

An Approach of Tumor Using Fractals

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ABSTRACT

The intent is to manifest that the external developments sample in tumors are 2-D fractal. The fractal dimension dispartate on the report to histological kind and drop of cell is captured. To observe the fractal dimension by employing three methods namely Box Counting Method, Mass Radius Method and Radius of gyration. In this regard it is assumed that fractal is a device to discover the dimension of the tumor. This will be considerate to the pathologist to inspect whether the tumor swelling is benign or malignant.

Keywords: Fractal dimension, Tumor, Box Counting Dimension, Self – Similarity.

INTRODUCTION

In general, tumors appear to occur when there is a problem with the dividing of cells in the body. Typically, the division of cells in the body is strictly controlled. New cells are created to replace older ones or to perform new functions. If the balance of cell division and death are disturbed, a tumor may form problems with the body's immune system can lead to tumors. There are two types of tumor namely benign and malignant. Here the growth is an important parameter for the formation of tumor. For that we take cells population growth. The application of fractal geometry to life sciences has brought about significant progress in understanding complex functional properties and morphological

features that characterize cells and tissue. Angiogenesis is the physiological process involving the formation of new blood vessels from preexisting vessels. This is a normal process in growth and development, as well as in wound healing. The body controls angiogenesis by producing a precise balance of growth and inhibitory factors in healthy tissues [8].

In the real world, self-similarity becomes an even less well-defined concept. Accordingly, structures are generally defined as 'fractal-like' or by means of truncated fractals. First, real structures, although similar to segments, possess a 'thickness' which adds some 'noise' to the ideal fractal structure to which it resembles. Moreover, the minimal and

maximal values within which the scaling behavior is restricted (i.e. self-similarity is satisfied). This can be further reduced by the structure itself. This point is of great importance for the biological systems, which have been recently investigated using scaling relationships by Brown and colleagues. The concept of fractal dimension was first introduced by Hausdorff as a generalization of the geometrical dimension, and subsequently developed by Kolmogorov and Tihomirov. By introducing a scale ε , according to which the original length of segmentation is partitioned, and counting the number N of self-similar parts resulting from the partitioning, the fractal dimension D is defined as:

$$D = \log_{\varepsilon} N$$

Here the growth of the tumor is modeled by Fractal Dimension. Various methods are used to find the dimension of the tumor [4, 7].

METHODS

In general, tumor appears to be caused by abnormal regulation of cell division. Typically, the division of the cells in the body is strictly controlled—new cells or to perform new functions. Cells which are damaged or no longer needed die to make room for healthy replacements. The following section gives the mathematical modeling of cell growth.

Mathematical Modeling of Cell

The human body is made up of millions of cells. These cells normally divide and multiply in an orderly fashion. New cells replace older cells and shape our growth

pattern by applying the specific genes and living habits of the body. Cell birth and renewal is the process occurs constantly in each and every living body.

The cell is the fundamental unit of structure and function in all living things except viruses. The understanding of cell function has been greatly facilitated through the quantitative study of the growth of cells. By the growth of a colony of unicellular microorganisms is usually meant changes in their number, rather than the change in size of the individual organisms. A common method for cells to reproduce and increase their number is binary fission, in which a cell divides into two cells. The cell number in a culture can be determined in a variety of ways, such as the determination of the cell count per unit volume, the cell mass, or the biochemical activity of the cells.

According to the law of mass action, if the population N were doubled, the change ΔN would also be doubled. So it can be written as [9]

$$\Delta N = KN \Delta t$$

(1)

where K is proportionality constant.

If we divide the equation (1) on both sides by Δt and take the limit as $\Delta t \rightarrow 0$, we obtain the derivative. Thus

$$\Delta t \rightarrow 0 \frac{\Delta N}{\Delta t} = KN$$

$$\text{i.e., } \frac{dN}{dt} =$$

$$KN \quad (2)$$

This is a relation between the quantity N and its derivative, which is assumed to hold true at any time. Such an equation is called a differential equation. The most fundamental method of solution is to take advantage of our familiarity with known

functions and their derivatives. Our familiarity with the exponential function might lead us to attempt as a solution

$$N = ce^{kt}$$

(3)

Where c is a constant. The meaning of the constant becomes clear if we specify the initial value N_0 of our population at time $t = 0$,

$$N_0 = ce^{k \cdot 0} = c, \tag{4}$$

So that the constant ‘ c ’ represents the initial value of the population. The solution of this equation may therefore be written as

$$N = N_0 e^{kt} \tag{5}$$

It can be proved that no other function satisfies the differential equation and the initial condition $N(0) = N_0$. Therefore the solution is said to be unique. The solution provides us the population number N at any time. An equation such as (2) must in the first instance be dimensionally correct to be at all meaningful. If we let the bracket [] denote “the dimensions of ” the quantity contained within them, we see from the preceding discussion that

$$\left[\frac{dN}{dt}\right] = \left[\frac{\Delta N}{\Delta t}\right] = \left[\frac{N}{t}\right] \tag{6}$$

From equation (2), the dimensions of $\frac{dN}{dt}$ must be the same as $[KN]$, and therefore $[K] = [1/t]$, or, K has the dimension of reciprocal time. We can also recognize this fact from equation (5), because the argument of the exponential function or exponent of e must be a pure number, hence $[Kt] = [1]$. From (2) we see that the fractional growth rate at any time ($N^{-1}dN/dt$) is a constant, and this constant is K . It is also called the specific growth rate.

Cell population growth is a type of exponential growth called doubling. Thus each generation of cells should be twice as numerous as the previous generation. However the number of generations only gives a maximum figure as not all cells survive in each generation. Under normal conditions, the cells in the human body divide and grow in an orderly, controlled manner. Cell growth can be expressed by “transformation”. It is an operation which converts a mathematical expression to a different but equivalent form. The transformation of cell growth can be expressed by Laplace transformation, because it satisfies two conditions such as [1]

$\Rightarrow f(t)$ Should be continuous or piecewise continuous in the given closed interval $[a, b]$ where $a > 0$.

$\Rightarrow f(t)$ should be in exponential order i.e., $L[f(t)] = \int_0^\infty e^{-st} f(t) dt, t > 0$.

Mathematical Model of Infectious Disease

An infectious disease (formation of tumor) is said to be endemic when it can be sustained in a population without the need for external inputs. This means that, on average, each infected cell is infecting *exactly* one other cell (anymore and the number of people infected will grow exponentially and there will be an epidemic, any less and the disease will die out). In mathematical terms, that is

$$R_0 \times S = 1 \tag{7}$$

The basic reproduction number (R_0) of the disease, assuming everyone is susceptible, multiplied by the proportion of the population that is actually susceptible (S)

must be one (since those who are not susceptible do not feature in our calculations as they cannot contract the disease). Notice that this relation means that, for a disease to be in the endemic steady state, the higher the basic reproduction number, the lower the proportion of the population susceptible must be, and vice versa [9].

Under the first assumption (above), let us say that everyone in the population lives to age L and then dies. If the average age of infection is A , then, on an average, individuals younger than A are susceptible and those older than A are immune (or infectious). Thus the proportion of the population that is susceptible is given by

$$S = \frac{A}{L} \tag{8}$$

But the mathematical definition of the endemic steady state can be rearranged to give

$$S = \frac{1}{R_0} \tag{9}$$

And therefore, since things equal to the same thing are equal to each other

$$\frac{1}{R_0} = \frac{A}{L} \\ R_0 = \frac{L}{A} \tag{10}$$

This provides us with a simple way to estimate the parameter R_0 using easily available data. For a population with an exponential age distribution, it turns out that

$$R_0 = 1 + \frac{L}{A} \tag{11}$$

Where,

R_0 – The basic reproduction number. The average number of individual each infected

individual will infect in a population that has no immunity to the disease.

S – The proportion of the population who are susceptible to the disease (neither immune nor infected).

A – The average age at which the disease is contracted in a given population.

L – The average life expectancy in a given population.

Thus the mathematics is required to calculate this little more complicated. However, this does allow us to work out the basic reproduction number of a disease given A and L in either type of population distribution. From this we can conclude that whether the tumor is benign or malignant.

Computation of Fractal Dimension

The tumor image is treated as two dimensional and the coordinates are defined as

(x, y) . Then the (x, y) coordinates are partitioned into grids which measure $s \times s$, where s is the image pixel size in the tissue. If the minimum and the maximum binary image levels in the $(i, j)^{th}$ grid fall into the k^{th} and l^{th} boxes respectively, the contribution of n_r in the $(i, j)^{th}$ grid is defined as $n_r(i, j) = l - (k - 1)$

$$n_r(i, j) = l - k + 1 \tag{12}$$

In this method $N(r)$ is defined as the summation of the contributions from all the grids that are located in a window of the image

$$N(r) = \sum_{i,j} n_r(i, j) \tag{13}$$

If $N(r)$ is computed for different values of

scaling r , then the fractal dimension can be estimated as the slope of the line that best fits points $(\log(1/r), \log N(r))$ [5].

Algorithm 1

Step 1: The image is divided into regular meshes with a mesh size of r .

Step 2: Count the number of square boxes that intersect the image $N(r)$.

Step 3: The number $N(r)$ is dependent on the choice of r .

Step 4: We repeat for several size values and count the corresponding number $N(r)$.

Step 5: We find out the slope D formed by plotting $\log N(r)$ against $\log(1/r)$.

Step 5 indicates the degree of complexity or dimensions of the fractal. Finally a straight line is fitted to the plotted points in the diagram using the least squares method. The linear regression equation used to estimate the fractal dimension is

$$\log N(r) = \log k +$$

$$D \log(1/r) \quad (14)$$

Where K is constant and D denotes the dimension of the fractal set (slope) [6]. The above algorithm has been applied to many patients and the dimension of their tumor cells have been found out. The above algorithm has been programmed and run in MATLAB.

Mass Radius Methods

The mass radius relation is useful for estimating the dimension of cluster like objects. It consists of selecting an origin point in the object (usually the center of mass) and counting the number of particles (mass = pixels) that make up the object at a radius r from the origin. For a

two-dimensional Euclidean object (a plane) the mass radius relation is

$$M(r) \propto r^2$$

The exponent is therefore the dimension, but the mass of a fractal object embedded in two dimensions changes with a fractional exponent:

$$M(r) \propto r^D \quad (15)$$

Then, the fractal dimension $D_{\text{mass-radius}}$ is obtained from;

$$D_{\text{mass-radius}} = \frac{\log M(r)}{\log(r)} \quad (16)$$

Then, compute the slope of the linear regression of $\log M(r)$ on $\log(r)$. The graphical implementation in image analysis of mass radius method dimensions has two sources of error. The first is associated with the estimation of area of the circle scanned in a square matrix; the second is associated with large estimations of areas at small radii. The mass dimension defines the relationship between the area located within a certain radius and size of this radius (or) box. This is performed for various radii as well as from various points of origin. The mass dimension can be estimated from the log – log plot of the area as a function of the radius.

The radius of the tumor can be calculated as $r = \left(\frac{\text{Area}}{\pi}\right)^{1/2}$. From this formula we can get the radius for the different types of tumor cells. Depending upon the radius of the cells the tumor grows in the organ [2]

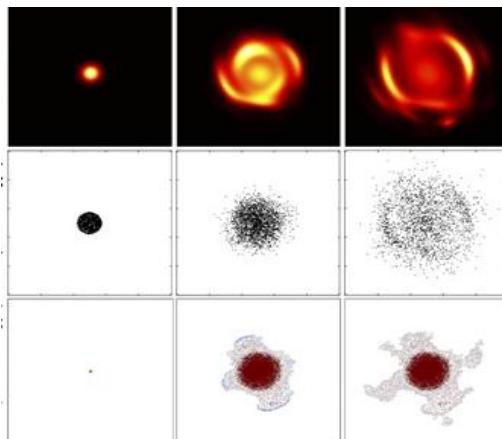


Fig. 1 Radius of Gyration

Radius of Gyration

Radius of gyration is the name of several related measures of the size of an object, a surface, or an ensemble of points. It is calculated as the root mean square distance of the object parts from either its center of gravity or an axis.

The “radius of gyration” R_g of an object also can be used to estimate D . In growth processes, in which the cluster size can be monitored as a function of time, R_g is calculated as

$$R_g = \sqrt{\frac{1}{N} \sum_{i=1}^N r_i^2} \quad (17)$$

Where N is the number of particles in the cluster at a given time and r_i is the distance from the i^{th} particle to the center of mass of the cluster. If R_g can be calculated for several N and the object is self-similar, then the following relation allows computation of the fractal dimension [6].

$$N \sim R_g^D$$

$$\log N = D$$

$$\log R_g$$

$$D =$$

$$\frac{\log N}{\log R_g} \quad (18)$$

The slope of the linear regression of $\log(N)$ on $\log(R_g)$ is D .

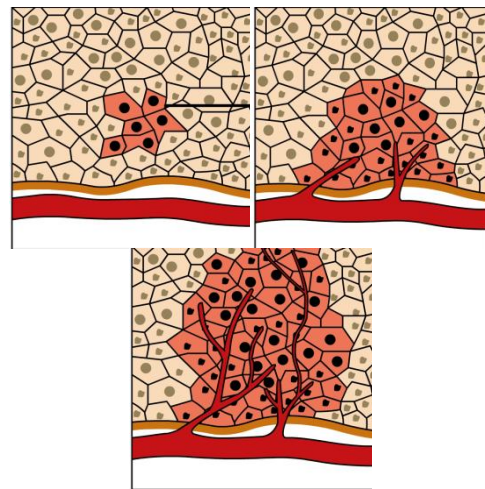


Fig.2 Growth of Tumor

RESULTS

The results of Box Counting Method of different images of the tumor are presented in Table 1(i) and (ii). In order to use the algorithm I, let r be the box (mesh) size in pixels and $N(r)$ be the number of boxes that cover objects (cells). Using linear regression method we find the lines at fit the points of $\log N(r)$ versus $\log(1/r)$. The fractal dimension is nothing but the slope of the line. The mass of the tumor depends upon the radius of the cell as well as the blood vessel growth. Fig. 1 shows the radius of gyration increased by time. Fig 2 shows the mass radius of the tumor [10]. From this we conclude that the mass radius method and the radius of gyration show the self-similarity that characterizes the cell growth in the tumor [3]. Scaling properties are actually assumed originated by the micro vascular structure, which is responsible for the delivery nutrients to body cells.

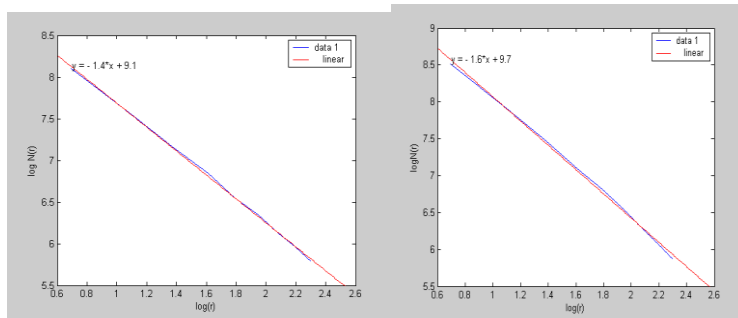
Table 1 (i) Data Analysis of different Brain Tumor using Box Counting Method

Scaling	1	D _B	2	D _B	3	D _B	4	D _B	5	D _B
2	1148		376		863		1975.5		3294.5	
3	687.33		294.67		583.55		1108.668		1889.6674	
4	440		235.75		397		695.720		1265.25	
5	300		194		285		467.4		938.0011	
6	209	1.7	158.67	1.02	206.56	1.5	333.1667	1.8	700.8336	1.4
7	159.97		126.14		157.83		246.1836		568.4286	
8	124		105.25		121		190.7813		456.2344	
9	96.65		89.33		97.54		150.7407		388.336	
10	80		72		80		122.1		325	

Table 1 (ii) Data Analysis of other parts of the organ using Box Counting Method

Scaling	1	D _B	2	D _B	3	D _B	4	D _B	5	D _B
2	605		841.5		3316		674		22,935	
3	402.8892		756.6666		2083.6670		420		13,295.70	
4	325.7		700.25		1513.5		345		8052.5	
5	271.59994		661.6002		1209.2		266.8		5245.98	
6	226.8890	1.02	633.8334	1.23	989.6668	1.5	208.78	1.67	3656.32	1.8
7	209.3470		589.5715		854.7145		176.55		2690.43	
8	192.6875		558.6250		745.75		145.5		2059.62	

9	173.3580		516.0001		671.4445		132.23		1628.14	
10	168.2000		525.1002		6145.3001		103.2		1318.4	



Graphical representation of Brain tumor and in other organs

CONCLUSION

This study shows that the surface of the cell in the tumor has a fractal structure, and the fractal dimension may differ according to histological grades. The fractal dimension varies in the brain tumor and the other parts of the organ. The variation of cell’s dimension is due to the blood vessel growth in the part of the organ. This shows that when the dimension is low, the tumor is benign. When the dimension is high the tumor is malignant. i.e., it leads to the cancer. We believe that fractal geometry gives insights into tumor morphology and becomes an important tool for analyzing complex and irregular tumor growth patterns mathematically.

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