QUEUING THEORY

CERTIFICATE

This is to certify that the project report entitled **QUEUING THEORY** submitted to the University of Kerala, in partial fulfilment of the requirement of the FDP in Bachelor of Science (Mathematics).

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NUMERICAL ANALIYSIS

Project Report submitted to the University of Kerala. Thiruvananthapuram in partial fulfilment of the requirement for the completion of the FDP in Bachelor of Science in Mathematics in affiliated colleges.

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NONLINEAR DIOPHANTINE EQUATIONS

Project Report submitted to the University of Kerala,
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THE FIBONACCI SEQUENCE AND THE GOLDEN RATIO

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A STUDY ON CODING THEORY

Project Report submitted to the University of Kerala,
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requirement for the completion of the FDP in Bachelor
of Science in Mathematics in affiliated colleges.

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NETWORK MODELS IN OPERATIONS RESEARCH

Project Report submitted to the University of Kerala, Thiruvananthapuram in partial fulfilment of the requirement for the completion of the FDP in Bachelor of Science in Mathematics in affiliated colleges.

by

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A STUDY ON FRACTALS

Project Report submitted to the University of Kerala, Thiruvananthapuram in partial fulfilment of the requirement for the completion of the FDP in Bachelor of Science in Mathematics in affiliated colleges.

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DECLARATION

We hereby declare that the project report entitled **A STUDY ON FRACTALS** submitted to the University of Kerala, in partial fulfilment of the requirement of the FDP in Bachelor of Science (Mathematics) is a Bonafide work carried out by us and it has not been submitted earlier or elsewhere for similar purposes according to the best of our knowledge and belief.

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ACKNOWLEDGEMENT

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April 2022

Contents

INTRODUCTION

Fractals are infinitely complex patterns that are self-similar across different scales.Since its introduction in 1975, the concept of the fractal has given rise to a new system of geometry that has had a significant impact on diverse fields like physical chemistry, physiology, and fluid mechanics. Fractals is a new branch of mathematics and art.Most physical systems of nature and many human artifacts are not regular geometric shapes of the standard geometry derived from Euclid. Fractal geometry offers almost unlimited ways of describing, measuring and predicting these natural phenomena.Although fractal geometry is closely connected with computer techniques, some people had worked on fractals long before the invention of computers. Those people were British cartographers, who encountered the problem in measuring the length of Britain coast. The coastline measured on a large scale map was approximately half the length of coastline measured on a detailed map. The closer they looked, the more detailed and longer the coastline became. They did not realize that they had discovered one of the main properties of fractals.

Fractals are common in nature and are found nearly everywhere. An example is broccoli. Every branch of broccoli looks just like its parent stalk. The surface of the lining of your lungs has a fractal pattern that allows for more oxygen to be absorbed. Such complex real-world processes can be expressed in equations through fractal geometry. Even to the everyday person, fractals are generally neat to look at even if you don't understand what a fractal is. But to a mathematician, it is a neat subject area.

This project explain the concepts of fractals.The project includes four chapters.The first chapter 'An introduction to fractals' deals with some of the basic concepts like definition,classification,properties,techniques for generating fractals and a short discussion about fractals and chaos.The second chapter 'The fundamentals of fractal geometry' explain the concepts of Hausdorff measure and dimensions and some examples of fractals.The third chapter discuss about self similarity and the fourth chapter points out the various applications of fractals in various fields.

Chapter 1

AN INTRODUCTION TO FRACTALS.

1.1 Definition of fractal.

A fractal is a never-ending pattern.There are several definitions of fractals. One of them is based on an important property of the fractal called the self-similarity. Thus, the definition of fractal is most usually defined on the basic ideas of self-similarity and the unusual relationship fractals have with the space they are embedded in. Many fractals possess the property of self-similarity, at least approximately, if not exactly. A self-similar object is one whose component parts resemble the whole. This reiteration of details or patterns occurs at progressively smaller scales and continue indefinitely, so that each part of each part, when magnified, will look basically like a fixed part of the whole object.

One often cited description that Mandelbrot published to describe geometric fractals is "a rough or fragmented geometric shape that can be split into parts, each of which is (at least approximately) a reduced-size copy of the whole"; this is generally helpful but limited. Because of the trouble involved in finding one definition for fractals, some argue that fractals should not be strictly defined at all.

1.2 Role of Mathematicians.

The term fractal, derived from the Latin word fractus ("fragmented," or "broken"), was coined by the Polish-born mathematician Benoit B. Mandelbrot.

The lion's share of the credit for the development of fractal geometry goes to Benoit Mandelbrot, many other mathematicians in the century preceding him had laid the foundations for his work. Moreover, Mandelbrot owes a great deal of his advancements to his ability to use computer technology – an advantage that his predecessors distinctly lacked; however, this in no way detracts from his visionary achievements. Nevertheless, while acknowledging and understanding the accomplishments of Mandelbrot, it undoubtedly helps to have some familiarity with the relevant works of Karl Weierstrass, Georg Cantor, Felix Hausdorff, Gaston Julia, Pierre Fatou and Paul Lévy – not only to make Mandelbrot's work clearer – but to see its connections to other branches of mathematics.Although the key concepts associated with fractals had been studied for years by mathematicians, Mandelbrot was the first to point out that fractals could be an ideal tool in applied mathematics.

1.3 Classification of fractals.

There are a lot of different types of fractals. The most popular types are Complex number fractals and Iterated Function System (IFS) fractals.

1.3.1 Complex number fractals

Two leading researchers in the field of complex number fractals are Gaston Maurice Julia and Benoit Mandelbrot. Inspired by Julia's work, and with the aid of computer graphics, Mandelbrot was able to show the first pictures of the most beautiful fractals known today. Mandelbrot set and Julia set explain the complex number fractals.

1.3.2 Iterated Function System Fractals

Iterated Function System (IFS) fractals are created on the basis of simple plane transformations: scaling, dislocation and the plane axes rotation. The most famous IFS fractals are the Sierpinski Triangle and the Koch Snowflake.

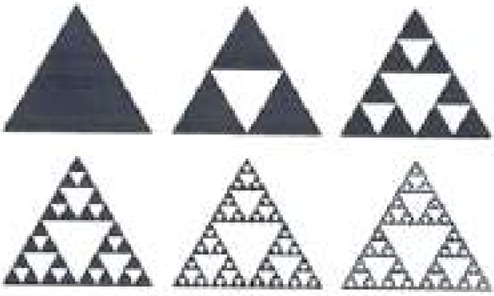
1.4 Properties of fractals.

Two of the most important properties of fractals are self-similarity and non-integer dimension.

1.4.1 Self-Similarity:

One of the basic properties of fractal images is the notion of self-similarity. This idea can be explained using the example of Sierpinski Triangle.Sierpinski Triangle also called as Sierpinski Gasket or Sierpinski Sieve. It is a fractal with a shape of an equilateral triangle. The Sierpinski triangle **S** can be constructed from an equilateral triangle by repeated removal of triangular subsets:

1. Start with an equilateral triangle.
2. Subdivide it into four smaller congruent equilateral triangles and remove the central triangle.
3. Repeat step 2 with each of the remaining smaller triangles infinitely.

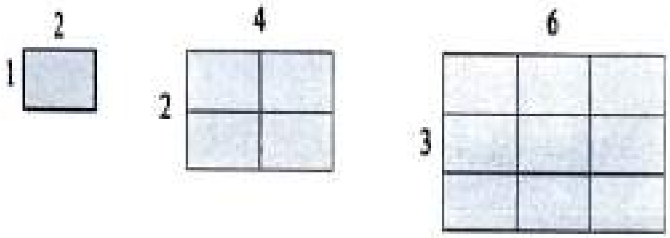


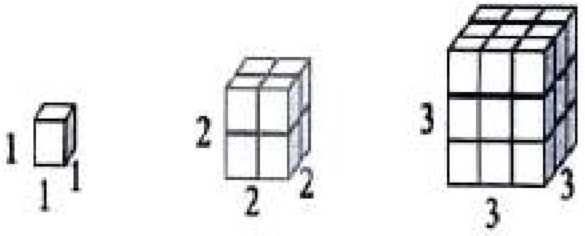
Note that **S** may be decomposed into 3 congruent figures, each of which is exactly half the size of **S** as shown in the figure. That is to say, if we magnify any of the 3 pieces of **S** by a factor of 2, we obtain an exact replica of **S**. That is, **S** consists of 3 self-similar copies of itself, each with magnification factor 2. **S** can be further decomposed into 9 self-similar copies of itself, each with magnification factor 4. Or it can be decomposed into 27 self-similar pieces, each with magnification factor 8 and so on. In general, we may divide **S** into 3^n self-similar pieces, each of which is congruent, and each of which may be magnified by a factor of 2^n to yield the entire figure. This type of self-similarity at all scales is a hallmark of the images known as fractals.

1.4.2 The non-integer dimension

The non-integer dimension is more difficult to explain. Classical geometry deals with objects of integer dimensions: zero dimensional points, one dimensional lines and curves, two-dimensional plane figures such as squares and circles, and three-dimensional solids such as cubes and spheres.However, many natural phenomena are better described using a dimension between two whole numbers. So, while a straight line has a dimension of one, a fractal curve will have a dimension between one and two, depending on how much space it takes up as it twists and curves. The more the flat fractal fills a plane, the closer it approaches two dimensions. Likewise, a "hilly fractal scene" will reach a dimension somewhere between two and three. So, a fractal landscape made up of a large hill covered with tiny mounds would be close to the second dimension, while a rough surface composed of many medium-sized hills would be close to the third dimension.

The concept of a fractal dimension rests in unconventional views of scaling and dimension. For example, notice that each step of the Sierpinski gasket iteration removes one quarter of the remaining area. If this process is continued indefinitely, we would end up essentially removing all the area, meaning we started with a 2-dimensional area, and somehow end up with something less than that, but seemingly more than just a 1-dimensional line (approximately 1.585).





Consider a line segment. If we shrink it to half its size, then, we need 2 copies of the new object to cover the original object. If we shrink it to one-third of its size, then we need 3 copies of the new object to cover the original object. Now consider a rectangle. If we shrink it to half of its size, then we need 4 copies of the new object to cover the original object. If we shrink it to one-third of its size, then we need 9 copies of the new object to cover the original object. Next, consider a cube. If we shrink it to half of its size, then we need 8 copies of the new object to cover the original object. If we shrink it to one-third of its size, then we need 27 copies of the new object to cover the original object.

Suppose that, when we reduce the scale of an object by a factor of k (i.e., we shrink it to 1/k th of its original size), we require N copies of the new object to cover the original one. For the line segment, $N = k$; for the square, $N = k^2$; and for the cube, $N = k^3$. In general, if$N = k^d$, we may refer to d as a kind of dimension of the object.This notion, when generalized suitably to apply to objects that do not have the property of self-similarity, gives the Hausdorff–Besicovitch dimension of the object. The topological dimension and Hausdorff–Besicovitch dimension coincide for the line segment, the square and the cube. But there are objects for which the two do not coincide; such objects are known as fractals. The value of Hausdorff–Besicovitch dimension may be non-integral (which explains the name 'fractal' for such an object). Hence the Hausdorff– Besicovitch dimension is also sometimes called 'fractal dimension'.

1.5 Common techniques for generating Fractals.

Images of fractals can be created using fractal-generating software. Common techniques for generating fractals are:

1.5.1 Escape-time fractals

These are defined by a recurrence relation at each point in a space (such as the complex plane). Examples of this type are the Mandelbrot set, Julia set, the Burning Ship fractal and the Lyapunov fractal.

1.5.2 Iterated function systems

These have a fixed geometric replacement rule. Cantor set, Sierpinski gasket, Koch snowflake, Menger sponge are some examples of such fractals.

1.5.3 Random fractals

Generated by stochastic rather than deterministic processes. For example, Trajectories of the Brownian motion, fractal landscapes and the Brownian tree.

1.6 Fractals and Chaos

The relation between fractal and chaos is very strong. Fractal geometry is used to describe the behaviour of chaotic system we usually find in nature. Chaos theory is closely related to fractal theory. Many events were considered to be chaotic, unpredictable and random. A butterfly flapping its wings in a South American jungle, it is said, can lead to a hurricane in China. (Butterfly effect) This is the signature of chaos theory.

Chaos Theory deals with nonlinear things that are effectively impossible to predict or control, like turbulence, weather, the stock market, our brain states, and so on. Chaos is something which is very sensitive to initial condition. Chaotic systems are mathematically deterministic but nearly impossible to predict. For example, the weather is an example of chaotic system. System often becomes chaotic when there is a feedback present. Fractal is a never-ending pattern. They are created by repeating a simple process again and again in an ongoing feedback loop. To see just how far a fractal or certain conditions can diverge from its starting point, we can iterate with two initial conditions that differ by just a very small amount.

The result of any IFS is fixed point which is called the attractor. As the function iterates it generates some sequence of points which finally converges to the attractor. Basin of attraction is an area which bounds the solution. Points which are not bounded by basin of attraction can approximate to infinity or further from attractor. Fractals that bear this particular trait are called escape-time fractals. Points which are outside from basin of attraction are called Repellers. Some of the attractor discovered are most surprising in form called strange attractors. Strange attractor differs from regular attractors in that it is impossible to tell where they will be. Fractal are related to chaos because they are complex systems that have definite properties.

Chapter 2

THE FUNDAMENTALS OF FRACTAL GEOMETRY.

2.1 Dimension and Measure

A point has a dimension of zero, a line has a dimension of one, a square has a dimension of two, and a cube has a dimension of three. Our understanding of dimension is discrete; we sort all of the objects surrounding us into one of the above categories. It turns out that we can't classify quite all objects into an integer-dimension category; those objects which behave in strange ways with regards to dimension are called fractals.

Suppose we have a ball of radius r, $B_r \subset \mathbb{R}^d$, where d is a positive integer. Let v denote the d-dimensional volume of B_r . The dimension d is related to the volume v and radius r of B_r. Notice that if $d = 1$, then B_r is simply a line segment, so $v \propto r$ (in this case, v is the length of B_r). If $d = 2$, then B_r is a circle, so $v \propto r^2$ (in this case, v is the area of B_r). If $d = 3$, then B_r is a sphere, so $v \propto r^3$. Therefore, we expect that $v \propto r^d$, or $d \propto \log(v)/\log(r)$. Now, notice that our intuitive definition of dimension relies on two concepts, radius (distance) and volume.

Definition 2.1.1. *Let $S \subset \mathbb{R}^n$. A measure μ on S is a function $\mu : S \to \mathbb{R}_{\geq 0} \cup \{\infty\}$ which satisfies the following conditions:*
(a) $\mu(\emptyset) = 0$
(b) $\mu(A) \leq \mu(B)$ if $A \subset B$
(c) $\mu\left(\bigcup_{i=1}^{\infty} A_i\right) \leq \sum_{i=1}^{\infty} \mu(A_i)$, where $\{A_i \in \mathbb{R}^n : i \in I\}$ is a countable collection of sets.

Intuitively, a measure determines the size of a set. Let's examine a simple example of a measure, the point mass. Fix some specific element a. If a set M contains a, then $\mu(M) = 1$; if the set M does not contain a, then $\mu(M) = 0$. Let's check that the point mass is indeed a measure:

1. $\mu(\varnothing) = 0$, since $\varnothing$ contains no points, and in particular, does not contain a.

2. Suppose $A \subset B$. If $a \in A$, then clearly $a \in B$, so $\mu(A) = \mu(B) = 1$. If $a \notin A$, then $\mu(A) = 0$. Since $\mu(B) = 0$ or $\mu(B) = 1$, we have $\mu(A) \le \mu(B)$.

3. Let A_i be a countable collection of sets, where $\{A_i \in \mathbb{R}^n : i \in I\}$. If $a \in \bigcup_{i=1}^{\infty} A_i$, then $\mu\left(\bigcup_{i=1}^{\infty} A_i\right) = 1$. Since $a \in \bigcup_{i=1}^{\infty} A_i$, we must have $a \in A_i$ for at least one $i \in I$. Hence $\sum_{i=1}^{\infty} \mu(A_i) \ge 1$, so$\mu\left(\bigcup_{i=1}^{\infty} A_i\right) \le \sum_{i=1}^{\infty} \mu(A_i)$. Now, if $a \notin \bigcup_{i=1}^{\infty} A_i$, then $\mu\left(\bigcup_{i=1}^{\infty} A_i\right) = 0$. In addition, this means that $a \notin A_i$ for all $i \in I$. Hence $\sum_{i=1}^{\infty} \mu(A_i) = 0$, and thus $\mu\left(\bigcup_{i=1}^{\infty} A_i\right) \le \sum_{i=1}^{\infty} \mu(A_i)$.

Definition 2.1.2. *Let $x, y \in \mathbb{R}^n$, where $x = (x_1, x_2, \ldots, x_n)$, and $y = (y_1, y_2, \ldots, y_n)$. Then the Euclidean distance between x and y is defined as*

$$d(x, y) = \sqrt{(x_1 - y_1)^2 + (x_2 - y_2)^2 + \cdots + (x_n - y_n)^2}.$$

Definition 2.1.3. *Let $S \subset \mathbb{R}^n$. The diameter of S is defined to be the largest distance between any two points of S, $|S| = \sup\{d(x, y) : x, y \in S\}$.*

Definition 2.1.4. *Let $S \subset \mathbb{R}^n$. A δ-cover of S is defined as $\{U_i \in \mathbb{R}^n : i \in I\}$, a finite or countable collection of sets, where $S \subset \bigcup_{i=1}^{\infty} U_i$ and $0 \le |U_i| \le \delta$.*

2.2 Hausdorff measure

Now, let's begin to define the concept of Hausdorff measure, developed by Felix Hausdorff, a great German mathematician. First, let's understand the quantity $H_\delta^s(S)$. Suppose $S \subset \mathbb{R}^n$, and $s \ge 0$. Given a fixed $\delta > 0$, we define

$$H_\delta^s(S) = \inf\left\{ \sum_{i=1}^{\infty} |U_i|^s : \{U_i\} \text{ is a } \delta\text{-cover of } S \right\}.$$

Given a $\delta > 0$, we consider all of the δ-covers of S. Note that these covers may have diameter equal to or less than δ. For a visual of this expression, consider Figure 2.1 . In this diagram, $s = 2$. The area enclosed by the black outline is our set S. Now, consider the sets U_i and U_j, two components of a δ-cover of S. For each cover, we are summing the square of the diameter of each component of the cover, and then taking the infimum over all covers; this gives us $H^2_\delta(S)$.

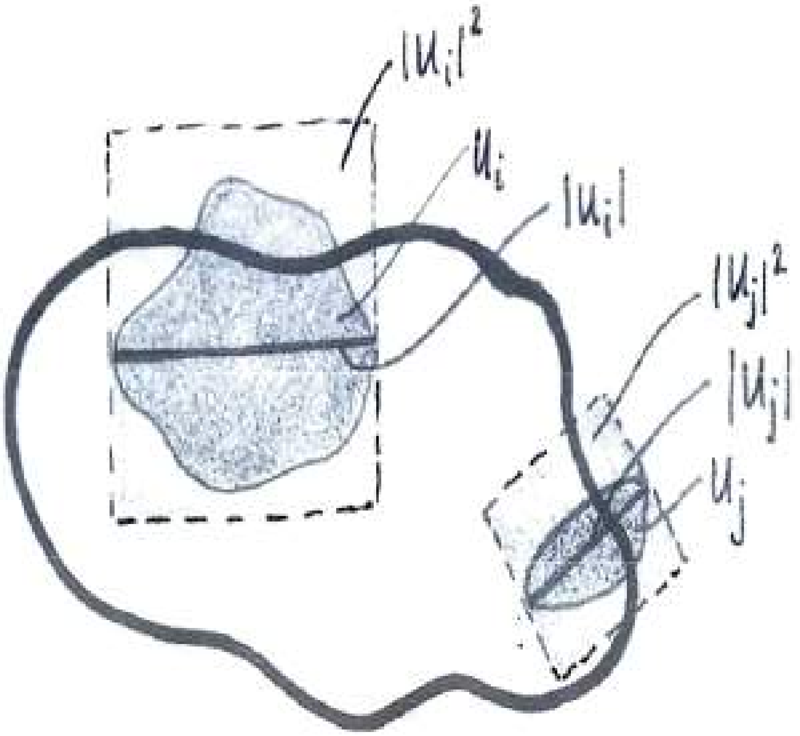


Figure 2.1: Computing the 2-dimensional Hausdorff measure of a set. The area enclosed by the black outline is the set S. The blue sets U_i and U_j are two components of a δ-cover of S, see details in text.

Now, let's consider what happens to $H^s_\delta(S)$ as $\delta \to 0$. As δ decreases, there are less and less δ-covers of S; hence, as $\delta \to 0$, the infimum could increase or not change, but it cannot decrease. That is, as $\delta \to 0$, we have a monotonically increasing sequence. Since this sequence is not bounded, we have that $\lim_{\delta \to 0} H^s_\delta(S)$ exists, but could be infinite.

Definition 2.2.1. *Let $S \subset \mathbb{R}^n$. The s-dimensional Hausdorff measure of S is $H^s(S) = \lim_{\delta \to 0} H^s_\delta(S)$.*

Let's briefly convince ourselves that the s-dimensional Hausdorff measure is indeed a measure:

1. We need to show that $H^s(\varnothing) = 0$. Well, the empty set admits all possible δ-covers. In particular, it admits the cover $\{0\}$, i.e., $\varnothing \subset \{0\}$. For this cover, $H^s_\delta(\varnothing) = \sum_{i=1}^{\infty} |U_i|^s = \sum |\{0\}|^s = 0$. Clearly, this is the infimum over all δ-covers, and thus, $H^s(\varnothing) = 0$.

2. Suppose $A \subset B$. We need to show that $H^s(A) \leq H^s(B)$. Well, note that if some U_i is a cover of B, then U_i must be a cover of A. There are, however, covers of A that are not covers of B. Therefore, for all $\delta > 0, H^s_\delta(A) \leq H^s_\delta(B)$, since the extra covers of A could give a smaller value for $\sum_{i=1}^{\infty} |U_i|^s$. Hence $H^s(A) \leq H^s(B)$.

3. The proof of this part was adapted from [3]. Suppose $\{A_i \in \mathbb{R}^n : i \in I\}$ is a countable collection of sets. We need to show that $H^s\left(\bigcup_{i=1}^{\infty} A_i\right) \leq \sum_{i=1}^{\infty} H^s(A_i)$. Assume that the s-dimensional Hausdorff dimension of each set is finite, that is $H^s(A_i) < \infty$ for all $i \in I$. Now, given $\epsilon > 0$, for all $i \in I$,there exists a δ-cover $\left\{U_j^{(i)}\right\}$ (that depends on i) of A_i such that

   $$\sum_j \left|U_j^{(i)}\right|^s < H^s_\delta(A_i) + \frac{\epsilon}{2^k}.$$

   Now, summing over all $i \in I$, we have

   $$\sum_i \sum_j \left|U_j^{(i)}\right|^s < \sum_{i=1}^{\infty} H^s_\delta(A_i) + \epsilon$$

   Since $\left\{U_j^{(i)}\right\}$ is a cover of A_i for each $i \in I$, the collection $\bigcup_{i \in I} \left\{U_j^{(i)}\right\}$ is a cover of $\bigcup_{i \in I} A_i$, so we have

   $$H^s_\delta\left(\bigcup_{i \in I} A_i\right) \leq \sum_i \sum_j \left|U_j^{(i)}\right|^s < \sum_{i=1}^{\infty} H^s_\delta(A_i) + \epsilon$$

If we let $\epsilon \to 0$,

$$H^s_\delta\left(\bigcup_{i\in I} A_i\right) \le \sum_{i=1}^{\infty} H^s_\delta\left(A_i\right)$$

for any $\delta > 0$. Letting $\delta \to 0$, we then have

$$H^s\left(\bigcup_{i\in I} A_i\right) \le \sum_{i=1}^{\infty} H^s\left(A_i\right).$$

Hence the s-dimensional Hausdorff measure is indeed a measure.

2.3 Hausdorff dimension

Now, note that if $\delta < 1$, then for any set $S \subset \mathbb{R}^n$, as s increases, $H^s_\delta(S)$ is non-increasing; hence $H^s(S)$ is likewise non-increasing. Let $t > s$, and suppose $\{U_i\}$ is a δ-cover of S. Then

$$\sum_{i=1}^{\infty} |U_i|^t \le \sum_{i=1}^{\infty} |U_i|^{t-s} |U_i|^s \le \delta^{t-s} \sum |U_i|^s$$

Taking the infimum of both sides, we get
$H^t_\delta(S) \le \delta^{t-s} H^s_\delta(S)$. Now, let $\delta \to 0$. If $H^s(S) < \infty$, then $H^t(S) = 0$. Likewise, if $H^t(S) > 0$, then we must have $\lim_{\delta\to 0} H^s_\delta(S) = \infty$. That is, there is no more than one value of s such that $0 < H^s(S) < \infty$. Visually, this means that on a graph of $H^s(S)$ vs. s, there is a value of s at which $H^s(S)$ jumps from ∞ to 0 (see Figure 2). It is this value of s which we define as the Hausdorff dimension of S.

Definition 2.3.1. *Let $S \subset \mathbb{R}^n$. The Hausdorff dimension of S, or* $\dim_H S$, *is*

$$\dim_H S = \inf\left\{s \ge 0 : H^s(S) = 0\right\}$$

$$= \sup\left\{s : H^s(S) = \infty\right\}$$

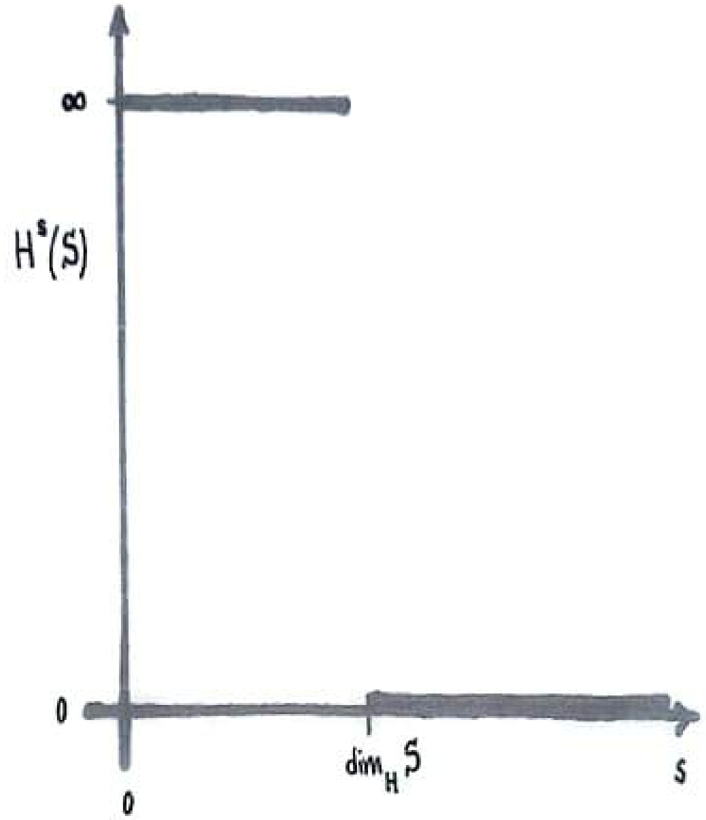


Figure 2.2: Graph of $H^s(S)$ vs. s for a set S. As we can see, there is a jump from ∞ to 0 , and the Hausdorff dimension of S is the value of s at which this jump occurs.

To intuitively understand the Hausdorff dimension, let's test this definition on an object we are familiar with, such as the line segment $[0,1]$. First, suppose $\delta = 0.1$. Then, given a δ-cover of our line segment, all the components of the cover have diameter less than or equal to 0.1, that is $|U_i| \leq 0.1$ for all i. Of course, there are many ways we could cover this line segment with these U_i. However, note that we can cover $[0,1]$ with exactly ten of these components if they are arranged appropriately, for instance, if each $|U_i| = 0.1$, and the sets do not overlap. Now, analogously, suppose we have a δ-cover, with the diameter of each component $|U_i| = \delta$. We then have that $\sum_{i=1}^{\infty} |U_i|^s = \sum_{i=1}^{1/\delta} \delta^s = \frac{1}{\delta}\delta^s = \delta^{s-1}$. Now, when $s > 1$, if we let $\delta \to 0$, we have $\delta^{s-1} \to 0$. When $s < 1$, if we let $\delta \to 0$, we have $\delta^{s-1} \to \infty$. That is, if $s < 1, H^s([0,1]) = \infty$, and if $s > 1, H^s([0,1]) = 0$. Since the jump between 0 and ∞ occurs at $s = 1$, the Hausdorff dimension of the line the jump between 0 and ∞ occ segment $[0,1]$ is 1, as expected.

2.4 Examples of Fractals and their Hausdorff dimensions.

2.4.1 Cantor set

Start with the unit interval [0, 1]. Delete the open middle third of the segment, leaving behind two closed segments: [0, 1/3] and [2/3, 1]. Note that, each has length 1/3. Repeat the same construction for each of them, namely, delete their open middle thirds. After this step, four closed intervals are left: [0, 1/9], [2/9, 1/3], [2/3, 7/9] and [8/9, 1]. Each of these has length 1/9. Repeat the construction yet again; namely, delete the open middle thirds of each closed interval remaining. Continue these steps indefinitely. The construction is depicted in Figure.

Now, examine carefully the portion of the object corresponding to the initial one-third of the original segment. It is an exact replica of the complete object, but at one-third its scale. Note, moreover, that you need 2 copies of the scaled-down object to cover the object at full-scale. Hence, if the Hausdorff–Besicovitch dimension is d, then $3^d = 2$, giving $d = log2/log3 \approx 0.631$, a non-integral quantity. The topological dimension of the Cantor set may be shown to be 0.

2.4.2 Koch Snowflakes

The Koch snowflake (also known as the Koch star and Koch island) is a mathematical curve and one of the earliest fractals to have been described. The Koch snowflake is based on the Koch curve.
Construction: The Koch curve can be constructed by starting with an equilateral triangle, then recursively altering each line segment that forms a side of the figure as follows:

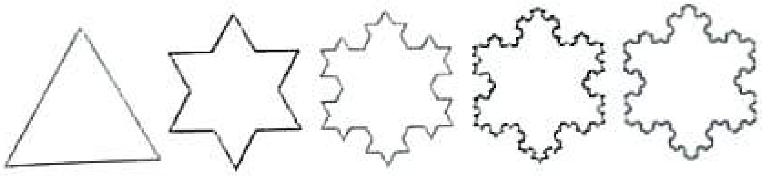
1. Divide the line segment into three segments of equal length.

2. Draw an equilateral triangle that has the middle segment from step 1 as its base and points outward.

3. Remove the line segment that is the base of the triangle from step 2.

4. After one iteration of this process, the result is a shape similar to the Star of David.

5. The Koch curve is the limit approached as the above steps are followed over and over again.



(Fractal dimension is $log4/log3 \approx 1.26$)

2.4.3 Mandelbrot set

The Mandelbrot set introduced by John Briggs is known to be the most famous fractal in modern mathematics, mainly because of its haunting beauty. The Mandelbrot set is a group of numbers defined by a simple formula

$$z_{n-1} = z_{n+2} + c$$

Some numbers belong to the Mandelbrot set, and others don't. In this formula, c is the number being evaluated, and z is a sequence of numbers $(z_0, z_1, z_2, z_3 \ldots)$ generated by the formula. The first number z_0 is set to zero; the other numbers will depend on the value of c. If the sequence of z_n stays small ($z_n \geq 2$ for all n), c is then classified as being part of the Mandelbrot set. For example, let's evaluate the point $c = 1$. Then the sequence of z_n is $0, 1, 2, 5, 26, 677 \ldots$. Clearly this sequence is not staying small, so the number 1 is not part of the Mandelbrot set.

FIGURE 1

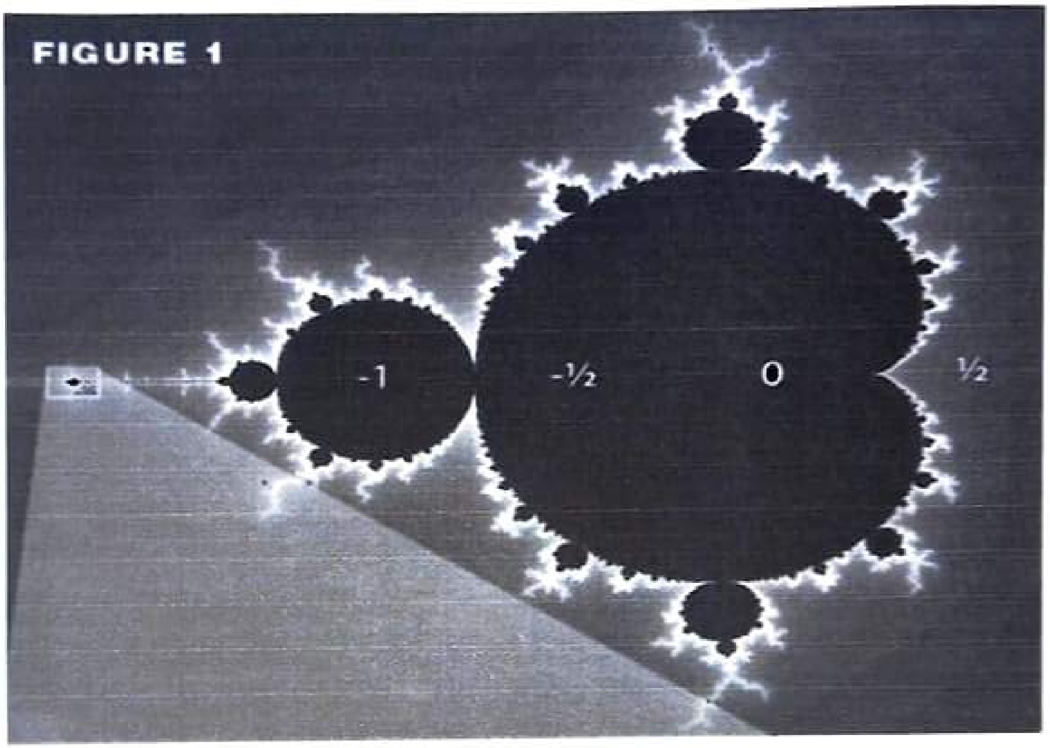


FIGURE 2

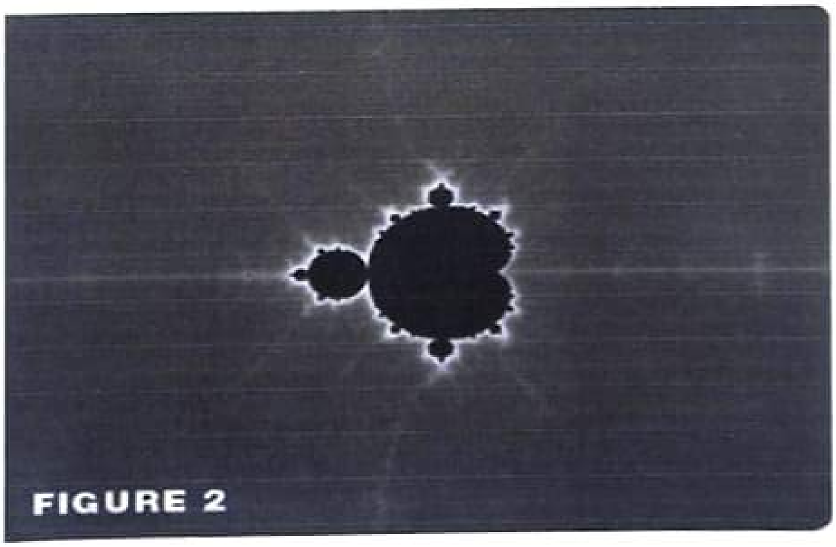
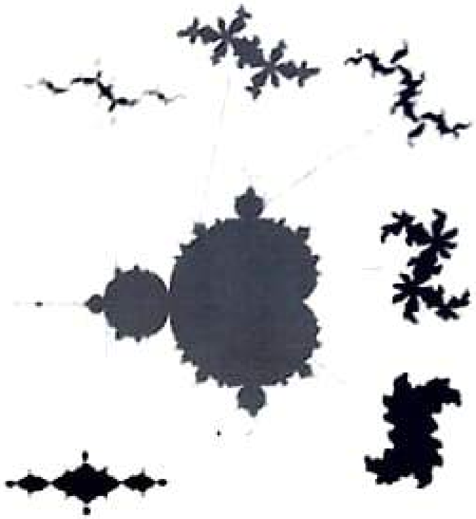


Figure 1 is a plot—a graph that shows which numbers are part of the Mandelbrot set. Points that are black represent numbers that are part of the set. So, the numbers, -1, -1/2, and 0 are part of the Mandelbrot set.

2.4.4 Julia set

Julia sets are strictly connected with the Mandelbrot set. The iterative function that is used to produce them is the same as for the Mandelbrot set. The only difference is the way this formula is used. In order to draw a picture of the Mandelbrot set, we iterate the formula for each point C of the complex plane, always starting with.



If we want to make a picture of a Julia set, C must be constant during the whole generation process, while the value of varies. The value of C determines the shape of the Julia set; in other words, each point of the complex plane is associated with a particular Julia set.
A Julia set is either connected or disconnected. The most important relationship between Julia sets and Mandelbrot set is that while the Mandelbrot set is connected (it is a single piece), a Julia set is connected only if it is associated with a point inside the Mandelbrot set. The disconnected sets are often called dust, they consist of individual points no matter what resolution they are viewed at.

Chapter 3

SELF-SIMILARITY

Self-similar fractals are those which are composed of scaled copies of themselves; that is, to construct the next iteration of the fractal, we perform simple translations or rotations on smaller versions of the shapes of the previous iteration. In the following definitions, we will rigorously define these maps, called contractions.

Definition 3.0.1. *Let* $D \subset \mathbb{R}^n$ *be a closed subset. A map* $S : D \to D$ *is called a contraction if there exists a number* c*, where* $0 < c < 1$*, such that* $|S(x) - S(y)| \leq c|x - y|$ *for all* $x, y \in D$*. We call* S *a contracting similarity if equality holds, that is, if* $|S(x) - S(y)| = c|x - y|$*, and we call* c *the ratio of similarity.*

Definition 3.0.2. *A finite collection of contractions* $\{S_1, S_2, \ldots, S_k\}$*, where* $k \geq 2$*, is called an iterated function system.*

Definition 3.0.3. *A non-empty compact set* $A \subset D$ *is called an attractor if* $A = \bigcup_{i=1}^{k} S_i(A)$*, where* $\{S_1, S_2, \ldots, S_k\}$ *is an iterated function system.*

Hence, self-similar fractals are attractors; that is, they are completely described by some collection of contracting similarities. The theorem below will allow us to calculate the Hausdorff dimension of self-similar fractals by utilizing the ratios of the similarities which define them. This calculation method is much more simple and intuitive than direct calculation of the dimension.

Theorum 1. *Let* F *be a fractal such that*

$$F = \bigcup_{i=1}^{m} S_i(F),$$

where $S_1, \ldots, S_m$ are similarities with ratios $c_1, \ldots, c_m$. Then, $\dim_H F = s$, *where s is given by*

$$\sum_{i=1}^{m} c_i^s = 1$$

In addition, $H^S(F)$ is a finite positive number. Proof. To prove this theorem, we will bound $H^s(F)$ from above and from below, and thus show that $H^s(F)$ is a finite positive number. Hence, since it is this particular value of s which makes $H^s(F)$ finite, we will have $\dim_H F = s$. *The first half of the proof (the upper bound), provided below, shows that $H^s(F)$ is finite; for the proof that $H^s(F)$ is positive (the lower bound), see Falconer's Fractal Geometry [1]. Suppose we have $\sum_{i=1}^{m} c_i^s = 1$. Now, consider all compositions of the similarities $S_1, \ldots, S_m$ of length k, where $k \geq 1$. (Note that we can repeat similarities; for instance, a composition of length $k = 3$ could be $S_1 \circ S_1 \circ S_2$). Let I_k be an indexing set for all such compositions of k. Then, by applying (4.5) k times, we have*

$$F = \underbrace{\bigcup_{i=1}^{m} S_i \left(\bigcup_{i=1}^{m} S_i \left(\bigcup_{i=1}^{m} S_i(\ldots) \right) \right)}_{k\text{-times}} = \bigcup_{I_k} S_{i_1} \circ \cdots \circ S_{i_k}(F)$$

That is, F is equal to the union of the images of all possible compositions of length k of the similarities over F.

Note that the above equality holds for all $k \in \mathbb{N}$, and for all k, this union of images is a cover of F. Now, since the mapping $S_{i_1} \circ \cdots \circ S_{i_k}$ is a similarity itself, with ratio $c_{i_1} \cdots c_{i_k}$, we have

$$\sum_{I_k} |S_{i_1} \circ \cdots \circ S_{i_k}(F)|^s = |F|^s \sum_{I_k} (c_{i_1} \cdots c_{i_k})^s$$

$$= |F|^s \left(\sum_{i_1} c_{i_1}^s \right) \cdots \left(\sum_{i_k} c_{i_k}^s \right) = |F|^s$$

where the last equality is by (4.6). Note that

$$|S_{i_1} \circ \cdots \circ S_{i_k}(F)| = c_{i_1} \cdots c_{i_k} |F|$$

$$\leq (\max\{c_1, \ldots, c_m\})^k \, |F|$$

Now, using the expression above, since our choice of k is unbounded, for any $\delta > 0$, we can find a k such that $|S_{i_1} \circ \cdots \circ S_{i_k}(F)| \leq \delta$. Therefore, these images are not just covers of F, but are δ-covers of F. However, there are many more possible covers of F. Thus we have an inequality in $H^s_\delta(F) \leq |F|^s$, and hence $H^s(F) \leq |F|^s$. Since $|F|$ is finite, is bounded above.

Chapter 4

APPLICATIONS OF FRACTALS.

4.1 Fractals in nature.

4.1.1 Fractals in Trees.

Fractals are seen in the branches of trees from the way a tree grows limbs. The main trunk of the tree is the origin point for the Fractal and each set of branches that grow off of that main trunk subsequently have their own branches that continue to grow and have branches of their own. Eventually the branches become small enough they become twigs, and these twigs will eventually grow into bigger branches and have twigs of their own. This cycle creates an "infinite" pattern of tree branches. Each branch of the tree resembles a smaller scale version of the whole shape.

4.1.2 Fractals in Animal Bodies.

Another incredible place where Fractals are seen is in the circulatory and respiratory system of animals. Consider the human respiratory system, a fractal that begins with a single trunk (similar to the tree) that branches off and expands into a much more fine-grained network of cavities can be observed.

4.1.3 Fractals in Snowflakes.

Every snowflake is unique and one of the contributing factors to the uniqueness of snowflakes is that they form in fractal patterns which can allow for incredible amounts of detail and also variation. In the case of ice crystal formations, the starting point of the fractal is in the centre and the shape expands outward in all directions. As the crystal expands, the fractal structures are formed in each direction. Each iteration of the shape gets smaller and more detailed, which also contributes to the overall complexity of the shape.

4.1.4 Fractals in Lightning

A lightning storm is one of the nature's most powerful displays of Fractals. When the current passes through the air, it becomes superheated. Superheating of the air changes its electrical conductivity and allows the current to fragment out. This process repeats for each level of fragmentation and finally results in a fractal. The inverted image of a lightning strike or electrical discharge has a great resemblance to a tree.

4.1.5 Fractals in Plants and Leaves

Plants and leaves, just like animals, have internal structures that distribute nutrients through a network of Fractals. These structures allow for easy distribution of liquids and other life sustaining materials to travel through the plant and support the life of every cell. Beyond the cellular level, some types of plants themselves are very fractal in look. One of the most notable examples is a type of broccoli called Romanesco broccoli. This type of broccoli has an incredible structure of spires which emanate from a single source (similar to the Fractal Snowflake) that in turn have their own spires which continue on to the tip of the plant. A fern is another great example of a fractal. Ferns are essentially made up of the same general structure repeated over and over again.

4.1.6 Fractals in Clouds.

Clouds also display characteristics of Fractals. The turbulence that is found within the atmosphere has an interesting impact in the way water particles interact with each other. Turbulence is fractal in nature and therefore has a direct impact on the formation and visual look of clouds. The amount of condensation, ice crystals, and precipitation expelled from the clouds all impacts the state of the cloud and the system's structure.

4.1.7 Fractals in Crystals.

Like ice formations, other natural forms of crystals like those created from minerals can also exhibit Fractal properties. Depending on the specific formation of crystal and the minerals used some are more fractal in appearance than others. A great example of this would be the cubic nature of some formations of Amethyst or pyrite.

4.2 Fractals in technology.

4.2.1 Fractal antenna

A fractal antenna is an antenna that uses a fractal, self-similar design to maximize the effective length, or increase the perimeter (on inside sections or the outer structure), of material that can receive or transmit electromagnetic radiation within a given total surface area or volume.

4.2.2 Fractal Dimension on network.

Fractal analysis is useful in the study of complex networks, present in both natural and artificial systems such as computer systems, brain and social networks, allowing further development of the field in network science. Complex networks have been studied extensively owing to their relevance to many real systems such as the world-wide web, the Internet, energy landscapes and biological and social networks.

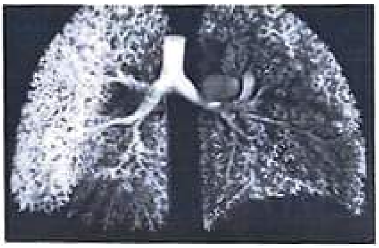
4.3 Fractals in medicine.

With the use of modern medicine, malfunctioning in the human body can be detected. Because human body is full of fractals, fractal math can be used to quantify, describe, diagnose and perhaps soon to help cure diseases. The fractal dimension of the lung appears to vary between healthy and sick lungs, potentially aiding in the automated detection of the disease. To diagnose Cancer, fractal analysis is helpful.

4.4 Fractals in market analysis.

Benoit Mandelbrot introduced a new fractal theory which is helpful to analyse the market. After plotting price data of market for a month some rises and fall will be appeared in the graph. Even if this graph is plotted for weak or even for a day same rises and fall will be appeared. This is self-similar property of fractal.

Fractals in trees.

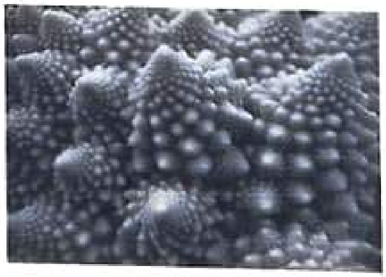


Fractals in animal bodies.

Fractals in snowflakes.

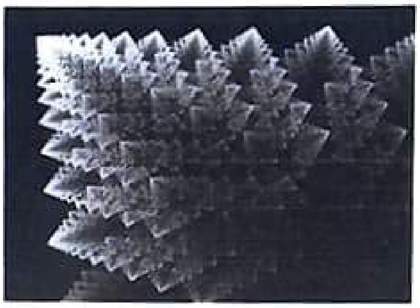
Fractals in lightning.

Fractals in ferns.

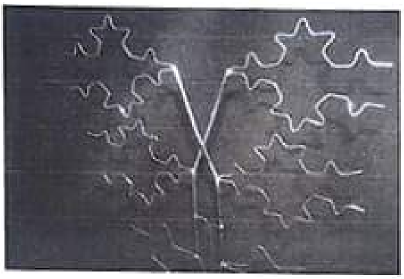


Fractals in plants.

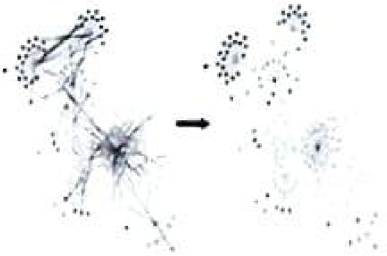
Fractals in clouds.



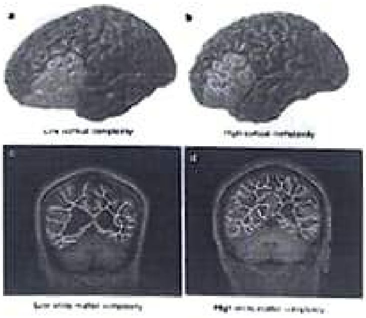
Fractals in crystal



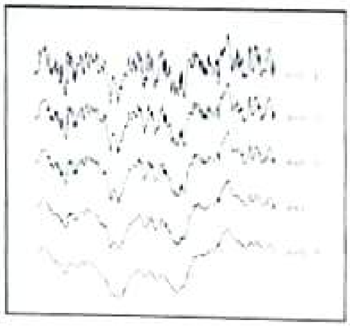
Fractals in antenna.



Fractal dimension on network.



Fractals in medicines.



Fractals in market analysis.

4.5 Conclusion

A fractal is a recursively created never-ending pattern that is usually self-similar in nature. Separate from Euclidean geometry, fractal geometry addresses the more non-uniform shapes found in nature, such as mountains, clouds and trees.Fractals provide a systematic method to capture the "roughness" of some objects. This method to capture roughness has uses in a wide variety of fields ranging from programming to medicine.

Fractals are all around us. Mathematicians have developed and are continuing to develop equations to generate these fractals. Maybe the stock market and weather will be even more predictable in the future. At first, when looking at the colourful picture of a fractal, one might think that it is just a creative piece of artwork. However, after studying the mathematical background behind them, they have so much more depth than being just a piece of art.

Even though the subject of fractal geometry is purely math, many people have found ways to take it outside math into computer science, health science, and even fashion and the arts. Fractals are used to make our movies look more amazing than life, and to make our computer and video games feel like we are right there in them. The discovery of fractals has allowed us to decrease the size of our cell phones every year and at the same time they have helped doctors anticipate heart problems in our bodies way before they happen. Without the discovery of fractals, our technology, entertainment, our health, etc. would not be where it is today.

This project explained the concepts of fractals through four chapters.The first chapter 'An introduction to fractals' dealt with some of the basic concepts like definition,classification,properties,techniques for generating fractals and a short discussion about fractals and chaos.The second chapter 'The fundamentals of fractal geometry' explained the concepts of Hausdorff measure and dimensions and some examples of fractals.The third chapter discussed about self similarity and the fourth chapter pointed out the various applications of fractals in various fields.

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14. `https://tse2.mm.bing.net/th?id=OIP.uYrY3IFO6zYjZLkqAuvUBQHaE8&pid=Api&P=0&w=261&h=174`
15. `https://tse1.mm.bing.net/th?id=OIP.2pWNyP19QULip1KQhpJ3kwHaFJ&pid=Api&P=0&w=236&h=163`

PANDEMIC MATHEMATICS

-the math behind the prevention of COVID-19 Pandemic.

PANDEMIC MATHEMATICS

Project Report submitted to the University of Kerala, Thiruvananthapuram in partial fulfilment of the requirement for the completion of the FDP in Bachelor of Science in Mathematics in affiliated colleges

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CERTIFICATE

This is to certify that the project entitled "PANDEMIC MATH" is based on work carried out by Sandra Sanal , Sneha E.M , Stemy S.L , Aarya Gopan , and Amina Anwar , under the guidence of Smt.Sebina Mathew , Assistant Professor of Mathematics , All Saint's College , Thiruvananthapuram and no part of this work has formed the basis for award of any degree or diploma to any other University.

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May 2, 2022 — Head Of Department

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CONTENTS

PRELIMINARY

Pooled Distribution and It's Testing

In Mathematical Statistics, "pooling" describes the practice of gathering together small sets of data that are assumed to have the same value of a characteristic (e.g., a mean) and using the combined larger set (the "pool") to obtain a more precise estimate of that characteristic.

In traditional lab testing , we analyze a single sample to detrmine whether it is positive or negative . But in this method , the use of resources is very high and is time consuming.

So, the method of pool testing is performed .

If pooled test result is negative , then all samples in the particular pool are considered negative .

If the pooled sample test is positive then all samples of the pool are assumed postive and are tested individually to determine which is positive.

It appears most often in the two sample **t-test**, which is used to test whether or not the means of two populations are equal.

Two Sample t-test OR Pooled Testing

The two-sample t-test (also known as the independent samples t-test) is a method used to test whether the unknown population means of two groups are equal or not.

Since the testing population is normally distributed , this is the most preferred method.

How to perform the two-sample t-test

For each group, we need the average, standard deviation and sample size.

This difference in our samples estimates the difference between the population means for the two groups.

Next, we calculate the pooled standard deviation. This builds a combined estimate of the overall standard deviation.

Next we calculate pooled varience ;

$$s_p = \frac{((n_1 - 1)s_1^2) + ((n_2 - 1)s_2^2)}{n_1 + n_2 - 2} \tag{1}$$

where n_1, n_2 and s_1, s_2 represent the sample sizes and standard deviations of first and second pools(populations).

Next, we take the square root of the pooled variance to get the pooled standard deviation.

We now have all the pieces for our test statistic. We have the difference of the averages, the pooled standard deviation and the sample sizes. We calculate our test statistic as follows:

$$t = \frac{\text{difference of group means}}{\text{standard error of difference}} \tag{2}$$

where ,

$$\text{standard error} = \frac{S.D}{\sqrt{1/n_1 + 1/n_2}}$$

the significance level ($\alpha = 0.05$) and the degrees of freedom $= df = n_1 + n_2 - 2$ are also known and hence we calculate t_α. Now , We compare the value of t_α to the t value.

If $t > t_\alpha$ we reject the null hypothesis .

Mathematical Modeling

Mathematical modeling is the process of describing a real world problem in mathematical terms, usually in the form of equations, and then using these equations both to help understand the original problem, and also to discover new features about the problem.

The aim of epidemic modeling (Mathematical Modeling in Epidemology) is to understand and if possible control the spread of the disease.

That is , we can get an idea about

- How fast the disease spreads ?
- How much of the total population is infected or will be infected ?
- Control measures.
- Effects of Migration/ Environment/ Ecology, etc. .
- Persistence of the disease.

INTRODUCTION

Coronavirus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus. The disease is spreding rapidly and hence there is a need to put an end to its spread.

To improve our understanding of how a disease spreads, scientists use a combination of mathematics and data for mathematical modeling. Mathematical models provide a way to formulate simple rules to approximate how a virus like SARS-CoV-2 spreads (and thereby approximate the spread of the associated disease COVID-19). When creating and studying a mathematical model, scientists seek to improve the accuracy of forecastsA type of prediction that gives a range of possibilities of future outcomes. A scientist may forecast a range for the number of people who get COVID-19 during a particular period of time and how a disease will spread. They also try to test the effects of possible responses, such as everyone staying at home, to reduce the number of infections that result from the spread of a disease. Their research can help inform the people who make guidelines or policies to protect others from diseases Scientists who specialize in these studies are often called **Mathematical Epidemologists**

The method of pooled testing (statistical method of testing of hypothesis) helps us to test large number of samples and thus monitor the spread of the virus.

Mathematical models and computation have played a major role in influencing the responses of governments to the COVID-19 pandemic. These models are much more detailed than the SIR model.The current COVID-19 pandemic illustrates the importance of the mathematical modeling of infectious diseases. Mathematical and computational approaches allow people to make progress toward reducing the spread of a disease while researchers develop vaccines and treatments. They also help efforts to design interventions and vaccination programs.

1 POOLED TESTING

When testing for a disease such as COVID-19, the standard method isindividual testing: we take a sample from each individual and test these samples separately. Under the convenient mathematical model of perfect testing, a sample from an infected individual always gives a positive result, while a sample from a noninfected individual always gives a negative result. For N individuals, this requires N tests, and we can accurately classify all the individuals as infected or noninfected. The infected ndividuals can be advised to self-isolate and their contacts can be traced, while the noninfected individuals are reassured that they are free of the disease.

An alternative to individual testing is pooled testing, also called group testing. Instead of testing individual samples, we can instead pool samples together and test that pooled sample. Again under the convenient model of perfect testing, a pool consisting entirely of uninfected samples gives a negative result, while a pool containing one or more infected samples gives a positive result. Thus a negative result demonstrates that every individual in the pool is noninfected, while a positive result requires further information to work out which individuals in the pools are infected.

when the prevalence of a disease is low enough and the accuracy of a test is high enough, pooled testing can accurately classify individuals as infected or noninfected in fewer than N tests. This can be more efficient—and often much more efficient—than individual testing.

Testing for COVID-19 Testing people for coronavirus is a public health measure that reduces the spread of coronavirus .In the real world, testing is not perfect. We distinguish between two types of test errors:

- False positive test errors, where a sample (individual or pool) that does not contain any infection wrongly gives a positive result. The probability that an infection-free sample correctly gives a negative result is called the specificity.
- False negative test errors, where a sample (individual or pool) that does contain infection wrongly gives a negative result. The probability that an infected sample correctly gives a positive result is called the sensitivity.

So, in order to avoid these errors and to get a more precise test result , we use the method of **Pool Testing**

The Math Of Pool Testing If you know that the probability (p) that a sample is infected, you can compute the optimal number of samples (k) to combine into a pooled sample. Here "optimal" means "resulting in the fewest tests, on average."

Suppose you want to test a large number, N, of individual samples. If each pooled sample contains k individual samples, then:

- There are about N/k pooled samples, so you need that many tests for the first round of testing.
- For each pooled sample, the probability that the sample does NOT test positive is the probability of having zero positive samples in a random set of k independent samples. This probability is given by the binomial distribution: $\text{Binom}(0, p, k) = (1-p)k$. Consequently, the probability that a pooled sample DOES test positive is $p_2 = 1-(1-p)k$.
- From the preceding calculation, the expected number of positive pooled samples is p_2N/k.
- Each positive test from the first round triggers k additional tests in the second round, so the expected number of tests in the second round is p2N.
- the expected number of TOTAL tests is $N_{Tot} = N(1/k + p_2)$.

If you don't use pooling, you have to do N tests, so pool testing reduces the total number of tests by the expected fraction $1/k + p_2$ or $f(k;p) = 1/k + 1-(1-p)k$.

Stages of a Pooled Testing

Pooled testing was first proposed in 1943 by Dorfman for the detection of cases of syphilis in those called up for US army service during the Second World War.

Suppose we have N individuals, and we wish to identify who among those N individuals is infected.

- We choose a pool size s, and we divide the N individuals into N/s disjoint groups of size s each. (We assume, for simplicity, that N is an exact multiple of s.) We take a sample from each of the N individuals, and then, for each of the N/s groups, we pool the samples from that group into a single pooled sample. We then run a test on each of the N/s pooled samples.
- 1. If a pool tests negative, we know all the individuals in the corresponding group are noninfected.
  2. If a pool tests positive, we then follow up by individually test all the individuals in the corresponding group. These individual tests discover which of the samples in the pool were infected or noninfected.

At the end of this process, under our perfect testing model, we have correctly classified all the individuals as infected or noninfected.

Thus pooled testing has the potential to develop into a mass testing strategy where large number of people can be tested quickly.

The pool size and population are denoted by s and N respectively. The rate of infection and non infection respectively by p and $q = 1p$. where p is,

$$p = \frac{Number of infected}{Population size}$$

1.1 DORFMAN'S ALGORITHM

In the early 1940s, group testing (pooled testing) has been used to reduce costs in a variety of applications, including infectious disease screening, drug discovery, and genetics. In such applications, the goal is often to classify individuals as positive or negative using initial group testing results.Many decoding algorithms have been proposed, but most fail to acknowledge, and to further exploit, the heterogeneous nature of the individuals being screened.

In 1943, Robert Dorfman a professor of political economy at Harvard University who made great contributions to the fields of economics, statistics, group testing and in the process of coding theory , studied group testing which is a relatively new field of applied mathematics that can be applied to a wide range of practical applications and is an active area of research today.He suggested the Dorfman's algorithm.

Dorfman's algorithm was the first group testing Algorithm. This entailed pooling together biological specimens from several individuals and testing these pools of specimens rather than testing each individual specimen. If a pool tested negative, all specimens in that pool were declared negative. Otherwise, further testing on individual specimen from the pool were employed to identify all positive individuals.Mathematically, Dorfman's algorithm partitions the set in the first stage, then individually tests each item in the positive sets in the second stage.

Considering the Dorfman's Algorithm, we move on to the diffrent types of pooled testing which is operated under the principle of Dorfman's Algorithm.

1.2 ONETIME POOLING

The onetime pooling consists of two steps of tests. In the first round, a pool of individuals are formed and tested. If the result is negative all individuals in the pool are declared negative. If the result is positive, each person in the pool is individually tested. This is the simplest of pooled testing strategy.

Expected number of tests

For a pool size of s, the probability that no one has infection is q^s and the probability that at least one person is infected in the pool is $1 - q^s$.

Therefore expected number of tests is

$$\begin{aligned}\mathbf{Exp}(s, q) &= q^s + (s+1)(1 - q^s) \\ &= s(1 - q^s) + 1\end{aligned}$$

No of tests required in worst cases

The expected number of testing need not happen all the time. Therefore, we cannot use this to determine the number of testing kits required. In this subsection, we identify the number of tests required in the worst case. Let us assume we do pooled testing on a population of size N and pool size s.Let p be the infection rate. Then pN individuals are infected. In a worst case partitioning of the pool, we will have all the pN individuals to be in different pools. Therefore $\frac{N}{s} - pN$ many pools are not infected. Therefore the maximum number of tests required is

$$\frac{N}{s} + (pN) * s$$

1.3 MULTI POOLING

The multi-pooling strategy consists of multiple pooling tests. At first level we use a pool size of s. In the next round all positive pools are split into two. That is, we consider pools of size $\frac{s}{2}$. In the third round, we split the positive pools from the second round into two (size $\frac{s}{4}$ each). The process is continued until the pool size becomes one or all individuals are tested separately. This is the best strategy to reduce the number of tests. Unfortunately, it takes multiple pooling tests taking too much time for a positive individual to know the result of the test. Moreover, multi-pooling strategy works only if the rate of infection is low.

Expected number of tests

In this subsection we find the expected number of tests required. Let N_1 be the initial population size, q_1 the rate of non-infection and s be the starting pool size. The total number of infected is

$q_1\ N_1$ and the total number of tests in the first round (denoted by $\mathbf{ET}_1)is$

$$ET_1 = \frac{N_1}{s}$$

The probability that a pool is infected in the first round is $1 - q_1^s$ Hence the expected number of positive pools in the first round is

$$P_1 = \frac{N_1}{s}(1 - q_1^s)$$

and the population to be tested is $N_2 = N_1(1 - q_1^s)$.

Let us now calculate the number of tests in the second round. The probability of non-infection in the second round is $q_2 = \frac{q_1 N_1}{N_2}$ We now partition the N_2 individuals into pools of size s and tests them. This gives us, the total number of tests in this round to be $\frac{2N_2}{s}$. Now , Look at a pool from the first round which contains exactly one positive individual. The second round splits the pool into two. Testing the non-positive split will immediately tell us that the other split is positive an information we gauged without testing that pool. The expected number of pools with exactly one infection is Singleton Pool S_1 , $S_1 = N_1(1 - q_1)q_1^{s-1}$.

Therefore the expected number of tests in the second round is

$$ET_2 = 2(p_1 - S_1) + \frac{3}{2}S_1$$

We progress by considering further reduction in the pool size. Thus the expected number of tests in this multi-pooling strategy comes out to be ΣET_k for k rounds of pooling (k = log s).

The above analysis can be approximated by assuming that the a positive pool in the first round will contain only one infected individual. If the infection is low, this is almost surely going to happen. The expected number of tests required if a pool of size s contains one infected individual is approximately

$$\frac{3}{2}\log s + 1$$

Assuming a population of size N and a probability of infection of p we get the expected number of tests required to be

$$Exp(s,p) \approx \frac{3pN}{2}\log s + \frac{N}{s}$$

1.4 ADVANTAGES OF POOLED TESTING

Pooling—sometimes referred to as pool testing or pooled testing means combining the same type of specimen from several people and conducting laboratory test on the combined pool of specimens to detect SARS-CoV-2, the virus that causes COVID-19. Pooled tests that return positive results will require each specimen in the pool to be retested individually to determine which individual(s) are positive.

Pooling allows laboratories to test more samples with fewer testing materials Which means that more people can be tested in locations where testing resources are limited. Testing has been touted as one of the best ways to prevent the spread of the virus. Yet, throughout the pandemic, access to testing has often been limited, people have had to wait in long lines, and results have been delayed at times for several weeks due to a backlog of tests at laboratories.Hence it saves time and manpower.

Pooled testing lowers manpower and increases the testing capacities of labs and also speeds up results . It allows testing facilities to process a large number of samples rapidly .More samples can be processed in a short time period . It reduces the total number of tests that needs to be done .

Pooling samples reduces the use of limited reagents , which is difficult to get when the demand is high . A study shows that pooling anywhere from 4 to 30 individual samples is an efficient strategy to defect the SARS-CoV-2 virus without sacrificing test sensitivity .

Pooled testing is better than traditional testing when the rate of infection is less than 20 % . It can be done even for an infection rate of 20-22 % .Pooled testing becomes significantly better when the rate of infection is very low.

1.5 DISADVANTAGES OF POOLED TESTING

The idea of pooled COVID testing seems like a great idea at first glance, but it comes with its own set of issues. Pooled testing is defined as "combining respiratory samples from several people and conducting one laboratory test on the combined pool of samples."

Unfortunately, there are problems with pooling COVID tests. Pooling can only be used in areas or situations where the number of positive test results is expected to be low-for example, in locations with a low prevalence of SARS-CoV-2 infections. When infection rates are high, too many pools come back with positive results.This would require more individual tests, thus making the pooling method less efficient and more complicated.

Pooled COVID testing can increase the number of false-negative cases (when someone who is infected with the virus falsely tests as not having it) as well as decrease the sensitivity of COVID-19 detection, especially in people who are asymptomatic or had a low viral load.

False negatives can increase the risk of an outbreak, defeating the whole point of testing.Additionally, while pooled testing can decrease the number of tests needed, the need to retest all the individuals in pools that tested positive lessens the decrease (and expense savings).

Pooled testing is effective only if prevalence and transmission of the disease are low in the population . Pooled testing is not meant for people at high risk ,like close contacts ,health workers or those who come under high risk .

Pooled testing is useful for population screening and resource-restricted settings, due to its ability to stretch COVID-19 testing supplies, increase the number of patients tested, and increase the number of cases detected. However, there are drawbacks, including the complicated workflow, lower sensitivity, and the need to repeat tests from positive pool.

2 EPIDEMOLOGICAL MODELING

The idea that transmission and spread of infectious diseases follows laws that can be formulated in mathematical language is old. In 1766, Daniel Bernoulli published an article where he described the effects of smallpox variolation (a precursor of vaccination) on life expectancy using mathematical life table analysis . However, it was only in the twentieth century that the nonlinear dynamics of infectious disease transmission was really understood. In the beginning of that century there was much discussion about why an epidemic ended before all susceptibles were infected with hypotheses about changing virulence of the pathogen during the epidemic.

The central idea about transmission models, as opposed to statistical models, is a mechanistic description of the transmission of infection between two individuals. This mechanistic description makes it possible to describe the time evolution of an epidemic in mathematical terms and in this way connect the individual level process of transmission with a population level description of incidence and prevalence of an infectious disease. The rigorous mathematical way of formulating these dependencies leads to the necessity of analyzing all dynamic processes that contribute to disease transmission in much detail. Therefore, developing a mathematical model helps to focus thoughts on the essential processes involved in shaping the epidemiology of an infectious disease and to reveal the parameters that are most influential and amenable for control. Mathematical modeling is then also integrative in combining knowledge from very different disciplines like microbiology, social sciences, and clinical sciences.

In this paper, we develop a mathematical model for the spread and control of the coronavirus disease. Understanding the early spread dynamics of the infection and evaluating the effectiveness of control measures is crucial for assessing the potential for sustained transmission to occur in new areas.

Epidemiology is essentially a population biology discipline concerned with public health. As such, epidemiology is thus heavily influenced by mathematical theory. The reason is that most phenomena observed at a population level are often complex and difficult to deduce from the characteristics of an isolated individual. For example, the prevalence of a disease in a population is only indirectly connected to the course of disease in an individual. In this context, the use of mathematical models aims to unearth processes from a large-scale perspective.

The SIR Model Or The Differential Equation Model

As the first step in the modeling process, we identify the independent and dependent variables. The independent variable is time t, measured in days. We consider two related sets of dependent variables.

The first set of dependent variables counts people in each of the groups, each as a function of time:

$S = S(t)$ is the number of susceptible individuals, $I = I(t)$ is the number of infected individuals, and $R = R(t)$ is the number of recovered individuals.

The second set of dependent variables represents the fraction of the total population in each of the three categories. So, if N is the total population , we have

$s(t) = S(t)/N$, the susceptible fraction of the population, $i(t) = I(t)/N$, the infected fraction of the population, and $r(t) = R(t)/N$, the recovered fraction of the population.

At each time t, s(t) + i(t) + r(t) = 1.

1. The ODE of Susceptible is,

$$\frac{ds}{dt} = -bs(t)I(t) \tag{3}$$

where b is the number of contacts per day by the infected individuals that are sufficient to spread the disease.

2. The ODE of Recovered is $\frac{dr}{dt} = ki(t)$

   where k is the infected group that will recover during any given day.

3. The ODE of Infected is $\frac{ds}{dt} + \frac{di}{dt} + \frac{dr}{dt} = 0$

Finally, we complete our model by giving each differential equation an initial condition.

2.1 Development of a Mathematical Model

We segregated human beings into four contamination groups of pupils, as of the following. Susceptible, Revealed (not so far transmittable), Transmittable Separated (i.e., inaccessible, healthier, or else no longest transmittable).

In order to formulate the model mathematically, we have divided total population N(t) into seven mutually exclusive compartments on the basis of their disease status namely: susceptible ($S(t)$), exposed ($E(t)$), asymptomatic infected ($A(t)$), symptomatic infected but not quarantined ($I(t)$), symptomatic and quarantined infected ($Q(t)$), hospitalised and isolated infected ($H(t)$) and recovered ($R(t)$) population, So at any time t total population, $N(t) = S(t) + E(t) + A(t) + I(t) + Q(t) + H(t) + R(t)$

a susceptible person may be infected by the close contact with a infected person.

Now we move to the most important part ,
Let $S(t)$ be the total number of susceptibles of the disease.
$I(t)$ be the total number of infected any given point of time and
$R(t)$ be the total number of Removed people (that is the category of
population that is either recovered or dead) .
Now we make certain assumptions :

1. We make assumption that the pandemic is sufficently short and the total population remains constant.
2. The second assumption model relates the way in which disease is transmitted. ie. rate of infected proportion (r) α rate of contact between susceptbles and infected.
3. We assume a constant rate at which infectives die or recover and let it be R .

Now we can form certain linear ODE's based on these data:

$$\frac{dS}{dt} = -rIS \tag{4}$$

which denotes the increase in the number of susceptbles.

$$\frac{dI}{dt} = rIS - aI \tag{5}$$

which denotes the increase in the number of infectives.

$$\frac{dR}{dt} = aI \tag{6}$$

which is the rate of removed proportion.

Now , considering the initial conditions

$$S = S_0$$

$$I = I_0$$

and

$$R = 0$$

(since in the begining of pandemic no one is removed).

We know,

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{7}$$

$$\Longrightarrow \quad \frac{d(S + I + R)}{dt} = 0$$

From the initial conditions , we can write , $S+I+R = S_0+I_0$

Now we come to the important questions, **Will the disease spread ?**

Consider the equation,

$$\frac{dS}{dt} = -rIS \tag{8}$$

we know the value of r , I and S are always positive but we have a negative value for $\frac{dS}{dt}$.

So that means the value of S is always less than its initial value S_0.

$\Longrightarrow S \leq S_0$

so we get ,

$$\frac{dI}{dt} < I(rS_0 - a)$$

If

$$S_0 > \frac{a}{r} = \frac{1}{q},$$

then the disease will spread , where $q = \frac{r}{a}$, the **Contact Ratio** which is the fraction of population that comes into contact with an infected individual.

We can rearrange the inequality as

$$\frac{rS_0}{a} = R_0$$

where R_0 is the **Basic Reproductive Ratio** .

$$R_0 = \frac{rS_0}{a} > 1$$

This depicts the number of secondary infections possible. Thus R_0 gives us an idea about if a person is infected , the possible number of secondary infections caused by them . For a Seasonal Flu , it is somewhere between 1 to 1.5 , but for COVID -19 it has a value greater than 3 .

Now we come to another question,**What will be the maximum number of infectives at any given point of time ?**

From above equations we get ,

$$\begin{aligned} \frac{dI}{dS} &= \frac{rIS - aI}{-rIS} \\ &= -1 + \frac{a}{rS} \\ &= -1 + \frac{1}{qS} \end{aligned} \tag{9}$$

where

$$\frac{a}{r} = \frac{1}{q}$$

$$\implies I + S - \frac{1}{q}\ln S = I_0 + S_0 - \frac{1}{q}\ln S_0$$

So the maximum value of I occurs when ,

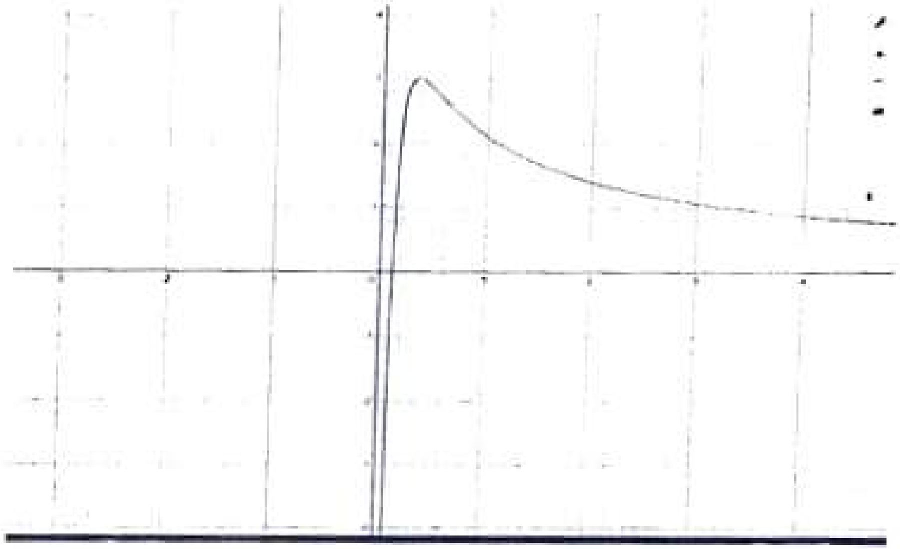

Figure 1:

$$S = \frac{1}{q}$$

$$\implies I_{max} = I_0 + S_0 - \frac{1}{q}\ln(qS_0)$$

Here the value of I_{max} depends on q (The Contact Ratio)

From this we plot a graph ,

In the begining of the pandemic , the value of q is supposed to be very high, since a large number of people are suscepted to be in contact.

$\Longrightarrow$ Maximum possiblity of infected people at any given time

$$= \text{Total Population} - f(x)$$

$$= I_0 + S_0 - \frac{1}{q}\ln(qS_0)$$

The function $f(x)$ depends completely on value of q.

How many people will be infected by this disease?

Assume total population as constant,
Solving this we get no: of removed population

$$R_{(\text{end})} = -S_{\text{end}} - I_0 + S_0$$

$$S_{(\text{end})} - \frac{1}{q}\ln(S_{\text{end}})$$

$$= I_0 + S_0 - \frac{1}{q}\ln(S_0)$$

This is the solution to our question.
We can represent this graphically as :
So, What does this mean for Covid-19 ?

- In short, the answer to our question 1 is , $R_0 = qS_0 > 1 \Longrightarrow$ the disease will spread if q is very large , this means

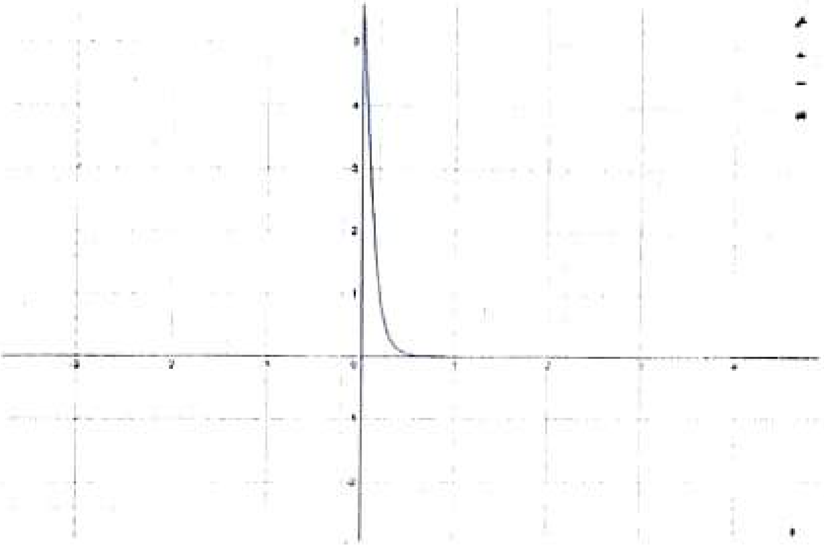

Figure 2:

that we should try to reduce the number of patients having contact with the infected

- Maximum number of infected people at a given point of time is [Total Population - $f(q)$], where $f(q)$ is a function of q(rate of people having contact with the infected).
- The total number of people that may be infected by the disease is [Total Population - $g(q)$], where $g(q)$ is another function of q

From the concept of Epidemological Modeling we can predict the pattern of spread of COVID-19 and this tells us how to alter things and to control the outbreak of pandemic by reducing the value of q. So we should strictly follow the guidelines made by government and Health Officials , maintain social distancing and use masks to prevent the spread and thus reducing the value of q which helps in controlling the disease outbreak.

CONCLUSION

Testing is necessary to reopen the economy and schools, however it's almost impossible to do this using conventional testing methods.The recently authorized technique called sample pooling significantly increase the number of people being tested.

Mathematical models are a key tool for guiding public health measures, and outputs from epidemological modeling analysis should be considered alongside numerous factors (such as potential economic and mental health effects of interventions) when deciding how to intervene. Perfect data are not available, so modeling requires assumptions made about the effects of different interventions on contact rates between hosts. 'Models demonstrated the need for the current lockdown, and modeling must remain a key tool for informing policy.

Thus we can conclude that Mathematics play a key role in this battle against COVID-19.Mathematical functions can be applied as tools to describe the dynamics of how infectious diseases propagate among people. Mathematical Modeling generates a picture or a 'model' of the dynamics of the disease, which can be visually represented by graphs, charts and comparative tables.

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