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Analysing The Invasiveness Of Skin Cancer Using Fractals

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ABSTRACT

Skin cancer, manifests itself as a dark lesion, most often with an irregular boundary. We model the skin cancer using fractals. The growth of the moles can be modeled by using fractals and its dimension can be calculated, through which we can detect the invasiveness of the cancer cells in an accurate manner. A new algorithm explains the spreading of cancer in the tissue. The Box Counting method and the Sausage method are used to find out the dimensions of the affected cells in an accurate manner. This fractal approach led to very promising results which improved the analysis of skin cancer. The estimation of skin cancer has been analysed through the statistical test which provides accurate results through which we can find the significance of the skin lesions.

Keywords: Box-Counting method, Fractals, Malignant Melanoma, Sausage method.

I. INTRODUCTION

A **fractal** is "a rough or fragmented geometric shape that can be subdivided into various parts, each of which is (at least approximately) a reduced-size copy of the whole". A fractal is an object which appears self-similar under varying degrees of magnification, and also an object with its own fractal dimension. Fractals themselves have their own dimension, which is usually a non-integer dimension that greater than their topological dimension D_T and less than their Euclidean dimension D_E. Self-similarity is the major characteristic of the fractal objects [5].Fractal objects and process are therefore said to display 'self-invariant' (self-similar or self-affine) properties [7]. Fractal structures do not have single length scale, while fractal process (time-series) cannot be characterized by a single-time scale. A suspected fractal object is examined by the box counting dimension. Let F be any non-empty bounded subset of R^n and let $N_\delta(F)$ be the smallest number of sets of diameter almost δ which can cover F, the box dimension of F

$$\dim_B F = \lim_{\delta \to 0} - \frac{\log N_\delta(F)}{\log \delta}$$

Sausage method or boundary dilation method is very closely related to the Minkowski dimension. The images were dilated with circles of increasing diameter. As an approximation for a circle we once again used the boxes with pixel sizes of $1\times1, 3\times3, 5\times5,...,17\times17$ the corresponding approximated radius *r* in pixels was calculated by

$$r = (A/\pi)^{1/2}$$

where *A* denotes the area in pixels. The slope k_S of the regression line of the double logarithmic plot of the counted pixels with respect to the radii give

$$D_S = 2 - k_S$$

The estimated fractal capacity dimension is D_S.

Skin cancer is a disease in which skin cells lose the ability to divide and grow normally. Healthy skin cells normally divide in an orderly way to replace dead cells and grow new skin. Abnormal cells can grow out of control and form a mass or 'tumor'. When abnormal cells originate in the skin, the mass is called a skin tumor.

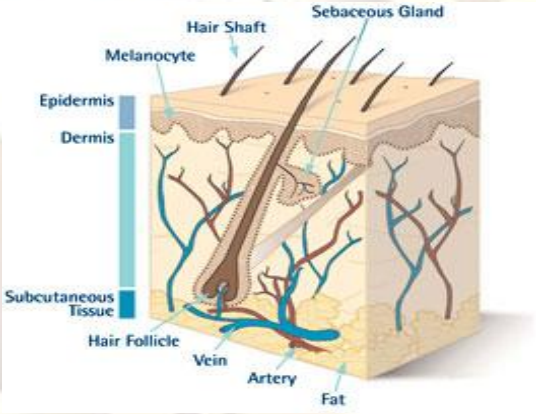


Figure-1. Malignant Melanoma

Melanoma is a malignant tumor of melanocytes. Melanoma is sometimes known as Cutaneous melanoma or Malignant melanoma. The tumor initially starts from the upper skin layer (epidermis) and later invades the dermis below. Fig 1.

Malignant melanoma can be characterized using some physical features such as shape, edge, color and surface texture. The border irregularity of pigmented skin lesions was identified by Keefe et al. [3] as the most significant diagnostic factor in clinical diagnosis of melanoma. Research by Morris Smith [6] revealed that "irregularity" is one of the major vocabulary terms used for describing border of the malignant melanoma in medical textbooks.

These findings coupled with the fact that border irregularity is one of the major features in the seven point checklist used for computing a "suspicious-ness" score for skin lesions [5] indicate that border irregularity is a very important factor in the diagnosis of malignant melanoma.

Several recent research studies have investigated early detection method using computer images analysis techniques. The previous article deals histologically with indentation and protrusion also the lesion border suggested the regression of a melanoma or excess cell growth.[4] In this Paper, we pointed out the structural dimension using Sausage method (Capacity dimension) and the overall dimension can be obtained by box-counting method (box-counting dimension) which is found out for few samples.

II. METHODOLOGIES

2.1 CIRCULATION METHOD

The circulation method is commonly modeled in a simple random way, which in one time unit advances one step of length a to a randomly chosen nearest-neighbor site on a given d-dimensional lattice. Assume that a random process starts at time $t = 0$ at the origin of the lattice. After't' time steps, the actual position of the process is described by the vector

$$r(t) = a\sum_{\tau=1}^{t} e_{\tau}$$

where e_{τ} denotes the unit vector pointing in the direction of the jump at the τ^{th} times. The above process can be explained through power law exponential. So, this is the main parameter for finding out the cells dimension. The construction of the model that follows a hierarchical rule is shown in the Fig 2. The network is built in an iterative fashion, the iteration is repeating and reusing the cells generated as follows [8]:

2.1.1 ALGORITHM

Step 1: Start form a single node, and then designate that as the root of the graph.

Step 2: Add two more nodes and connect each of them to the root.

Step 3: Add two points of three nodes, each unit identical to the network created in the previous iteration (step2), and then connect each of the bottom nodes (see figure) of these two units to the root. That is, the root will gain four more new links.

Step 4: Add two units of nine nodes each, identical to the units generated in the previous iteration, and connect all eight bottom nodes of the two new units to the root. These rules can be easily generalized. Indeed, step *n* would involve the following operation.

Step *n* : Add two units 3^{n-1} of nodes each, identical to the network created in the previous iteration (step *n*-1) and connect each of the 2^n bottom nodes of these two units to root of the network.

The above algorithm has been programmed and run by using C++.

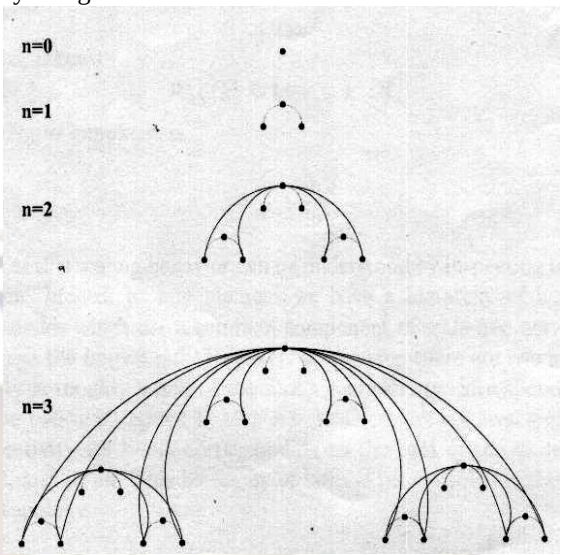


Figure-2. Hierarchical model for cell growth

2.2 PERCOLATION MODEL

A single percolation cluster is generated in the way of the cancer spreading in the organ. In a square lattice, each site represents an individual which can be infected with probability (p) and which is immune with probability (1-p). At an initial time *t=0* the individual at the centre of the lattice (cell) is infected. We assume now that in one unit of time this infected site infects all non-immune nearest neighbor sites. In the second unit of time, these infected sites will infect all their non immune nearest neighbor sites, and so on. In this way, after ***t*** time steps all non immune sites of the l^{th} square grid around the cells are infected, i.e. the maximum length of the shortest path between the infected sites and the cell is $l \equiv t$. This process of randomly infecting individuals is exactly the same as that of randomly occupying sites in the site percolation, where the sites of a lattice have been occupied randomly, when the bonds between the sites are randomly occupied, we speak of bond percolation. So far, we considered on either site or bond percolation, where either sites or bonds of a given lattice have been chosen randomly. This site bond percolation can be relevant for the spreading of the cancer in the tissue.

2.2.1 ALGORITHM

Step 1: The origin of an empty lattice is occupied.

Step 2: The nearest neighbor sites from the origin are either occupied with probability (p) or blocked with probability (1-p).

Step 3: The empty nearest neighbors sites proceed as step 2 with probability (p) and blocked with probability (1-p).This process continues until no sites are available for growth. Thus percolation

clusters are generated with a distribution of cluster size s. i.e, sn_s (p). The factor s comes from the site of the cluster and has the same chance of being the origin of the cluster, and thus exactly the same cluster can be generated in s ways, enlarging the distribution sn_s (p) by a factor of s. (Fig-3)

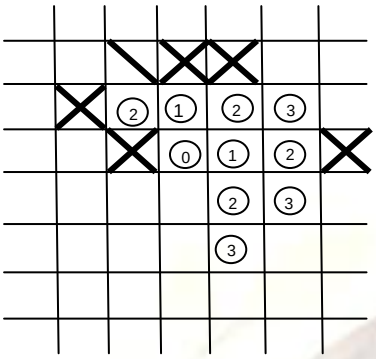


Figure-3. First four steps for the percolation model

The above method is particularly useful for studying the structure and physical properties of single percolation cluster. From this the irregular border of the cancer is formed. The above algorithm has been programmed and run by using C++ [1].

2.3 DISTANCE MEASURE

Distance measure is the distance from the centre of mass to the perimeter point (x_i, y_i). So the radial distance is defined as

$$d(i) = \sqrt{(x(i) - \bar{x})^2 + (y(i) - \bar{y})^2}$$

i=0, 1,2,…… .N-1

Here $d(i)$ is a vector obtained by the distance measure of the boundary pixels. A normalized vector $r(i)$ is obtained by dividing $d(i)$ by the maximum value of $d(i)$ [2].

The quantitative parameters such as Area, Perimeter, Formfactor and Invaslog can found out using Sausage method. Perimeter stands for the sum of all individual perimeters of all individual objects in the image and was calculated correspondingly.

$$Formfactor = 4\pi\, Area / perimeter^2$$

$$Invaslog = -\log(Formfactor)$$

The value of Invaslog has been specially proven to be a strong quantitative measure for the invasiveness in the skin cancer.

III. RESULTS BASED ON SKIN LESION IMAGES

The dimension D of the cancer cell images have been estimated using Box-counting Method (D_B) and Sausage Method (D_s).The amount of invasiveness of the cancer cells in the skin are found out by Form Factor and Invaslog. The above factors have been calculated for the original image as well as dermatologist image. The statistical report also provides the level of significance through which we can analyse the invasiveness of the cancer cells.

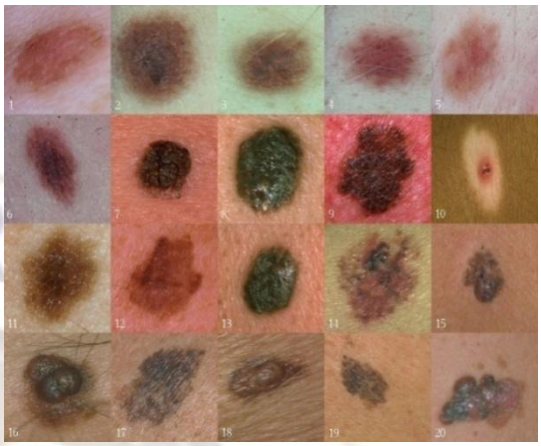


Figure -4. Original Image

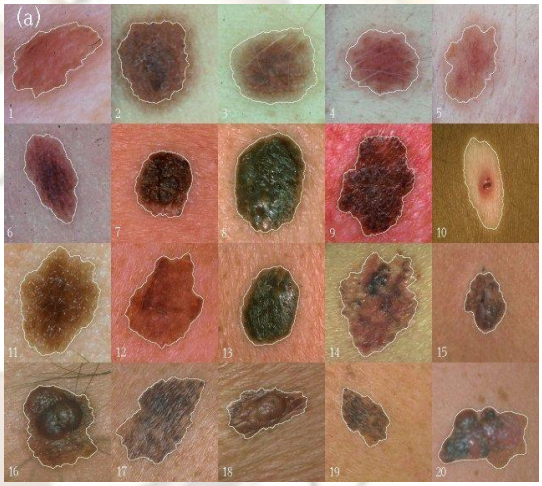


Figure -5. Dermatologist Image

SKIN LESION 2 (ATYPICAL)

Table -1. Box-Counting Method

Scaling	Original image						Dermatologist					
	Area	Perimeter	Total area	Form factor	Invasl og	Dimension D_b	Area	Perimeter	Total area	Form factor	Invasl og	Dimension D_b
2	6783	488	7271	0.358	0.446		1757	277	2034	0.288	0.541	
3	2923	389	3312	0.243	0.614		738	197	935	0.239	0.622	
4	1612	293	1905	0.235	0.629		400	140	540	0.256	0.592	
5	1009	231.6	1240.6	0.236	0.627		245	108	353	0.264	0.578	
6	683	194.8333	877.8333	0.226	0.646	1.9	165	88	253	0.268	0.572	1.9078
7	490	170	660	0.213	0.672		118	71	189	0.294	0.532	
8	376	137	513	0.252	0.599		88	59	147	0.318	0.498	
9	283	128.8889	411.8889	0.214	0.670		68	46	114	0.404	0.394	
10	229	107.3	336.3	0.250	0.602		53	40	93	0.416	0.381	

Table-2. Sausage method

Scaling	Original image				Dermatologist			
	Area	Radius	K_s	$D_s = 2 - K_s$	Area	Radius	K_s	$D_s = 2 - K_s$
3	2923	30.503			738	15.327		
5	1009	17.921			245	8.831		
7	490	12.489			118	6.129		
9	283	9.491	0.79	1.21	68	4.652	0.48	1.52
11	185	7.674			42	3.656		
13	127	6.358			28	2.985		
15	92	5.412			19	2.459		
17	68	4.652			14	2.111		

SKIN LESION 13 (BENIGN)

Table-3. Box-Counting Method

Scaling	Original image						Dermatologist					
	Area	Perimeter	Total area	Form factor	Invasl og	Dimension D_b	Area	Perimeter	Total area	Form factor	Invasl og	Dimension D_b
2	4722	1167	5889	0.044	1.357		1189	451	1640	0.073	1.137	
3	1935	852.3342	2787.3342	0.033	1.482		454	322	776	0.055	1.260	
4	1036	585.5	1624.5	0.038	1.420		228	228	456	0.035	1.456	
5	620	457.0002	1077.0002	0.037	1.432		134	162	296	0.064	1.194	
6	412	346.2224	758.2224	0.433	1.37	1.9	83	131	214	0.061	1.215	1.9
7	283	283.9389	566.9389	0.044	1.357		55	105	106	0.063	1.201	
8	209	229.4688	438.4688	0.050	1.301		40	84	124	0.071	1.149	
9	160	185.8766	345.8766	0.058	1.237		29	71	100	0.072	1.143	
10	114	170.9801	284.9801	0.049	1.310		22	61	83	0.074	1.131	

Table-4.Sausage method

Scaling	Original image				Dermatologist			
	Area	Radius	K_s	$D_s = 2 - K_s$	Area	Radius	K_s	$D_s = 2 - K_s$
3	1935	24.818			454	12.021		
5	620	14.048			134	6.531		
7	283	9.491			55	4.184		
9	160	7.136	0.63	1.37	29	3.038	0.29	1.71
11	94	5.470			16	2.257		
13	54	4.146			10	1.784		
15	37	3.432			8	1.596		
17	22	2.646			4	1.128		

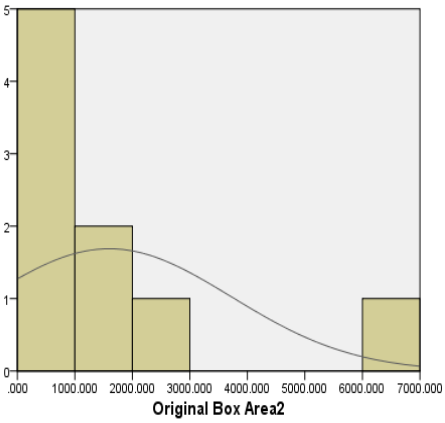
SKIN LESION 20 (MALIGNANT MELANOMA)

Table-5. Box-Counting Method

Scaling	Original image						Dermatologist					
	Area	Perimeter	Total area	Form factor	Invasl og	Dimension	Area	Perimeter	Total area	Form factor	Invasl og	Dimension
2	5065	1993.5	7058.5	0.016	1.80		1130.5	545.5	1676	0.048	1.319	
3	2036.6669	1478.6671	3515.3340	0.012	1.92		461	350.0001	811.0001	0.047	1.328	
4	1084.6250	1023.0	2107.6250	0.013	1.8		234	252.75	486.75	0.046	1.337	
5	658.0400	763.8004	1421.8403	0.014	1.85		137.2	189.6	326.8	0.048	1.319	
6	430.8333	588.8336	1019.6670	0.015	1.82	1.8	85	150.9445	235.9445	0.047	1.328	1.8
7	297	477.5714	774.5714	0.016	1.80		56	123.1632	179.1632	0.046	1.337	
8	228	362.7188	590.7188	0.022	1.66		44	95.3750	139.3750	0.060	1.222	
9	162.0741	324.5556	486.6296	0.019	1.72		27	89.3457	116.3457	0.043	1.367	
10	122.20	282.9602	405.1602	0.019	1.72		20	72.28	92.28	0.048	1.319	

Table-6. Sausage method

Scaling	Original image				Dermatologist			
	Area	Radius	K_s	$D_s = 2 - K_s$	Area	Radius	K_s	$D_s = 2 - K_s$
3	2036.6669	25.462			461	12.114		
5	658.0400	14.473			137.2	6.608		
7	297	9.723			56	4.222		
9	162.0741	7.183	0.65	1.350	27	2.932	0.19	1.81
11	95	5.499			9	1.693		
13	62	4.442			6	1.382		
15	38.0267	3.479			2	0.801		
17	28	2.985			3	0.977		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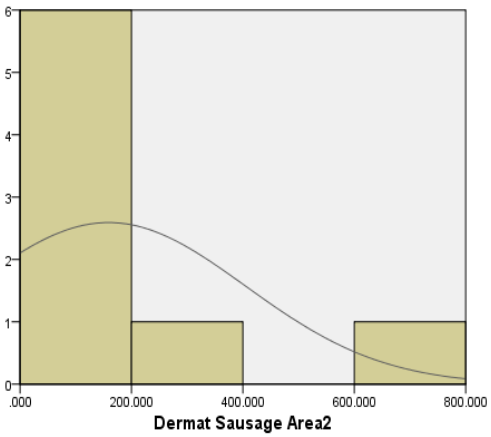
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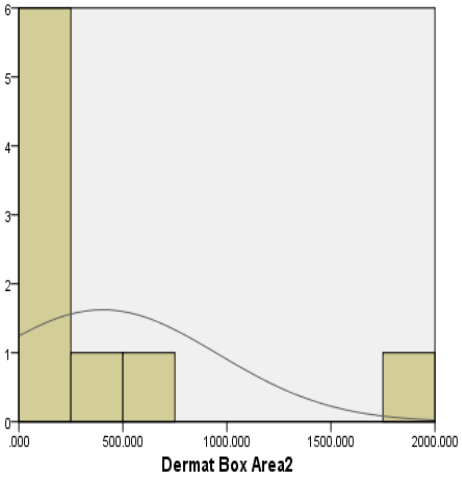
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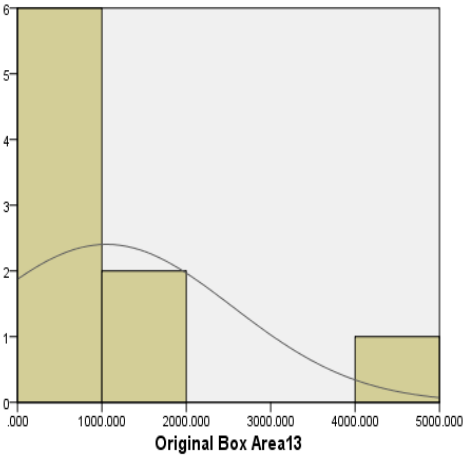
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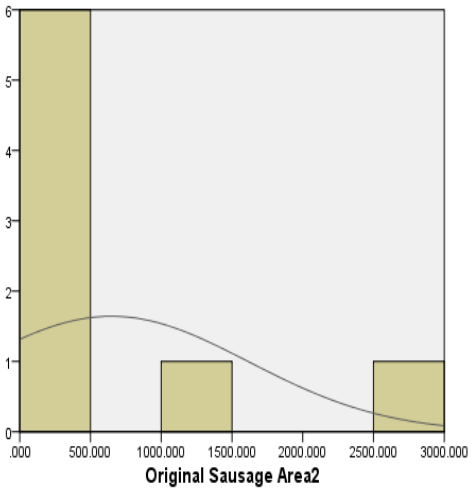
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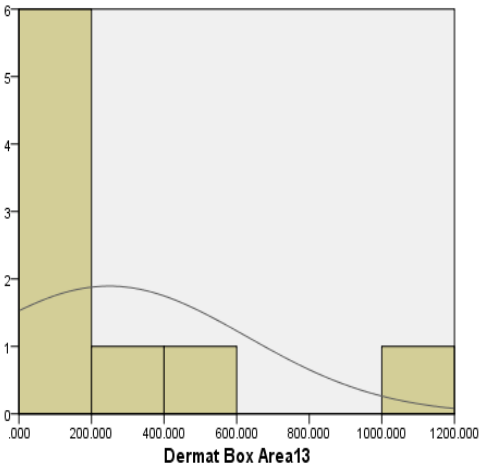
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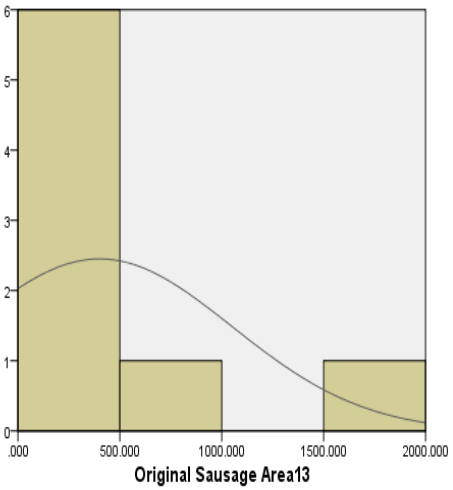
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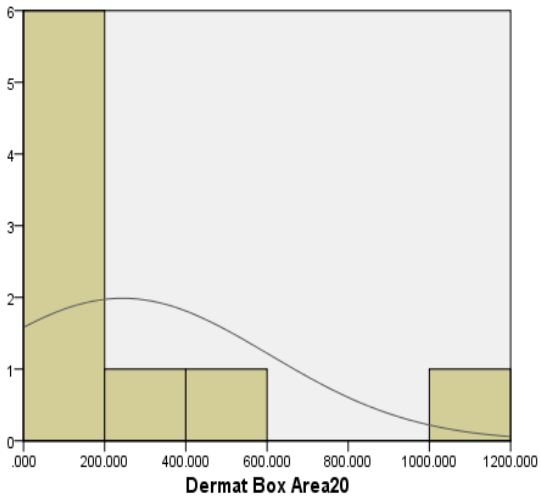
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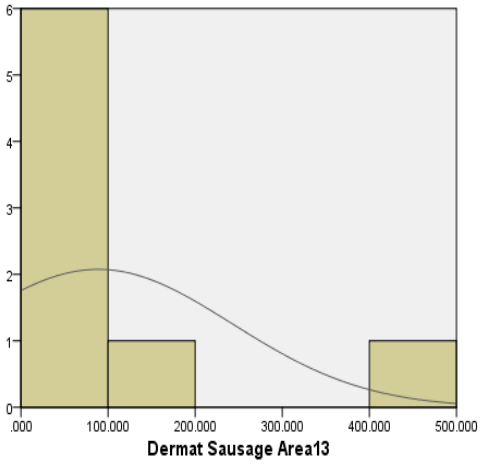
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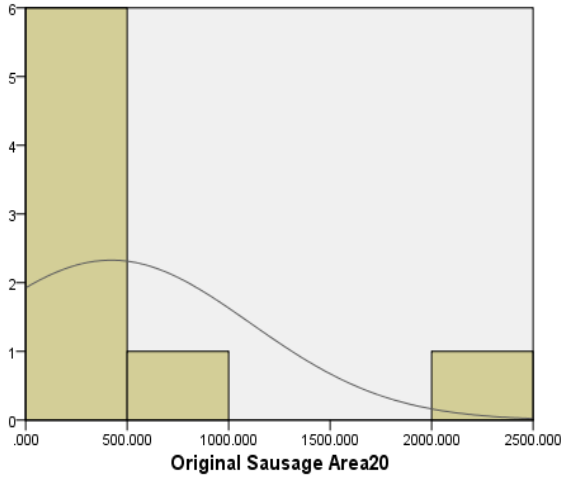
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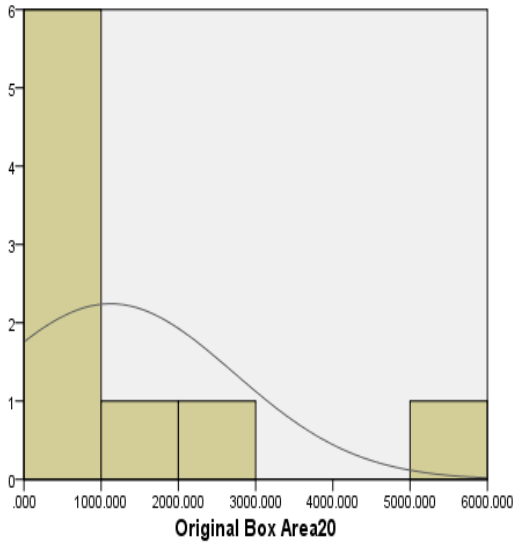
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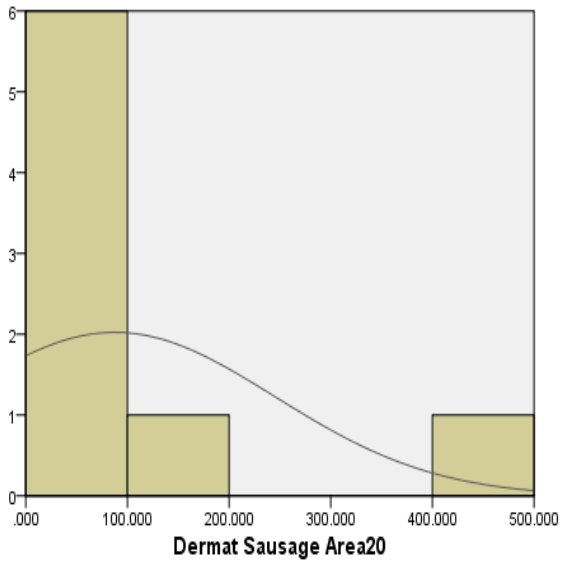
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IV. CONCLUSION

In our proposed model, a new measure of border irregularity for pigmented skin lesions based on the cell potential has been proposed. The Box-counting method and Sausage method are analyzed for the original image as well as the image given by the dermatologist. The comparison between the two methods for the original image as well as the dermatologist image shows us the Sausage method gives the affordable results. The Box Counting method gives the maximum boundary value of the irregular border of the original image. As the dimension increases the invasiveness of the cancer cells also increases which can be found by sausage method and from this results we can analyse the invasiveness of the affected cells easily.

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