal dimension used to provide information on the irregularity of an object contour or selfsimilarities of a texture. Fractal analysis was largely applied for discrimination between different types of forms and textures ([7]).

On the other hand, time series analysis deals with time series that are sets of values of a single variable function, usually measured as function of time (dynamic features). Nonlinear methods were developed in the last 20 years, motivated by the concept of deterministic chaos which was proved to exist within many real systems in chemistry, physics, biology, medicine, electronics ([1], [2], [3], [4]). The time series in medicine are recordings of the electrical activity – electrocardiograms, electroencephalograms and physiological parameters – blood pressure, breathing ([2], [5], [8]).

Although, these two branches of chaos theory aim at different types of applications – static - purely geometric, images (spatial chaos), respectively, dynamic features - recordings of different body activities over time (temporal chaos); the connection between them is obvious. A chaotic dynamical system converges, as time passes, to a domain generally having a fractal structure (system’s attractor) so many chaotic systems are generating fractals.

In the domain of pathological anatomy – especially when analyzing CT, RMN images and frozen tissues samples, one deals with static – not varying with respect to time - structures.

This fact generally leads to the employment of fractal analysis methods for classification and discrimination. The most used method is the box-counting method that provides the fractal (box-counting) dimension of the analyzed object.

In this paper, for CT image analysis, aside from the classical use of the box counting method, we consider measurements with respect to a one-dimensional spatial axis – instead of temporal axis so that methods of nonlinear dynamical analysis can be applied as well; in fact pertinent examples from chemistry ([9], [10]) geography ([11]) are well known.

We consider a series of CT images containing the kidney tissue that have fractal – like tissue
structures. The basic idea is to make the distinction between modified and normal kidney tissues by computing the box-counting dimensions and, respectively, the correlation dimensions of the attractors of the time (spatial) series associated to the images. The two methodologies and their associated methods are presented and the obtained statistical results are compared in terms of trustworthiness.

The conclusion of the study on the selected set of CT images is that distinction between normal and malign tissues can be obtained by both methods, but higher accuracy and significantly better results are obtained when using nonlinear time series analysis.

2 Materials and methods

For this study, a series of 100 CT images were used. 50 of them contain malign modified kidney tissue and the rest of 50 images – present normal kidney tissue.

2.1 Box-counting method and dimension

The box counting method provides a measure – fractal (box/counting) dimension \( d_f \) for the complexity of the texture of the kidney tissue. The fractal dimension is computed using the box/counting algorithm because, in comparison to other methods, it offers two major advantages: it is easy to implement and can be applied for images no matter how complex.

The \( d_f \) derived from the Hausdorff coverage dimension, is given by the following approximation:

\[
  d_f = \lim_{s \to 0} \frac{\log(N(s))}{\log(1/s)},
\]

where: \( N(s) \) is the number of squares with side length \( s \) that contain information when grid covering the image.

Relation (1) is the equation of the slope \( d_f \) of the regression line associated to the points \( \log(N(s)), \log(1/s) \) for different values of the square’s side - \( s \).

The box-counting algorithm assumes to determine the \( d_f \) in accordance with the dependence of the texture upon the used scale factor. It consists in image binarization, successively covering it with squares with equal sides \( (2, 2^2, 2^3, ..) \) and counting every time the squares that contain some part of the analyzed object. The points of coordinates \( \log(N(s)), \log(1/s) \) are approximately positioned in a line and its slope will be the fractal dimension in “box-counting” sense.

To exemplify how the algorithm is used, we’ll consider the image of a kidney (fig 1. a)) from which we’ll extract a binary version by neglecting all the pixels over a certain threshold (fig. 1. b)).

![Image](image1.png)

Fig. 1. a) The original image; a) binary image c) extracted contour

Next, we’ll apply the box-counting algorithm, described above, for different scale values \( s \), using our specially designed software - MorfoFractal.

The method can be also used to determine the self similarities of an object contour (Fig.1 c)), but in our case, due to the fact that the kidney capsule is not necessary affected, the texture is more important.

A general problem of this method is the use of an ad hoc threshold when creating the binary image. This fact leads to incomplete or noisy object in the binary image and sometimes importantly affects the fractal dimension value.

2.2 The CT image associated time series attractor and the correlation dimension

By investigating time series, one can observe the behavior and properties of dynamical systems.

A dynamical system \( T : N \times M \to M \) is said to be a discrete dynamical system if there is a map \( f : M \to M \) such that:

\[
  T(n,x) = (f \circ f \circ ... \circ f)(x) = f^n(x),
  \forall n \in N, \forall x \in M.
\]

A nonempty set of states \( K \subset M \) is called an attractor or attracting set for the system \( T \) if the following properties hold:

1. \( K \) is closed
2. \( K \) is invariant,
3. there is a neighborhood \( U \) of \( K \) such that:

\[
  \lim_{i \to \infty} d(T(t,x),K) = 0, \forall x \in U.
\]

A real valued map \( F : M \to R \) is interpreted as a
measure on the state space. If \( \forall t,s \in S \) are fixed \( t \) is called delay) and \( x \in M \) is a fixed state, then a sequence of measurements:

\[
F(T(t,x)), F(T(t+s,x)), F(T(t+2s,x)), \\
\ldots, F(T(t+(d-1)s,x))
\]

is called a time series starting from \((t, x)\) associated to the system \( T \). If \( T \) is a discrete dynamical system defined by the map \( f \), then the associated time series starting from \((0, x)\) is:

\[
F(x), F(f(x)), F(f^2(x)), \ldots, F(f^n(x)).
\]

One can reconstruct the attractor of a dynamical system from the time series generated by the system, by using the Taken’s Embedding Theorem ([13], [10]). The theorem was written for an infinite time series, but it can be implemented for a long enough finite series also.

Below we present a version of Taken’s theorem due to T. Sauer, J. Yorke, M. Casdaglia.

Let \( T: \mathbb{R} \times M \to M \) be a smooth dynamical system of class \( C^2 \) on \( M \) and let \( F: M \to \mathbb{R} \) be a measure of class \( C^2 \). Let \( t \in \mathbb{R} \) be a fixed moment and let \( \tau > 0 \) be a delay. If \( K \) is a compact invariant set of \( T \) and \( b \) is the box-counting dimension of \( K \), then the map:

\[
H : K \to \mathbb{R}^{2b+1}
\]

defined by:

\[
H(x) = (F(T(t,x)), F(T(t-\tau,x)), \ldots, F(T(t-2b\tau,x)))
\]

is generically injective (a property is called generic if it is true on a set that contains a countable intersection of open dense sets).

Presuming that the fractal dimension of the attractor is known, the attractor can be reconstructed from a univariable time series in a higher dimensional space (that is at least twice plus one its fractal dimension ([15], [16], [12], [10], [18]).

In practice, \( b \) is unknown, so, there are a series of methods for reconstructing the attractor without knowing its dimension.

The correlation dimension - \( d_c \) - is a simple way to distinguish a random signal from a signal generated by a possibly chaotic set. A random process correlation dimension is infinite, that means that the higher the embedding space dimension is, the higher is the \( d_c \) value (the orbit of a random process is not expected to have any spatial structure). The \( d_c \) for a closed curve is 1 and for a two-dimensional surface is 2. The correlation dimension is calculated using formula (2):

\[
C(\varepsilon) = e^{d_c}, \varepsilon \to 0 \Rightarrow d_c = \lim_{\varepsilon \to 0} \frac{\ln C(\varepsilon)}{\ln \varepsilon} \tag{2}
\]

\( C(\varepsilon) \) is called the correlation integral and is defined by expression (3):

\[
C(\varepsilon) = \lim_{n \to \infty} \frac{1}{N^2} \sum_{i,j=1}^{N} H(\varepsilon - |y_i - y_j|), \tag{3}
\]

where:

- \( H(x) \) - is the Heaviside function,
- \( H(x) = \begin{cases} 1, x > 0 \\ 0, \text{otherwise} \end{cases} \);
- \( \varepsilon \) - maximal Euclidian distance allowed between pairs of points;
- \( y_i \) - is a point in the embedded phase space constructed from a single time series according to Taken’s theorem:

\[
y_i = (x_{i}, x_{i+\tau}, x_{i+2\tau}, \ldots, x_{i+(d_E-1)\tau});
\]
- \( d_E \) - the dimension of the embedding space;
- \( i = N \cdot \tau (d_E + 1) \) - number of embedding vectors;
- \( N \) - initial time series length.

So, \( C(\varepsilon) \) gives the proportion of the number of pairs of points in the embedding space with the Euclidian distance less than a specified small \( \varepsilon \).

In order to perform nonlinear analysis on a CT normal or modified tissue image, a series of steps must be made.

First, from a CT slice, the region containing the tissue to be analyzed must be isolated; a matrix containing values of each pixels shade is obtained (the value can vary between 0 and 255 corresponding to different shades of grey; 0 stands for black and 255 for white) ([3], [4]).

The time (spatial) series is generated in the following manner:

1. the matrix resulting from the original image is cut in horizontal strips of 1, 4, 8, … pixels, with respect to the initial image dimension and precision;
2. all strips are put together one after another and generate one single strip associated to the image;
3. the time (spatial) series - \( x(t) \) - is generated by computing either the mean value or the maximal (dominant) value of each columns of pixels within the strip.
As result of this procedure, the time (spatial) series associated to the section of the analyzed tissue is obtained (Fig. 2.).

Fig. 2. Kidney CT image and the associated time series (position in the strip vs. grey level)

For this study, since the analyzed CT regions are not extremely large, a 1-pixel strip was associated to each original image, this way not altering the information provided by the image.

Having the associated series, the next step of the procedure implies calculating the correlation dimension of the attractor. This value is the discrimination criterion.

However, in practical applications, in order to determine the dimension of an attractor, we cannot directly use the above formulae for $d_C$ due to the following aspects:
- limited time series;
- noisy time series;
- unknown fractal dimension of the attractor;
- for different $\tau$ - delay values different results due autocorrelations;
- unknown $d_E$ – leading to time correlations when reconstructing the series in a embedding space with unsuitable dimension;

That is why a series of methods for determining the delay, the suitable embedding space and the correlation dimension were refined over the years. Here are given the outlines for these methods. They were implemented as a nonlinear analysis toolbox using MATLAB.

The delay or lag value $\tau$ used to create the delayed embedding must be chosen carefully. A small value of the delay generates correlated vector elements, while large delay values yield to uncorrelated data and a random distribution in the embedding space. The delay can be chosen with good results as the moment of time where the autocorrelation function of the reconstructed series decays to $1/e$ of its initial value:

$$RN(\tau) < RN(1)(1-1/e).$$  \hspace{1cm} (4)

In order to determine this value, the MATLAB routine searches over a specified range, given by the user $[1, \tau_{max}]$ for the first value that satisfies relation (4). Generally, the lag value was found between 4 and 10, while the used search interval is $[1, 20]$.

The minimum allowed embedding dimension is the dimension where the number of so called false nearest neighbours (concept introduced by Kennel, Brown & Abarbanel (1992)) drops under a certain percent. A false neighbour is a point that under a certain higher dimensional embedding is projected near a point that that in the previous embedding was not in its vicinity.

In order to implement this procedure, each point of the delayed series is tested by taking its closest neighbor in $d_E$ dimensions, and computing the ratio of the distances between these two points in $d_E + 1$ dimensions and in $d_E$ dimensions. If this ratio is larger than a certain threshold $th$, the neighbor was false (this threshold is taken large enough to take in consideration points that exponential divergence due to deterministic chaos):

$$\frac{\|y_{i,d_E} - y_{j,d_E}\|}{\|y_{i,d_E} - y_{j,d_E}\|} > th$$  \hspace{1cm} (5)

where $\|\|\|$ is the Euclidian distance.

The MATLAB routine calculates the percentage of false neighbours over a range of embedding dimensions ($d_E$ between 2 and 15) until it reaches a value less than a specified limit; otherwise it considers the minimal obtained value.

Once a proper delay and a minimum allowed embedding dimension are determined, the correlation dimension is calculated over a range of different $\varepsilon$ - values and embedding dimensions higher than the first assuring a decreased number of false neighbours.

The $d_C$ differs from one embedding dimension to another due to the noise in the data, but there is a particular region, usually called the scaling region where $d_C$ stabilizes ([12]). This is the interval where a mean value for the correlation dimension of an attractor is calculated.

The $d_f$ and $d_C$ values obtained on the set of kidneys’ CT images are presented, statistically analyzed and commented in the next chapter.

3 Results and statistics

We start the analysis procedure by presenting a comparative study between the 2 kidneys of the same patient, one healthy while the second presenting a malign tumor.

In the next table, on each row there are the images of correspondent sections in the kidneys and
the values for the box-counting dimension and mean correlation dimension.

It can be observed that both dimensions for the unaffected kidney tissue vary accordingly to the complexity of the tissue in the analyzed section (in the middle of the kidney more complex than in the extremities). Generally, the $d_f$ and $d_c$ of the modified tissue varies correspondingly to the dimension of the affected region and the complexity of the tissue at the analyzed level with clearly larger differences in the case of $d_c$.

Table 1 Normal and modified tissue images, $d_f$, $d_c$

<table>
<thead>
<tr>
<th>$d_f$</th>
<th>$d_c$</th>
<th>Normal tissue</th>
<th>Malign tissue</th>
<th>$d_f$</th>
<th>$d_c$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.83</td>
<td>1.7</td>
<td><img src="image1" alt="Normal tissue" /></td>
<td><img src="image2" alt="Malign tissue" /></td>
<td>1.89</td>
<td>2.15</td>
</tr>
<tr>
<td>1.75</td>
<td>1.73</td>
<td><img src="image3" alt="Normal tissue" /></td>
<td><img src="image4" alt="Malign tissue" /></td>
<td>1.90</td>
<td>2.14</td>
</tr>
<tr>
<td>1.72</td>
<td>1.77</td>
<td><img src="image5" alt="Normal tissue" /></td>
<td><img src="image6" alt="Malign tissue" /></td>
<td>1.83</td>
<td>2.16</td>
</tr>
<tr>
<td>1.8</td>
<td>1.82</td>
<td><img src="image7" alt="Normal tissue" /></td>
<td><img src="image8" alt="Malign tissue" /></td>
<td>1.81</td>
<td>2.19</td>
</tr>
<tr>
<td>1.81</td>
<td>1.89</td>
<td><img src="image9" alt="Normal tissue" /></td>
<td><img src="image10" alt="Malign tissue" /></td>
<td>1.81</td>
<td>2.21</td>
</tr>
<tr>
<td>1.81</td>
<td>1.87</td>
<td><img src="image11" alt="Normal tissue" /></td>
<td><img src="image12" alt="Malign tissue" /></td>
<td>1.8</td>
<td>2.11</td>
</tr>
<tr>
<td>1.73</td>
<td>1.83</td>
<td><img src="image13" alt="Normal tissue" /></td>
<td><img src="image14" alt="Malign tissue" /></td>
<td>1.76</td>
<td>2.09</td>
</tr>
<tr>
<td>1.85</td>
<td>1.79</td>
<td><img src="image15" alt="Normal tissue" /></td>
<td><img src="image16" alt="Malign tissue" /></td>
<td>1.73</td>
<td>2.1</td>
</tr>
<tr>
<td>1.79</td>
<td>1.47</td>
<td><img src="image17" alt="Normal tissue" /></td>
<td><img src="image18" alt="Malign tissue" /></td>
<td>1.75</td>
<td>1.69</td>
</tr>
</tbody>
</table>

The same procedure was applied to all the 100 CT’s.

Statistical methods were performed in order to test the trustworthiness of these two different types of discrimination methods.

For the statistical analysis, descriptive and comparison procedures were performed. The subjects were divided in two samples each containing 50 CT images (normal and modified, respectively).

3.1 Statistical results for box-counting method

For each sample, the average, standard deviation, standard skewness and standard kurtosis were computed. In order to compare the samples, the $t$ test and Kolmogorov-Smirnov test were applied. Both comparison tests show no significant difference between the two distributions at the 95.0% confidence level.

![Fig. 3. Frequency histogram of the two samples](image19)

![Fig. 4. Comparison of density traces](image20)
Table 2 Descriptive $d_C$ statistical methods results

<table>
<thead>
<tr>
<th>Descriptive methods</th>
<th>Normal tissue $d_C$</th>
<th>Modified tissue $d_C$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Average</td>
<td>1.73667</td>
<td>1.76875</td>
</tr>
<tr>
<td>Std. Deviation</td>
<td>0.0589522</td>
<td>0.0715853</td>
</tr>
<tr>
<td>Std. Skewness</td>
<td>0.769626</td>
<td>0.827251</td>
</tr>
<tr>
<td>Std. Kurtosis</td>
<td>-1.0833</td>
<td>0.0478851</td>
</tr>
<tr>
<td>95.0% confidence interval for mean</td>
<td>[1.71177,1.76156]</td>
<td>[1.73852,1.79898]</td>
</tr>
</tbody>
</table>

Table 3 Comparison statistical methods results ($d_t$)

<table>
<thead>
<tr>
<th>Test</th>
<th>Normal tissue $d_t$</th>
<th>Modified tissue $d_t$</th>
</tr>
</thead>
<tbody>
<tr>
<td>t Test</td>
<td>0.0968575 &gt; 0.05</td>
<td></td>
</tr>
<tr>
<td>Kolmogorov-Smirnov Test</td>
<td>0.0684376 &gt; 0.05</td>
<td></td>
</tr>
</tbody>
</table>

These results yield that the trustworthiness level of the analysis made by computing the box-counting dimension of the considered CT samples is low.

### 3.2 Statistical results for nonlinear time series method

The same procedures were applied for values obtained by means of nonlinear time series analysis. For each sample, the average, standard deviation, standard skewness and standard kurtosis were computed.

In order to compare the samples the $t$ test and Kolmogorov-Smirnov test were performed. Both comparison tests show significant difference between the two distributions at the 95.0% confidence level.

Table 4 Descriptive $d_C$ statistical methods results

<table>
<thead>
<tr>
<th>Descriptive methods</th>
<th>Normal tissue $d_C$</th>
<th>Modified tissue $d_C$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Average</td>
<td>1.72988</td>
<td>1.97475</td>
</tr>
<tr>
<td>Std. Deviation</td>
<td>0.240782</td>
<td>0.242743</td>
</tr>
<tr>
<td>Std. Skewness</td>
<td>2.27774</td>
<td>2.35657</td>
</tr>
<tr>
<td>Std. Kurtosis</td>
<td>3.66811</td>
<td>1.26397</td>
</tr>
<tr>
<td>95.0% confidence interval for mean</td>
<td>[1.6282,1.83155]</td>
<td>[1.87225,2.07725]</td>
</tr>
</tbody>
</table>

Table 5 Comparison statistical methods results ($d_C$)

<table>
<thead>
<tr>
<th>t Test</th>
<th>Normal tissue $d_C$</th>
<th>Modified tissue $d_C$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kolmogorov-Smirnov Test</td>
<td>0.00101879 &lt; 0.05</td>
<td></td>
</tr>
</tbody>
</table>

The confidence level in this case is better than for the previously analyzed methodology. This conclusion can be justified by the fact that the box-counting method is using a certain threshold, this way loosing some information on the tissue texture while nonlinear analysis is more precise and use all the information in the images.

### 4 Conclusion

The conclusions of the study on the selected set of CT images are:
- there are significant differences between the correlation dimension of the normal tissue and the correlation dimension of the modified tissue.
- there are differences between the box-counting dimension of the normal tissue and the box-counting dimension of the modified tissue.
- the discrimination methodology based on nonlinear time series analysis proves itself to be of high confidence level
- using box-counting method for discrimination
between renal tissue textures captured from CT-images is not reliable. It can be used only as auxiliary method.

Future work, using nonlinear time series methods, aims at:
- enlarging the CT images data base;
- measuring, where it is possible, the percentage of the modified tissue in a kidney CT slice in order to provide information on what is causing the increase in \( d_c \) (percentage of affected tissue or \( d_c \) value of modified tissue);
- determining the position of tumors masses in an affected organ when considering horizontal slices and respectively reconstructed transversal slices in that organ.
- incorporate medical diagnostics.

References: