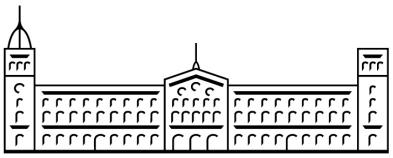

Treball final de grau

GRAU DE MATEMÀTIQUES

Facultat de Matemàtiques
Universitat de Barcelona

FRACTAL STUDY OF TUMORS

Edelweiss Mármol Pérez

Director: Dr. Àlex Haro Provinciale
Realitzat a: Departament de Matemàtica Aplicada i Anàlisi

Barcelona, June 27, 2016

Abstract

Fractal geometry was first invented by mathematicians of the late 19th and early 20th century to study problems as abstract as the existence of continuous functions non derivable at any point, the continuum hypothesis, or the existence of topological spaces with strange properties. It was not until the second half of the 20th century that fractal geometry became popular, and it was applied to the study of natural phenomena by the hand of B. Mandelbrot.

The study of tumor growth using fractal geometry is relatively recent. This study is based on the fractal character of tumor contours. One of their most important features is roughness, since its increase is related to the tumor growth. Tumor growth dynamic can be described by a function that depends on both time and position, known as local width function, as well as by some power law exponents, called critical exponents.

The aim of this final degree project is to study all these concepts in connection with fractals. Elementary concepts of the theory of fractals will also be studied, as the iterated function systems, the fractal dimension and the fractal interpolation functions. Since fractal dimension can only be computed accurately for some specific mathematical objects, we will study some methods that estimate fractal dimension of tumors based on its fractal characteristics. Finally, we will develop some Matlab programs which will compute the fractal dimension of tumors, as well as the roughness of their contours. Furthermore, we will compare our results with the experimental data.

Acknowledgments

I would like to express my gratitude to my director Àlex Haro, who has kindly helped and guided me throughout this project. Furthermore, I would like to thank all his time and his useful advices.

I would like to thank as well my classmates and friends, who have helped me with the bitmap image file.

Last, but not least, I want to thank my family and my partner for their constant support.

Contents

1 Introduction

This work stems from my interest in mathematics applied to medicine, specially in tumors.

This project revolves around fractals and their relationship with natural objects, in particular, tumors. To start, we could define a fractal as a mathematical model or a real object that maintains its essential form, irregular and fragmented, against changes in the scale of observation. We distinguish two types of fractals: the artificial fractals and the natural fractals. On the one hand, *artificial fractals* are objects whose parts, at infinitely many levels of magnification, appear geometrically similar to the whole. That is, they look the same at all scales. Examples of artificial fractals are, for instance, the Cantor set, the Sierpinski triangle or the Koch snowflake. On the other hand, *natural fractals* are real objects that display this "self-similarity" for only a range of magnifications or scales. The mathematical object will of course only be an accurate model within this particular range. In nature, the contour or bone fissures, of coastlines or tumor contours as well are examples of natural fractals.

On the one hand, artificial fractals are defined from iterated function systems (IFS), using concepts such as metric spaces or contraction mappings. We can compute their fractal dimension by means of the Box Counting Theorem, although we will study some other methods that relate the fractal dimension concept to the IFS one. Furthermore, we are going to study the so-called fractal interpolation functions. These are functions that interpolate data as complex as those of the stock market, of cardiograms or of seismograms as well. The graph of these functions possesses fractal characteristics, in particular, it is constructed from IFS once more. Therefore, we can use the aforementioned methods for compute the fractal dimension of these graphs.

On the other hand, natural fractals are more complicated to study since there is no method or mathematical formula that defines them. However, we are going to focus on tumors, and we are going to study their fractal characteristics and their growing dynamics. As we will later see, what determines the growth dynamic of tumors is the morphology of their contours. These contours possess fractal characteristics, so a fractal study of tumor will determine the growing dynamic behavior. Finally, other concept related to tumor growth is the fractal dimension. We are going to study some methods that estimate tumor dimension based on their fractal nature. The question then will be if the box counting dimension of tumors is the same as the one obtained by the studied methods. A program will be used to answer this question.

Structure of the Project

The aim of this project is to study fractal geometry in order to apply it to the study of tumors. The contents are developed through three chapters.

The study of artificial fractals takes place in Chapter 2. I start defining the metric space in which fractals live. Then, I define some elementary concepts, such as affine transformations and contraction mappings, to be able to study the Iterated Function Systems and The Collage Theorem. After this, through some theorems and properties, I define the fractal dimension. Finally, I give the formal definition of an artificial fractal.

Chapter 3 focuses on fractal interpolation functions. I start giving their definition to then study their relation with fractals. Lastly, I define the fractal dimension of these functions. Besides, I create a Matlab program to test it with some examples.

The fractal study of tumor develops throughout chapter 4. I start defining tumors and studying their fractal character. Later, I do a dynamic scaling analysis to define the critical exponents and then I use these exponents to determine the tumor growth dynamic. Finally, I study the fractal dimension of tumors, and I create a Matlab program to test it with a real example.

The code of the programs is attached and explained in the Appendix.

2 Artificial Fractals and Fractal Dimension

Let's start talking about **artificial fractals**. As we said before, they are mathematical objects that maintain their essential form against changes in the scale of observation. In other words, they are self-similar objects that look the same at infinitely levels of magnification. We will focus on deterministic fractals, that are the ones created with no randomness involved. The aim, however, is to find an accurate definition of these complex objects, which, from now on, we just call them fractals, as well as to study how they are constructed and what their main properties are.

2.1 The Metric Space $(\mathcal{H}(X), h)$: The Place Where Fractals Live

In order to give an exact definition of a fractal, we first need to define a space in which to study them. We may start working in some metric spaces which we denote by (X, d), such as $(\mathbb{R}^2, Euclidean)$. But then, when we wish to discuss pictures, drawings, or subsets of the space, it becomes natural to introduce the space $(\mathcal{H}(X), h)$.

Definition 2.1. *Let (X, d) be a metric space. Then $\mathcal{H}(X)$ denotes the set whose elements are the nonempty compact subsets of X.*

In order to define this metric space in which to study fractal geometry, we need a distance (also called metric). Its definition will follow the following steps.

Definition 2.2. *Let (X, d) be a metric space, $x \in X$, and $B \in \mathcal{H}(X)$. Define*

$$d(x, B) = min\{d(x, y) : y \in B\}.$$

*$d(x, B)$ is called the **distance from the point x to the set B**.*

Remark. The existence of the minimum value of the set of real numbers $\{d(x, y) : y \in B\}$ follows from the compactness and nonemptyness of the set $B \in \mathcal{H}(X)$. Let's consider, given $x \in X$, the real-valued function $f : B \to \mathbb{R}$ defined by

$$f(y) = d(x, y) \text{ for all } y \in B.$$

From the definition of the metric it follows that f is continuous, viewed as a transformation from the metric space (B, d) to $\mathbb{R}$. Moreover, B is a nonempty and compact set due to the definition of $\mathcal{H}(X)$. Then, applying the Weierstrass Extreme Value Theorem, we obtain that f attains a maximum and a minimum value. That is, there exist numbers z_1 and z_2 in B such that $f(z_1) \leq f(y) \leq f(z_2)$ for all $y \in B$. In particular, there exists $z_1 \in B$ such that $f(z_1) = d(x, z_1) = min\{d(x, y) : y \in B\}$ which is what we wanted to show.

Definition 2.3. *Let (X, d) be a metric space. Let $A, B \in \mathcal{H}(X)$. Define*

$$d(A, B) = max\{d(x, B) : x \in A\}.$$

$d(A, B)$ is called the ***distance from the compact set A to the compact set B.***

Just as above, using the compactness and nonemptyness of the sets A and B, we can prove that this definition is meaningful. Specifically, there are points $\hat{x} \in A$ and $\hat{y} \in B$ such that $d(A, B) = d(\hat{x}, \hat{y})$.

This definition is not completely satisfying. In particular, it is not symmetric with respect to A and B. Moreover, if $A \subset B$, then $d(A, B) = 0$ (even if the inclusion is proper and the sets are different). We get a satisfactory definition of a distance in $\mathcal{H}(X)$ by symmetry of the previous definition.

Definition 2.4. *Let (X, d) be a metric space. Let $A, B \in \mathcal{H}(X)$. Then the* ***Hausdorff distance between the sets*** *A and B is defined by*

$$h(A, B) = max\{d(A, B), d(B, A)\}.$$

Proposition 2.1. *h is a metric on $\mathcal{H}(X)$. In other words, $(\mathcal{H}(X), h)$ is a metric space.*

Proof. Let $A, B, C \in \mathcal{H}(X)$. We have to show that h obeys the following axioms:

i) $0 \leq h(A, B) < \infty$, so $h(A, B) = d(a, b)$ for some $a \in A$ and $b \in B$ using the compactness of A and B. If $A \neq B$ we can assume there is an $a \in A$ so that $a \notin B$.

ii) $h(A, A) = 0$, so $h(A, A) = max\{d(A, A), d(A, A)\} = d(A, A) = max\{d(x, A) : x \in A\} = 0$ since d is a metric.

iii) $h(A, B) = h(B, A)$ given that the definition of h is symmetric.

iv) To show that $h(A, B) \leq h(A, C) + h(C, B)$ we first show that $d(A, B) \leq d(A, C) + d(C, B)$. We have, for any $a \in A$:

$$\begin{aligned} d(a, B) &= min\{d(a, b) : b \in B\} \\ &\leq min\{d(a, c) + d(c, b) : b \in B\} \quad \forall c \in C \\ &= d(a, c) + min\{d(c, b) : b \in B\} \quad \forall c \in C, \quad so \\ d(a, B) &\leq min\{d(a, c) : c \in C\} + max\{min\{d(c, b) : b \in B\} : c \in C\} \\ &= d(a, C) + d(C, B). \end{aligned}$$

Hence, $d(A, B) \leq d(A, C) + d(C, B)$. Similarly,

$$\begin{aligned} d(B, A) &\leq d(B, C) + d(C, A) \quad whence \\ h(A, B) &= max\{d(A, B), d(B, A)\} \\ &\leq max\{d(A, C), d(C, A)\} + max\{d(C, B), d(B, C)\} \\ &= h(A, C) + h(C, B) \quad as\ desired. \end{aligned}$$

Then h is a metric on $\mathcal{H}(X)$ as we wanted to see. $\square$

Therefore, we have that $(\mathcal{H}(X), h)$ is a metric space and we refer to it as the *space of fractals*. At this point and time, we define a *fractal* as any element of the set $\mathcal{H}(X)$ (i.e. as any nonempty compact subset of X).

The central result of this section is the completeness of the space of fractals, as well as its relation to the completeness of the metric space (X, d). This is shown in the theorem below.

Theorem 2.1. ***The Completeness of the Space of Fractals.*** *Let (X, d) be a complete metric space. Then $(\mathcal{H}(X), h)$ is a complete metric space. Moreover, if $\{A_n \in \mathcal{H}(X)\}_{n=1}^{\infty}$ is a Cauchy sequence, then*

$$A = \lim_{n\to\infty} A_n \in \mathcal{H}(X)$$

can be characterized as follows:

$$A = \{x \in X : \text{there is a Cauchy sequence } \{x_n \in A_n\}_{n=1}^{\infty} \text{ that converges to } x\}.$$

2.2 Construction of Fractals

The aim of this section is to define what is known as an *Iterated Function System* (IFS), which is a method of constructing fractals. But before that, we must define some important previous concepts such as affine transformations or contraction mappings.

2.2.1 Transformations on Metric Spaces

The goal of fractal geometry is to study "complicated" subsets of geometrically "simple" spaces such as $\mathbb{R}$, $\mathbb{R}^2$ or $\mathbb{C}$. Furthermore, deterministic fractal geometry focuses on those subsets of a space that are generated by, or possess invariance properties under, simple geometrical transformations of the space into itself. These simple transformations are, for instance, affine transformations in $\mathbb{R}^2$ such as rotations, translations or homothecies.

Let's see how these transformations are defined, to later be able to work in fractal geometry.

Definition 2.5. *Let (X, d) be a metric space. A* ***transformation*** *on X is a function $f : X \to X$, which assigns exactly one point $f(x) \in X$ to each point $x \in X$.*

Therefore, a transformation is merely a map. We now define the affine transformations in $\mathbb{R}^2$.

Definition 2.6. *A transformation $w : \mathbb{R}^2 \to \mathbb{R}^2$ of the form*

$$w(x_1, x_2) = (ax_1 + bx_2 + e, cx_1 + dx_2 + f),$$

where a, b, c, d, e and f are real numbers, is called a two-dimensional ***affine transformations****.*

An affine transformation is nothing more than a linear transformation followed by a translation, that is why we often use the following equivalent notation:

$$w(x) = w\begin{pmatrix} x_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} a & b \\ c & d \end{pmatrix}\begin{pmatrix} x_1 \\ x_2 \end{pmatrix} + \begin{pmatrix} e \\ f \end{pmatrix} = Ax + t.$$

Here $A = \begin{pmatrix} a & b \\ c & d \end{pmatrix}$ is a two-dimensional, 2×2 real matrix and t is the column vector $\begin{pmatrix} e \\ f \end{pmatrix}$. Such transformations have important geometrical and algebraic properties.

As we will see later with IFS's, sometimes the problem is to find an affine transformation that approximately transforms one given set into another given set in $\mathbb{R}^2$. The way of doing this is as follows.
Suppose that we want to find the affine transformation that almost takes set A to set B. Therefore we need to find the numbers a, b, c, d, e, and f defined above so that $w(A) \approx B$. We begin by introducing x and y coordinate axes. We mark three points on the initial set A and determine their coordinates (x_1, x_2), (y_1, y_2), and (z_1, z_2). Then we mark the corresponding three points on the set B, and determine again their coordinates; say $(\tilde{x}_1, \tilde{x}_2)$, $(\tilde{y}_1, \tilde{y}_2)$, and $(\tilde{z}_1, \tilde{z}_2)$ respectively. Then a, b and e are obtained by solving the three linear equations

$$\begin{aligned} x_1a + x_2b + e &= \tilde{x}_1, \\ y_1a + y_2b + e &= \tilde{y}_1, \\ z_1a + z_2b + e &= \tilde{z}_1; \end{aligned}$$

while c,d and f satisfy

$$\begin{aligned} x_1c + x_2d + f &= \tilde{x}_2, \\ y_1c + y_2d + f &= \tilde{y}_2, \\ z_1c + z_2d + f &= \tilde{z}_2. \end{aligned}$$

To finish, there are a kind of affine transformations, called *similitudes*, having this special form:

$$w\begin{pmatrix} x_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} r & 0 \\ 0 & r \end{pmatrix}\begin{pmatrix} \cos\theta & -\sin\theta \\ \sin\theta & \cos\theta \end{pmatrix}\begin{pmatrix} x_1 \\ x_2 \end{pmatrix} + \begin{pmatrix} e \\ f \end{pmatrix}$$

for some translation $(e, f) \in \mathbb{R}^2$, some real number $r \neq 0$, and some angle $\theta \in [0, 2\pi)$. We call θ the rotation angle and r the scale factor or scaling. Thus, we have that a similitude is the composition of a translation, a rotation and an homothecy.

2.2.2 Contraction Mappings

From the concept of transformation (or map), we are going to define what is known as *contraction mapping*. Afterwards, we will see the most important theorem so far, the *Contraction Mapping Theorem*, also known as Banach Fixed Point Theorem.

We start defining the following concept.

Definition 2.7. *Let $f : X \to X$ be a transformation on a metric space. A point $x_f \in X$ such that $f(x_f) = x_f$ is called a **fixed point** of the transformation.*

The fixed points of a transformation are very important, because they tell us which parts of the space are fixed (not moved) by the transformation.

Let's now define the contraction mappings.

Definition 2.8. *A transformation $f : X \to X$ on a metric space (X, d) is called contractive or a **contraction mapping** if there is a constant $0 \leq s < 1$ such that*

$$d(f(x), f(y)) \leq s \cdot d(x, y) \ \forall x, y \in X.$$

*Any such number is called a **contractivity factor** for f.*

The contraction mappings have the following properties, some of which we will use to prove the Contraction Mapping Theorem.

Lemma 2.1. *Let $w : X \to X$ be a contraction mapping on the metric space (X, d). Then w is continuous.*

Lemma 2.2. *Let $w : X \to X$ be a contraction mapping on the metric space (X, d) with contractivity factor s. Then $w : \mathcal{H}(X) \to \mathcal{H}(X)$ defined by*

$$w(B) = \{w(x) : x \in B\} \quad \forall B \in \mathcal{H}(X)$$

is a contraction mapping on $(\mathcal{H}(X), h)$ with contractivity factor s.

The above definitions lead us to the following theorem.

Theorem 2.2. ***The Contraction Mapping Theorem.***
Let (X, d) be a complete metric space. Let $f : X \to X$ be a contraction mapping with contractivity factor $0 \leq s < 1$. Then f possesses exactly one fixed point $x_f \in X$ and, moreover, for any point $x \in X$, the sequence $\{f^n(x) : n = 1, 2, \cdots\}$ converges to x_f. That is, for each $x \in X$,

$$\lim_{n \to \infty} f^n(x) = x_f.$$

In addition,

$$d(x, x_f) \leq (1-s)^{-1} \cdot d(x, f(x)) \quad \forall x \in X.$$

Proof. Let $x \in X$, and let $0 \leq s < 1$ be the contractivity factor for f. Then

$$d(f^n(x), f^{n+k}(x)) \leq s^n \cdot d(x, f^k(x)) \tag{2.1}$$

for all $n, k = 0, 1, 2, \cdots$, where we have fixed $x \in X$. In particular, for $k = 0, 1, 2, \cdots$ we have

$$\begin{aligned} d(x, f^k(x)) &\leq d(x, f(x)) + d(f(x), f^2(x)) + \cdots + d(f^{k-1}(x), f^k(x)) \\ &\leq (1 + s + s^2 + \cdots + s^{k-1}) \cdot d(x, f(x)) \leq (1-s)^{-1} \cdot d(x, f(x)) \end{aligned}$$

since $1 + s + s^2 + \cdots + s^{k-1}$ is a geometric series with common ratio $0 \leq s < 1$, and using that f is a contraction mapping. So substituting this into equation (2.1) we obtain that

$$d(f^n(x), f^{n+k}(x)) \leq s^n \cdot (1-s)^{-1} \cdot d(x, f(x)),$$

from which it immediately follows that $\{f^n(x)\}_{n=0}^{\infty}$ is a Cauchy sequence. Now since (X, d) is a complete metric space, this Cauchy sequence possesses a limit $x_f \in X$. Then, for each $x \in X$, we have that

$$\lim_{n\to\infty} f^n(x) = x_f.$$

Now we shall show that x_f is a fixed point of f. But since f is contractive, it is continuous (Lemma 2.1), and hence

$$f(x_f) = f(\lim_{n\to\infty} f^n(x)) = \lim_{n\to\infty} f^{n+1}(x) = x_f.$$

Finally, we have to show that f possesses exactly one fixed point $x_f \in X$. Let's suppose that it possesses more than one, for instance, let x_f and y_f be two fixed points of f. Then $x_f = f(x_f)$, $y_f = f(y_f)$, and

$$d(x_f, y_f) = d(f(x_f), f(y_f)) \leq s \cdot d(x_f, y_f),$$

where $(1-s) \cdot d(x_f, y_f) \leq 0$. But $0 \leq s < 1$, which implies that $d(x_f, y_f) = 0$ and hence $x_f = y_f$.

Lastly, we have to show that $d(x, x_f) \leq (1-s)^{-1} \cdot d(x, f(x)) \quad \forall x \in X$. But this follows from what we have proved above.

$$\begin{aligned} d(x, x_f) &= d(x, \lim_{n\to\infty} f^n(x)) = \lim_{n\to\infty} d(x, f^n(x)) \leq \lim_{n\to\infty} (1-s)^{-1} \cdot d(x, f(x)) \\ &= (1-s)^{-1} \cdot d(x, f(x)) \quad \forall x \in X. \end{aligned}$$

This completes the proof. □

2.2.3 Iterated Function Systems

Let (X, d) be a metric space and let $(\mathcal{H}(X), h)$ denote the corresponding space of nonempty compact subsets with the Hausdorff metric h.

We are not able yet to give an accurate definition of a fractal. Even so, we have agreed that they are elements of the set $\mathcal{H}(X)$. If we wanted to be a little more specific, we could define a fractal as a fixed point of a contractive transformation on the metric space $(\mathcal{H}(X), h)$. Therefore we need not only the underlying metric space (X, d) to be "geometrically simple", but also the contraction mapping to be constructed from simple and easily specified contraction mappings on (X, d).

The next lemma provides an important method for combining contraction mappings on $(\mathcal{H}(X), h)$ to produce new contraction mappings on $(\mathcal{H}(X), h)$. This method is different form the obvious one of composition.

Lemma 2.3. *Let (X, d) be a metric space. Let $\{w_n : n = 1, 2, \cdots, N\}$ be contraction mappings on $(\mathcal{H}(X), h)$. Let the contrativity factor for w_n be denoted by s_n for each n. Define $W : \mathcal{H}(X) \to \mathcal{H}(X)$ by*

$$W(B) = w_1(B) \cup w_2(B) \cup \cdots \cup w_N(B) = \bigcup_{n=1}^{N} w_n(B), \text{ for each } B \in \mathcal{H}(X).$$

Then W is a contraction mapping with contractivity factor $s = max\{s_n : n = 1, 2, \cdots, N\}$.

Now we are able to define what is known as *Iterated Function System*. An IFS is a method of constructing fractals based on the definition of a set of transformations in a metric space that, when iterated, they create fractal representations. One of its properties is that the resulting constructions are always self-similar (they are formed by parts that are "similar" to the whole). These are usually called IFS fractals and they can be of any number of dimensions, although are commonly computed and drawn in 2D.

The formal definition is the one below.

Definition 2.9. *An **iterated function system** consists of a complete metric space (X, d) together with a finite set of contraction mappings $w_n : X \to X$ with respective contractivity factors $0 \leq s_n < 1$ for $n = 1, 2, \cdots, N$. The notation for the IFS just announced is $\{X;\ w_n,\ with\ n = 1, 2, \cdots, N\}$ and its contractivity factor is $s = max\{s_n : n = 1, 2, \cdots, N\}$, $0 \leq s < 1$.*

The following theorem summarizes the main facts so far about an IFS.

Theorem 2.3. *Let $\{X;\ w_n,\ with\ n = 1, 2, \cdots, N\}$ be an iterated function system with contractivity factor s. Then the transformation $W : \mathcal{H}(X) \to \mathcal{H}(X)$ defined by*

$$W(B) = \bigcup_{n=1}^{N} w_n(B)$$

for all $B \in \mathcal{H}(X)$, is a contraction mapping on the complete metric space $(\mathcal{H}(X), h)$ with contractivity factor s. That is

$$h(W(B), W(C)) \leq s \cdot h(B, C)$$

for all $B, C \in \mathcal{H}(X)$. Its unique fixed point, $A \in \mathcal{H}(X)$, obeys

$$A = W(A) = \bigcup_{n=1}^{N} w_n(A)$$

and is given by $A = \lim_{n \to \infty} W^n(B)$ for any $B \in \mathcal{H}(X)$.

Definition 2.10. *The fixed point $A \in \mathcal{H}(X)$ described in the theorem is called the* ***attractor of the IFS****.*

With all this, we can now define a *fractal* as an attractor of an IFS.

2.2.4 The Collage Theorem

Once we have defined the concept of an Iterated Function System, we are going to see how to make fractal models by means of the Collage Theorem. This important theorem is based on the design of an IFS whose attractors are closed to given sets. Let's see this in detail.

Theorem 2.4. ***The Collage Theorem.***
Let (X, d) be a complete metric space. Let $L \in \mathcal{H}(X)$ be given, and let $\epsilon \geq 0$ be given too. Choose an IFS (or IFS with condensation) $\{X;\ (w_0), w_1, w_2, \cdots, w_N\}$ with contractivity factor $0 \leq s < 1$, so that

$$h(L, \bigcup_{n=1(n=0)}^{N} w_n(L)) \leq \epsilon,$$

where h is the Hausdorff metric. Then

$$h(L, A) \leq \epsilon/(1 - s),$$

where A is the attractor of the IFS. Equivalently,

$$h(L, A) \leq (1 - s)^{-1} \cdot h(L, \bigcup_{n=1(n=0)}^{N} w_n(L)) \quad \forall L \in \mathcal{H}(X).$$

This theorem tells us that to find an IFS whose attractor is "close to" or "looks like" a given set, one must find a set of transformations (i.e. contraction mappings on a suitable space where the given set lies) such that the union, or collage, of the images of the given set under the transformations is near to the given set. In other

words, given a set L, it tells us how to find an IFS for which L is the attractor. We use the Hausdorff metric to measure nearness.

The proof of the Collage Theorem is just the last part of the proof of the Contraction Mapping Theorem.

Finally, we have that an *artificial fractal* is an attractor of an IFS. Let's study now one of its main properties, the fractal dimension.

2.3 Fractal Dimension

From an early age, we learn that lines and curves are one-dimensional, planes and surfaces are two-dimensional, solids such as a cube are three-dimensional, and so on. In a formal way, we have the following definition.

Definition 2.11. *Let X be a subset of $\mathbb{R}^n$. We say that X has dimension zero if, for any point $p \in X$, there are arbitrarily small neighborhoods of p whose boundaries don't intersect the set. Inductively, we say that X has dimension n if there are arbitrarily small neighborhoods for any point $p \in X$ whose boundaries intersect X in a set of dimension $n-1$, being n the minimum natural number for which this is true.*

This notion of dimension is called the **topological dimension** of a set. Let's see some examples.

Example 1. Let's consider the set X as follows.

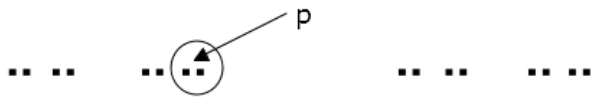

Figure 1: Set X

As we can see, for any point $p \in X$ there are arbitrarily small neighborhoods whose boundaries don't intersect the set. Then, according to the definition, the topological dimension of X is 0.

Example 2. Let's now consider the set Y shown in the image below.

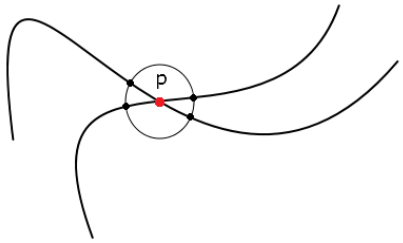

Figure 2: Set Y

We can observe that there are arbitrarily small neighborhoods for any point $p \in Y$ whose boundaries intersect Y in a set of dimension 0. Then, using the above definition, the topological dimension of the set Y is 1.

Example 3. Finally, let's consider the set Z as the one shown in the following image.

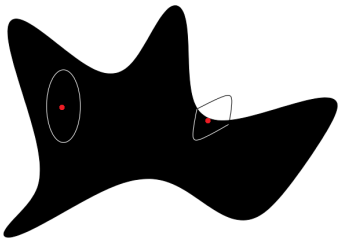

Figure 3: Set Z

According to Definition 2.11 once more, the topological dimension of Z is 2 (for any point of Z there are arbitrarily small neighborhoods whose boundaries intersect Z in a set of dimension 1).

Now, when it comes to fractals we need to be more specific. Imagine, for instance, that we want to know the dimension of the Koch Snowflake.

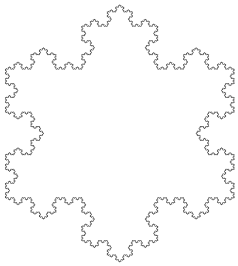

Figure 4: Koch Snowflake

According to Definition 2.11, it has topological dimension one (for any point of the Koch Snowflake, there are arbitrarily small neighborhoods whose boundaries intersect the fractal in a set of dimension zero). However, it is, by no means, a rectifiable curve (i.e. the length of the curve between any two points on the Koch Snowflake is infinite). No small piece of it is line-like, but consists of an infinite number of segments joined at different angles. The dimension of a curve can be explained intuitively thinking of a fractal line as an object too detailed to be one-dimensional, but too simple to be two-dimensional. Therefore, its dimension might best be described not by its usual topological dimension but by some other dimension, which in this case is a number between one and two. This new dimension is known as *fractal dimension*.

Fractal dimension is an attempt to quantify how densely a fractal occupies the metric space in which it lies. It is highly useful since it provides an objective means for comparing fractals, in particular, attractors of IFS's. Moreover, as we will see in next chapters, fractal dimension can be also applied in natural fractals where we can measure it approximately by experiments. In this way, fractal dimension is connected, for instance, to clouds, trees, coastlines, or to tumor interfaces as well. However, in this section we will focus on the fractal dimension of artificial fractals.

To start, we could give this informal definition. A **fractal dimension** is a ratio providing a statistical index of complexity comparing how detail in a fractal pattern changes with the scale at which it is measured. It does not have to be an integer.

Next, we are going to see formally the mathematical concept of fractal dimension, as well as some of its properties and theorems.

Let's focus on compact subsets of metric spaces. Let (X, d) denote a complete metric space, and let $A \in \mathcal{H}(X)$ be a nonempty compact subset of X. Let $\epsilon > 0$, and let $B(x, \epsilon)$ denote the closed ball of radius ϵ and center at a point $x \in X$. We define the integer $\mathcal{N}(A, \epsilon)$ as the least number of closed balls of radius ϵ needed to cover the set A. That is

$$\mathcal{N}(A, \epsilon) = \text{smallest positive integer } M \text{ such that } A \subset \bigcup_{n=1}^{M} B(x_n, \epsilon),$$

for some set of points $\{x_n : \ n = 1, 2, \cdots, M\} \subset X$. We know that there is such a number $\mathcal{N}(A, \epsilon)$ because of the compactness of the set A, since every open covering has a finite sub-covering.
The intuitive idea behind fractal dimension is that a set A has fractal dimension D if the number of closed balls needed to cover A grows exponentially fast when ϵ goes to zero. That is

$$\mathcal{N}(A, \epsilon) \approx C\epsilon^{-D} \text{ for some positive constant } C.$$

This notation means that $\lim_{\epsilon\to 0}\left\{\frac{\log(\mathcal{N}(A,\epsilon))}{\log(C\epsilon^{-D})}\right\}=1$. So, if we solve for D, we find that

$$D \approx \frac{\log(\mathcal{N}(A,\epsilon)) - \log C}{\log(1/\epsilon)}.$$

Since $\lim_{\epsilon\to 0}\left\{\frac{\log C}{\log(1/\epsilon)}\right\}=0$, it leads us to the following definition.

Definition 2.12. *Let $A \in \mathcal{H}(X)$ where (X,d) is a metric space. For each $\epsilon > 0$ let $\mathcal{N}(A,\epsilon)$ denote the smallest number of closed balls of radius $\epsilon > 0$ needed to cover A. If the limit*

$$D = \lim_{\epsilon\to 0}\left\{\frac{\log(\mathcal{N}(A,\epsilon))}{\log(1/\epsilon)}\right\}$$

*exists, then D is called the **fractal dimension of A**. We will also use the notation $D = D(A)$.*

Remark. But what happens if this limit doesn't exist? In order to avoid this problem, we are giving the following definition which provides a value for the fractal dimension for a wider collection of sets.

Let (X,d) be a complete metric space, and let $A \in \mathcal{H}(X)$. If

$$D_s = \lim_{\epsilon\to 0}\left\{\sup\left\{\frac{\log(\mathcal{N}(A,\tilde{\epsilon}))}{\log(1/\tilde{\epsilon})} : \tilde{\epsilon}\in(0,\epsilon)\right\}\right\} \overset{\texttt{DEF.}}{=} \limsup_{\epsilon\to 0}\left\{\frac{\log(\mathcal{N}(A,\epsilon))}{\log(1/\epsilon)}\right\}$$

exists, then D_s is called the **superior fractal dimension** of A.
In the same way, if

$$D_i = \lim_{\epsilon\to 0}\left\{\inf\left\{\frac{\log(\mathcal{N}(A,\tilde{\epsilon}))}{\log(1/\tilde{\epsilon})} : \tilde{\epsilon}\in(0,\epsilon)\right\}\right\} \overset{\texttt{DEF.}}{=} \liminf_{\epsilon\to 0}\left\{\frac{\log(\mathcal{N}(A,\epsilon))}{\log(1/\epsilon)}\right\}$$

exists, then D_i is called the **inferior fractal dimension** of A.

Therefore, if $D_s = D_i =: D$ we say that D is the fractal dimension of A.

As we can see, this extended definition is consistent with Definition 2.12. So if a set has dimension D according to Definition 2.12, then it has the same dimension according to the new one. Moreover, all the theorems we are going to see from now on apply with either definition. This latter definition is broader, so it provides a fractal dimension in some cases where the first one makes no assertion.

Theorem 2.5. *Let's consider the metric space $(\mathbb{R}^m, Euclidean)$, and let m be a positive integer. The fractal dimension $D(A)$ exists for all $A \in \mathcal{H}(\mathbb{R}^m)$. Let $B \in \mathcal{H}(\mathbb{R}^m)$ now be such that $A \subset B$, and let $D(B)$ denote the fractal dimension of B. Then $D(A) \le D(B)$. In particular,*

$$0 \le D(A) \le m.$$

In any case, the definition of fractal dimension of a set depends on the metric used. However, the following theorem tells us that metrically equivalent sets have same fractal dimension.

Theorem 2.6. *Let the metric spaces (X_1, d_1) and (X_2, d_2) be metrically equivalent. Let $\theta : X_1 \to X_2$ be a transformation that provides the equivalence of the spaces. Let $A_1 \in \mathcal{H}(X_1)$ have fractal dimension D. Then $A_2 = \theta(A_1)$ has fractal dimension D. That is*

$$D(A_1) = D(\theta(A_1)).$$

The next two theorems simplify the process of calculating the fractal dimension. Specially, they allow us to replace the continuous variable ϵ by a discrete variable.

Theorem 2.7. *Let $A \in \mathcal{H}(X)$, where (X, d) is a metric space. Let $\epsilon_n = Cr^n$ for real numbers $0 < r < 1$ and $C > 0$, and integers $n = 1, 2, 3, \cdots$ If*

$$D = \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}(A, \epsilon_n))}{\log(1/\epsilon_n)} \right\},$$

then A has fractal dimension D.

Proof. Let the real numbers r and C, and the sequence of numbers $E = \{\epsilon_n : \ n = 1, 2, 3, \cdots\}$ be as defined in the statement of the theorem. Define $f(\epsilon) = max\{\epsilon_n \in E : \ \epsilon_n \leq \epsilon\}$. Assume that $\epsilon \leq r$. Then

$$f(\epsilon) \leq \epsilon \leq f(\epsilon)/r \text{ and } \mathcal{N}(A, f(\epsilon)) \geq \mathcal{N}(A, \epsilon) \geq \mathcal{N}(A, f(\epsilon)/r).$$

Now, since $\log(x)$ is an increasing positive function of x for $x \geq 1$, it follows that

$$\left\{ \frac{\log(\mathcal{N}(A, f(\epsilon)/r))}{\log(1/f(\epsilon))} \right\} \leq \left\{ \frac{\log(\mathcal{N}(A, \epsilon))}{\log(1/\epsilon)} \right\} \leq \left\{ \frac{\log(\mathcal{N}(A, f(\epsilon)))}{\log(r/f(\epsilon))} \right\}. \tag{2.2}$$

Assume that $\mathcal{N}(A, \epsilon) \to \infty$ as $\epsilon \to 0$. If not, then the theorem is true. Therefore, the right-hand side of equation 2.2 obeys

$$\lim_{\epsilon\to 0} \left\{ \frac{\log(\mathcal{N}(A, f(\epsilon)))}{\log(r/f(\epsilon))} \right\} = \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}(A, \epsilon_n))}{\log(r/\epsilon_n)} \right\}$$

$$= \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}(A, \epsilon_n))}{\log(r) + \log(1/\epsilon_n)} \right\} = \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}(A, \epsilon_n))}{\log(1/\epsilon_n)} \right\}$$

since $f(\epsilon) = \epsilon_n$ for some $n = 1, 2, 3, \cdots$.

The left-hand side of equation 2.2 obeys

$$\lim_{\epsilon\to 0} \left\{ \frac{\log(\mathcal{N}(A, f(\epsilon)/r))}{\log(1/f(\epsilon))} \right\} = \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}(A, \epsilon_{n-1}))}{\log(1/\epsilon_n)} \right\}$$

$$= \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}(A, \epsilon_{n-1}))}{\log(1/r) + \log(1/\epsilon_{n-1})} \right\} = \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}(A, \epsilon_n))}{\log(1/\epsilon_n)} \right\}$$

since $f(\epsilon)/r = \epsilon_n/r = Cr^{n-1} = \epsilon_{n-1}$ for some $n = 1, 2, 3, \cdots$.

So as $\epsilon \to 0$, both the left-hand side and the right-hand side of equation 2.2 approach the same value claimed in the theorem. By the Sandwich Theorem of calculus, the limit as $\epsilon \to 0$ of the quantity in the middle of equation 2.2 also exist, and it equals the same value. That is

$$\lim_{\epsilon\to 0} \left\{ \frac{\log(\mathcal{N}(A, \epsilon))}{\log(1/\epsilon)} \right\} = \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}(A, \epsilon_n))}{\log(1/\epsilon_n)} \right\} \overset{\texttt{HIP}}{=} D.$$

This completes the proof. □

The most important result of this section is the theorem below, since it provides a very useful method of computing the fractal dimension of an object. In particular, an artificial fractal. But as we will see in the following chapters, it can be used to compute the fractal dimension of natural fractals as well.

Theorem 2.8. ***The Box Counting Theorem.***
Let $A \in \mathcal{H}(\mathbb{R}^m)$, where the Euclidean metric is used. Cover $\mathbb{R}^m$ with a grid whose square boxes have side length $1/2^n$. Let $\mathcal{N}_n(A)$ denote the number of boxes of side length $1/2^n$ which intersect the attractor. If

$$D = \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}_n(A))}{\log(2^n)} \right\},$$

then A has fractal dimension D.

Proof. Since the Euclidean metric is equivalent to the metric derived from the uniform norm (or sup norm), the fractal dimension is the same for both metrics. Therefore, we are going to use the second one to prove the theorem.
To start, we have that

$$2^{-m}\mathcal{N}_{n-1}(A) \le \mathcal{N}(A, 1/2^n) \le \mathcal{N}_{n-1}(A) \text{ for all } n = 1, 2, 3, \cdots$$

The first inequality holds because a square box of radius $1/2^n$ can intersect at most 2^m "on-grid" boxes of side length $1/2^{n-1}$. The second one, because $\mathcal{N}(A, 1/2^n)$ is the minimum closed covering of A. Now, since $\log(x)$ is an increasing positive function of x for $x \ge 1$, it follows that

$$\left\{ \frac{\log(2^{-m}\mathcal{N}_{n-1}(A))}{\log(2^n)} \right\} \le \left\{ \frac{\log(\mathcal{N}(A, 1/2^n))}{\log(2^n)} \right\} \le \left\{ \frac{\log(\mathcal{N}_{n-1}(A))}{\log(2^{n-1})} \right\}. \tag{2.3}$$

On the one hand, the right-hand side of the equation 2.3 obeys

$$\lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}_{n-1}(A))}{\log(2^{n-1})} \right\} = \lim_{n\to\infty} \left\{ \frac{\log(\mathcal{N}_n(A))}{\log(2^n)} \right\} \overset{\texttt{HIP}}{=} D.$$

On the other hand, the left-hand side of the equation 2.3 obeys

$$\lim_{n\to\infty}\left\{\frac{\log(2^{-m}\mathcal{N}_{n-1}(A))}{\log(2^n)}\right\} = \lim_{n\to\infty}\left\{\frac{\log(2^{-m})+\log(\mathcal{N}_{n-1}(A))}{\log(2^n)}\right\}$$

$$= \lim_{n\to\infty}\left\{\frac{\log(\mathcal{N}_{n-1}(A))}{\log(2^n)}\right\} = \lim_{n\to\infty}\left\{\frac{\log(\mathcal{N}_n(A))}{\log(2^n)}\right\} \overset{\texttt{HIP}.}{=} D.$$

So as $n \to \infty$, both the left-hand side and the right-hand side of equation 2.3 approach the same value. By the Sandwich Theorem of calculus again, the limit as $n \to \infty$ of the quantity in the middle of equation 2.3 also exist, and it equals the same value. Theorem 2.7 with $r = 1/2$ and $C = 1$ completes the proof.

$$D \overset{\texttt{HIP}.}{=} \lim_{n\to\infty}\left\{\frac{\log(\mathcal{N}(A,1/2^n))}{\log(2^n)}\right\} \overset{\texttt{Th 2.8}}{=} \lim_{\epsilon\to 0}\left\{\frac{\log(\mathcal{N}(A,\epsilon))}{\log(1/\epsilon)}\right\}.$$

□

We have used boxes of side $1/2^n$ in Theorem 2.8 as an example. We could equally well use boxes of side Cr^n, where $C > 0$ and $0 < r < 1$ are fixed real numbers.

Finally, we are going to connect the concept of fractal dimension to the IFS one. To do this, we are giving the following theorem which provides the fractal dimension of the attractor of an important class of IFS. It also allow us to estimate fractal dimensions simply using pictures of fractals.

Theorem 2.9. *Let $\{\mathbb{R}^m;\ w_1, w_2, \cdots, w_N\}$ be an IFS, and let A denote its attractor. Suppose that each w_n is a similitude of scaling factor $0 \le s_n < 1$ for each $n \in \{1, 2, \cdots, N\}$. If the IFS is totally disconnected or just-touching then the attractor has fractal dimension $D(A)$, which is given by the unique solution of*

$$\sum_{n=1}^{N} |s_n|^{D(A)} = 1, \quad D(A) \in [0, m].$$

If the IFS is overlapping, then $\overline{D} \ge D(A)$, where $\overline{D}$ is the solution of

$$\sum_{n=1}^{N} |s_n|^{\overline{D}} = 1, \quad \overline{D} \in [0, \infty).$$

Remark. We say that an IFS is *totally disconnected* if each point of its attractor possesses a unique address. In the same way, we say that an IFS is *just-touching* if it is not totally disconnected and if its attractor contains an open set $\mathcal{O}$ such that (i) $w_i(\mathcal{O}) \cap w_l(\mathcal{O}) = \emptyset$ for all $i, l \in \mathbb{N}$ and (ii) $\bigcup_{i=1}^{N} w_i(\mathcal{O}) \subset \mathcal{O}$. Finally, an IFS with some attractor A is said to be *overlapping* if for some w_i, w_j there exists an open set $\mathcal{P}$ such that $\mathcal{P} \subset w_i(A) \cap w_j(A)$.

In order to show this theorem, let's see some examples.

Example 4. Let's consider the totally disconnected IFS $\{[0,1]\,;\ w_1, w_2\}$, where

$$w_1(x) = \frac{1}{3}x$$

$$w_2(x) = \frac{1}{3}x + \frac{2}{3}$$

are two similitudes of scaling factor $\frac{1}{3}$. The attractor of this IFS is the Cantor set.

Figure 5: First iterations of the IFS whose limit is the Cantor set.

According to the theorem above, the dimension of the Cantor Set is the unique solution D of the equation

$$\sum_{n=1}^{2} |s_n|^D = 1 \iff |1/3|^D + |1/3|^D = 1 \iff 2 \cdot (1/3)^D = 1.$$

If we solve for D, we obtain that

$$D = \frac{\log(1/2)}{\log(1/3)} = \frac{\log(2)}{\log(3)} \approx 0.63.$$

Therefore, the fractal dimension of the Cantor Set (attractor of the totally disconnected IFS $\{[0,1]\,;\ w_1, w_2\}$) is 0.63.

Example 5. Let's now consider the metric space $(\mathbb{R}^2,\ \textit{Euclidean})$, and the similitudes w_1, w_2 and w_3 defined as follows

$$w_1 \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} 0.5 & 0 \\ 0 & 0.5 \end{pmatrix} \cdot \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \end{pmatrix},$$

$$w_2 \begin{pmatrix} y_1 \\ y_2 \end{pmatrix} = \begin{pmatrix} 0.5 & 0 \\ 0 & 0.5 \end{pmatrix} \cdot \begin{pmatrix} y_1 \\ y_2 \end{pmatrix} + \begin{pmatrix} 0.5 \\ 0 \end{pmatrix},$$

$$w_3\begin{pmatrix} z_1 \\ z_2 \end{pmatrix} = \begin{pmatrix} 0.5 & 0 \\ 0 & 0.5 \end{pmatrix} \cdot \begin{pmatrix} z_1 \\ z_2 \end{pmatrix} + \begin{pmatrix} 0 \\ 0.5 \end{pmatrix}.$$

Then, $\{\mathbb{R}^2;\ w_1, w_2, w_3\}$ is a just-touching IFS of three similitudes of scaling factor 0.5. Moreover, the attractor of this IFS is the Sierpinski Triangle.

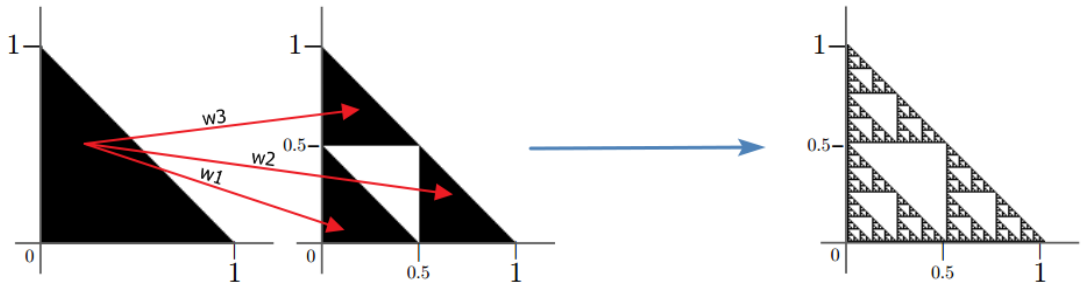

Figure 6: Similitudes and Attractor of the IFS

Now, according to Theorem 2.9, the fractal dimension of the Sierpinski Triangle is the unique solution D of the equation

$$\sum_{n=1}^{3} |s_n|^D = 1 \iff |0.5|^D + |0.5|^D + |0.5|^D = 1 \iff 3 \cdot (0.5)^D = 1.$$

If we solve for D, we find that

$$D = \frac{\log(1/3)}{\log(0.5)} = \frac{\log(3)}{\log(2)} \approx 1.58.$$

Therefore, the fractal dimension of the Sierpinski Triangle (attractor of the just-touching IFS $\{\mathbb{R}^2;\ w_1, w_2, w_3\}$) is 1.58.

Example 6. Finally, let's consider the metric space ($\mathbb{R}^2$, *Euclidean*) once more, and the similitudes w_1, w_2, w_3 and w_4 defined as follows

$$w_1\begin{pmatrix} x_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} 1/3 & 0 \\ 0 & 1/3 \end{pmatrix} \cdot \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \end{pmatrix},$$

$$w_2\begin{pmatrix} y_1 \\ y_2 \end{pmatrix} = \begin{pmatrix} 1/6 & -\sqrt{3}/6 \\ \sqrt{3}/6 & 1/6 \end{pmatrix} \cdot \begin{pmatrix} y_1 \\ y_2 \end{pmatrix} + \begin{pmatrix} 1/3 \\ 0 \end{pmatrix},$$

$$w_3\begin{pmatrix} z_1 \\ z_2 \end{pmatrix} = \begin{pmatrix} 1/6 & \sqrt{3}/6 \\ -\sqrt{3}/6 & 1/6 \end{pmatrix} \cdot \begin{pmatrix} z_1 \\ z_2 \end{pmatrix} + \begin{pmatrix} 1/2 \\ \sqrt{3}/6 \end{pmatrix},$$

$$w_4 \begin{pmatrix} t_1 \\ t_2 \end{pmatrix} = \begin{pmatrix} 1/3 & 0 \\ 0 & 1/3 \end{pmatrix} \cdot \begin{pmatrix} t_1 \\ t_2 \end{pmatrix} + \begin{pmatrix} 2/3 \\ 0 \end{pmatrix}.$$

Then, $\{\mathbb{R}^2;\ w_1, w_2, w_3, w_4\}$ is a just-touching IFS of four similitudes of scaling factor $1/3$. Moreover, the attractor of this IFS is the Koch Curve.

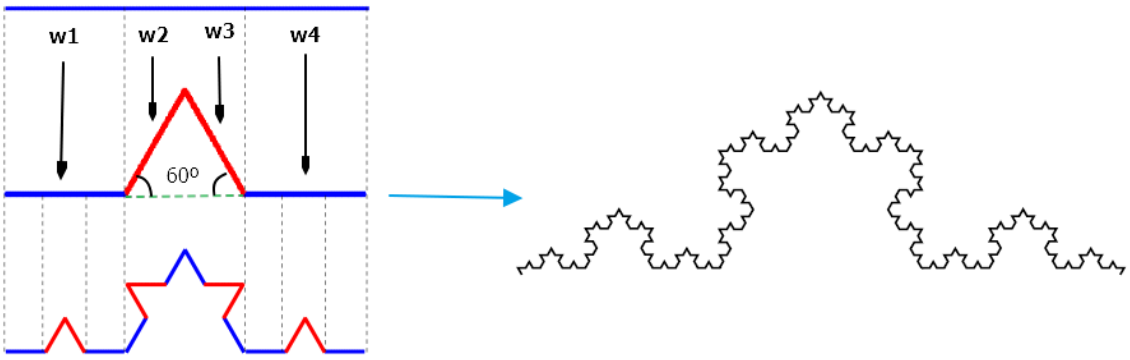

Figure 7: Similitudes and Attractor of the IFS

Now, according to Theorem 2.9 again, the fractal dimension of the Koch Curve is the unique solution D of the equation

$$\sum_{n=1}^{4} |s_n|^D = 1 \iff |1/3|^D + |1/3|^D + |1/3|^D + |1/3|^D = 1 \iff 4 \cdot (1/3)^D = 1.$$

If we solve for D, we find that

$$D = \frac{\log(1/4)}{\log(1/3)} = \frac{\log(4)}{\log(32)} \approx 1.26.$$

Therefore, the fractal dimension of the Koch Curve (attractor of the just-touching IFS $\{\mathbb{R}^2;\ w_1, w_2, w_3, w_4\}$) is 1.26.

With all this, we are finally able to define rigorously the fractal objects. To do this, we are using the box-counting dimension as follows.

Definition 2.13. *An **artificial fractal** is an object so that its fractal dimension is larger than its topological dimension.*

3 Fractal Interpolation

Another concept closely related to fractals, that will be developed throughout this chapter, is the fractal interpolation functions. As a preview, we say that a function f is a *fractal interpolation function* if its graph is the attractor of an IFS, under some conditions we later study.

What links these functions with fractals is that they present self-similarity, although only for a range of scales. Even so, its fractal character makes that we can apply them what we have studied so far. That is, we can use IFS's to construct these fractal interpolation functions as well as the Box Counting Theorem to compute the fractal dimension of their graphs.

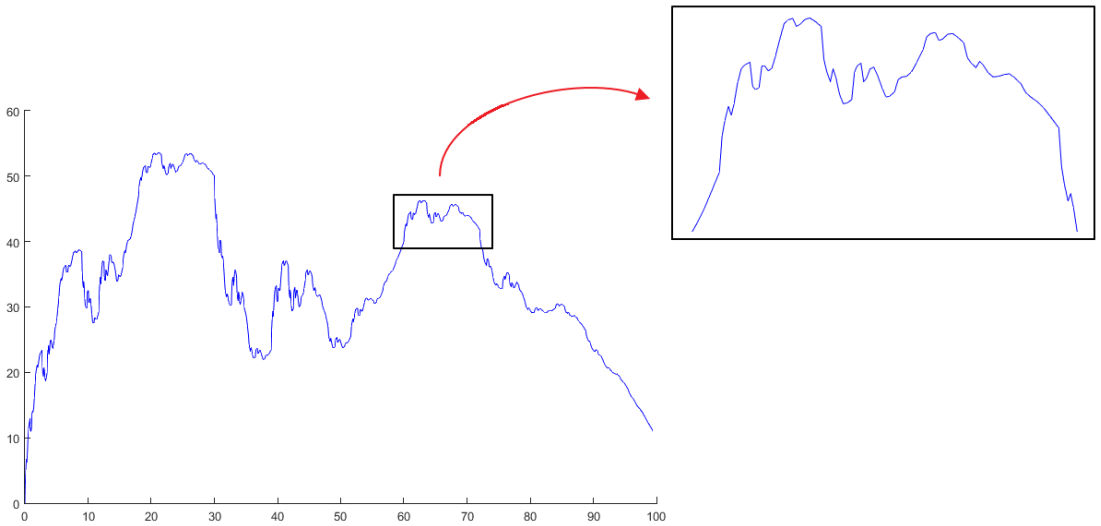

Figure 8: Self-similarity of fractal interpolation functions. The graph is made by running program A.1, see details in Appendix.

3.1 Introduction

Let $\{(x_i, y_i) : i = 0, 1, \cdots, N\} \subset \mathbb{R}^2$, $N > 1$, be a discrete data set such that $x_0 < x_1 < \cdots < x_N$. In many engineering and science tasks, we often have a number of data points, such as the one described above, obtained by sampling or experimentation, which represent the values of a function for a limited number of values of the independent variable. Interpolation is a method of constructing a continuous function f that fits the given points, that is, $f(x_i) = y_i$ for each $i = 0, 1, \cdots, N$. Usually, such a function is called an **interpolation function**. Interpolation can be employed for various purposes. One of the most common is to estimate the value of the implied function for an intermediate value of the independent variable (i.e., a value other that $x_0, x_1, \cdots, x_N$).

There are several interpolation methods that can be applied to a specific data set, according to the assumptions that underlie the model we investigate. Usually, these assumptions include smoothness and simplicity. The most popular methods are the piecewise constant interpolation, the piecewise linear interpolation and the polynomial interpolation. We can see an example of each below.

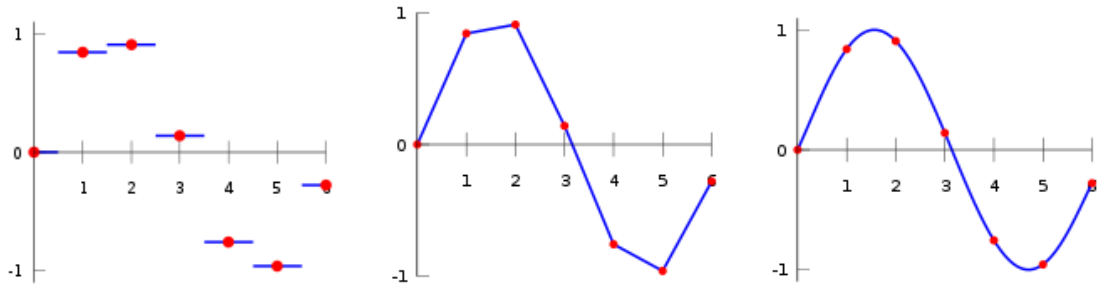

Figure 9: On the left, piecewise constant interpolation. In the middle, plot of a set of data with piecewise linear interpolation superimposed. And on the right, plot of a set of data with polynomial interpolation applied.

Most interpolation functions are given as linear combinations of elementary functions. For instance, a linear combination of monomials leads to polynomial interpolation functions. We can employ trigonometric, logarithmic, or exponential functions as well.

However, in the case where the given data set is more complex (for example, data that are generated by cardiogram, seismogram, stock exchange...) the models mentioned above, which usually assume smoothness, cannot give satisfactory results. In this cases, we will employ methods with functions whose graphs have fractal characteristics. Such functions are called **fractal interpolation functions**, and will be introduced over this chapter.

Fractal interpolation functions can be used to interpolate any form of experimental data, and their construction is based on the generation of an appropriate IFS whose attractors interpolate the given data. The graphs of these functions can be used to approximate image components such as the profiles of mountain ranges, the tops of clouds, or the interfaces of tumors as we will see in Chapter 4. In all these cases it is not sufficient to make a polynomial "least-squares" fit. That is why we need fractal interpolation functions to "fit" such experimental data. That is, the graph of the fractal interpolation function can be made close, in the Hausdorff metric, to the data. Moreover, we can ensure that the fractal dimension of the graph of the fractal interpolation function agrees with that of the data, over an appropriate range of scales.

Fractal interpolation functions share with elementary functions that they are of a geometrical character, that they can be represented by "formulas", and that they

can be computed rapidly. The main difference is their fractal character. Fractal interpolation functions can have a non-integer fractal dimension while the fractal dimension of elementary functions is always 1.

3.2 Fractal Interpolation Functions

Definition 3.1. *A **set of data** is a set of points of the form* $\{(x_i, y_i) \in \mathbb{R}^2 : \ i = 0, 1, 2, \cdots, N\}$*, where*

$$x_0 < x_1 < x_2 < x_3 < \cdots < x_N.$$

*An **interpolation function** corresponding to this set of data is a continuous function* $f : [x_0, x_N] \to \mathbb{R}$ *such that*

$$f(x_i) = y_i \quad for \quad i = 0, 1, \cdots, N.$$

The points $(x_i, y_i) \in \mathbb{R}^2$ *are called the **interpolation points**. We say that the function* f *interpolates the data and that (the graph of)* f *passes through the interpolation points.*

Let $\Delta = \{(x_i, y_i) \in \mathbb{R}^2 : \ i = 0, 1, 2, \cdots, N\}$ be a set of data. The question now is how to construct an IFS in $\mathbb{R}^2$ whose attractor, which we denote by G, is the graph of a continuous function $f : [x_0, x_N] \to \mathbb{R}$ which interpolates the data. We will restrict to IFS's whose maps are affine transformations.
Let's consider then an IFS of the form $\{\mathbb{R}^2;\ w_n : \ n = 1, 2, \cdots, N\}$, where the maps are affine transformations of the special structure

$$w_n \begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} a_n & 0 \\ c_n & d_n \end{pmatrix} \cdot \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} e_n \\ f_n \end{pmatrix}.$$

Such transformations are called *shear* transformation, because they map line segments parallel to the y-axis to line segments parallel to the y-axis. Moreover, the ratio of the length of $w_n(L)$ to the length of L is $|d_n|$ for all $n = 1, 2, \cdots, N$. We call d_n the **vertical scaling factor** in the transformation w_n.

Now, in order to ensure that the attractor of the IFS will pass through the interpolation points, we impose that w_n maps the endpoints of Δ, i.e. (x_0, y_0) and (x_N, y_N), to (x_{n-1}, y_{n-1}) and (x_n, y_n) respectively. We can see this fact in Figure 10 below.

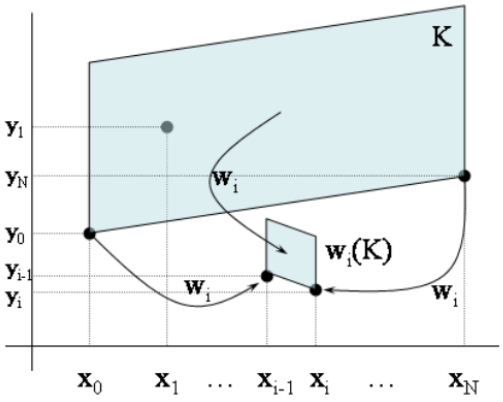

Figure 10: An affine map w_i.

Hence, we take:

$$w_n \begin{pmatrix} x_0 \\ y_0 \end{pmatrix} = \begin{pmatrix} x_{n-1} \\ y_{n-1} \end{pmatrix} \quad \text{and} \quad w_n \begin{pmatrix} x_N \\ y_N \end{pmatrix} = \begin{pmatrix} x_n \\ y_n \end{pmatrix} \quad \text{for} \quad n = 1, 2, \cdots, N.$$

Then the transformation w_n is specified by the five real numbers a_n, c_n, d_n, e_n, and f_n, which must obey the four linear equations

$$a_n \cdot x_0 + e_n = x_{n-1}, \tag{3.1}$$

$$a_n \cdot x_N + e_n = x_n, \tag{3.2}$$

$$c_n \cdot x_0 + d_n \cdot y_0 + f_n = y_{n-1}, \tag{3.3}$$

$$c_n \cdot x_N + d_n \cdot y_N + f_n = y_n. \tag{3.4}$$

Therefore we have 5N unknowns and 4N equations. It follows that there is effectively one free parameter in each transformation (i.e. a total of N). We choose this parameter to be d_n since w_n is a *shear* transformation. In this way, we are able to specify the vertical scaling produced by the transformation. With $d_n = 0$, for $n = 1, 2, \cdots, N$, the piecewise linear interpolation function is recovered. We will later see that these parameters determine the fractal dimension of the attractor of the IFS.

Assuming that d_n is the free parameter, the linear system has a unique solution for a_n, c_n, e_n, and f_n for every selection of interpolation points:

$$a_n = \frac{x_n - x_{n-1}}{x_N - x_0},$$

$$e_n = \frac{x_N x_{n-1} - x_0 x_n}{x_N - x_0},$$

$$c_n = \frac{y_n - y_{n-1}}{x_N - x_0} - \frac{d_n(y_N - y_0)}{x_N - x_0},$$

$$f_n = \frac{x_N y_{n-1} - x_0 y_n}{x_N - x_0} - \frac{d_n(x_N y_0 - x_0 y_N)}{x_N - x_0}.$$

The IFS arising from these conditions is $\{\mathbb{R}^2;\ w_n : n = 1, 2, \cdots, N\}$, and will be denoted as the *IFS associated to* Δ.

Let the vertical scaling factor d_n obey $0 \leq d_n < 1$ for $n = 1, 2, \cdots, N$. Even with this condition, the IFS is not, in general, hyperbolic on the metric space $(\mathbb{R}^2, \textit{Euclidean})$. This means that the affine transformations w_n are not necessarily contraction mappings. The question now would be, is there a metric such that the IFS is hyperbolic? The answer to this question is in the theorem below.

Theorem 3.1. *Let $N > 1$ be a positive integer. Let $\{\mathbb{R}^2;\ w_n :\ n = 1, 2, \cdots, N\}$ denote the IFS defined above, associated with the data set*

$$\{(x_n, y_n) : n = 0, 1, \cdots, N\}.$$

Let the vertical scaling factor d_n obey $0 \leq d_n < 1$ for $n = 1, 2, \cdots, N$. Then there is a metric d on $\mathbb{R}^2$, equivalent to the Euclidean metric, such that the IFS is hyperbolic with respect to d. In particular, there is a unique nonempty compact set $G \subset \mathbb{R}^2$ such that

$$G = \bigcup_{n=1}^{N} w_n(G).$$

Proof. Let's define a metric d on $\mathbb{R}^2$ by

$$d((x_1, y_1), (x_2, y_2)) = |x_1 - x_2| + \theta|y_1 - y_2|,$$

where θ is a positive real number which we specify below.

Let's prove that this metric d is equivalent to the Euclidean metric on $\mathbb{R}^2$. Since the Euclidean metric is equivalent to the Manhattan metric, it is enough to show that the metric d defined above and the Manhattan metric on $\mathbb{R}^2$ are equivalent. Recall that the Manhattan metric, d_M, is defined by $d_M((x_1, y_1), (x_2, y_2)) = |x_1 - x_2| + |y_1 - y_2|$. Let's consider the following cases:
If $\theta = 1$, then the two metrics d and d_M are the same. Therefore, equivalent.
If $\theta > 1$, then since $\theta|y_1 - y_2| \geq |y_1 - y_2|$ we have that $d((x_1, y_1), (x_2, y_2)) \geq d_M((x_1, y_1), (x_2, y_2))$. In the same way, since $\frac{1}{\theta}|x_1 - x_2| \leq |x_1 - x_2|$ we have that

$$\frac{1}{\theta} d((x_1, y_1), (x_2, y_2)) \leq d_M((x_1, y_1), (x_2, y_2)) \leq d((x_1, y_1), (x_2, y_2)).$$

Hence, both metrics are equivalent.
Finally, if $\theta < 1$ then we have, by the same argument, that

$$\theta \cdot d_M((x_1, y_1), (x_2, y_2)) \leq d((x_1, y_1), (x_2, y_2)) \leq d_M((x_1, y_1), (x_2, y_2)).$$

Again, both metrics are equivalent.
It is then proved that the metric d is equivalent to the Euclidean metric on $\mathbb{R}^2$.

Now, let $n \in \{1, 2, \cdots, N\}$. Let the numbers a_n, c_n, e_n, f_n be defined by equations (3.1), (3.2), (3.3), and (3.4). Then we have that

$$\begin{aligned} & d(w_n(x_1, y_1), w_n(x_2, y_2)) \\ & \qquad = d((a_n x_1 + e_n, c_n x_1 + d_n y_1 + f_n), (a_n x_2 + e_n, c_n x_2 + d_n y_2 + f_n)) \\ & \qquad = a_n \cdot |x_1 - x_2| + \theta \cdot |c_n(x_1 - x_2) + d_n(y_1 - y_2)| \\ & \qquad \leq (|a_n| + \theta \cdot |c_n|) \cdot |x_1 - x_2| + \theta \cdot |d_n| \cdot |y_1 - y_2| \end{aligned}$$

We notice that $|a_n| = |x_n - x_{n-1}|/|x_N - x_0| < 1$ since $N \geq 2$. If $c_i = 0$ for each $i = 1, \cdots, n$, then we choose $\theta = 1$. Otherwise we choose

$$\theta = \frac{\min\{(2 - |a_n|) \ : \ n = 1, 2, \cdots, N\}}{\max\{2 \cdot |c_n| \ : \ n = 1, 2, \cdots, N\}}.$$

Then it follows that

$$\begin{aligned} d(w_n(x_1, y_1), w_n(x_2, y_2)) & \leq (|a_n| + \theta \cdot |c_n|) \cdot |x_1 - x_2| + \theta \cdot |d_n| \cdot |y_1 - y_2| \\ & \leq a \cdot |x_1 - x_2| + \theta \cdot \delta \cdot |y_1 - y_2| \\ & \leq \max\{a, \delta\} \cdot d((x_1, y_1), (x_2, y_2)), \end{aligned}$$

where

$$\begin{aligned} a = (1 + a_n - \frac{\max\{|a_n| \ : \ n = 1, 2, \cdots, N\}}{2}) < 1, \\ \delta = \max\{|d_n| \ : \ n = 1, 2, \cdots, N\} < 1. \end{aligned}$$

Therefore, w_n is a contraction mapping for each $n = 1, 2, \cdots, N$. This completes the proof. □

Theorem 3.2. *Let $N > 1$ be a positive integer. Let $\{\mathbb{R}^2;\ w_n : \ n = 1, 2, \cdots, N\}$ denote the IFS defined above, associated with the data set $\{(x_n, y_n) : n = 1, 2, \cdots, N\}$. Let the vertical scaling factor d_n obey $0 \leq d_n < 1$ for $n = 1, 2, \cdots, N$, so that the IFS is hyperbolic. Let G denote the attractor of the IFS. Then G is the graph of a continuous function $f : [x_0, x_N] \to \mathbb{R}$, which interpolates the data $\{(x_i, y_i) : i = 1, 2, \cdots, N\}$. That is,*

$$G = \{(x, f(x)) : \ x \in [x_0, x_N]\},$$

where

$$f(x_i) = y_i \quad \textit{for} \quad i = 0, 1, 2, \cdots, N.$$

Proof. Let $\mathcal{F}$ denote the set of continuous functions $f : [x_0, x_N] \to \mathbb{R}$ such that $f(x_0) = y_0$ and $f(x_N) = y_N$. We define a metric d on $\mathcal{F}$ by

$$d(f, g) = \max\{|f(x) - g(x)| \ : \ x \in [x_0, x_N]\} \quad \text{for all} \quad f, g \in \mathcal{F},$$

so that $(\mathcal{F}, d)$ is a complete metric space. Let the real numbers a_n, c_n, e_n, f_n, be defined by equations (3.1), (3.2), (3.3), and (3.4). We now define a graph transformation $T : \mathcal{F} \to \mathcal{F}$ by

$$(Tf)(x) = c_n l_n^{-1}(x) + d_n \cdot f(l_n^{-1}(x)) + f_n$$

for $x \in [x_{n-1}, x_n]$ and for $n = 1, 2, \cdots, N$, where $l_n : [x_0, x_N] \to [x_{n-1}, x_n]$ is the invertible transformation $l_n(x) = a_n \cdot x + e_n$.

First, we are going to verify that T does indeed take $\mathcal{F}$ into itself. Let $f \in \mathcal{F}$. Then the function $(Tf)(x)$ obeys the endpoint conditions since

$$\begin{aligned}(Tf)(x_0) &= c_1 l_1^{-1}(x_0) + d_1 \cdot f(l_1^{-1}(x_0)) + f_n \\ &= c_1 x_0 + d_1 \cdot f(x_0) + f_n = c_1 x_0 + d_1 y_0 + f_n \\ &= y_0\end{aligned}$$

and

$$\begin{aligned}(Tf)(x_N) &= c_N l_N^{-1}(x_N) + d_N \cdot f(l_N^{-1}(x_N)) + f_N \\ &= c_N x_N + d_N \cdot f(x_N) + f_N \\ &= c_N x_N + d_N y_N.\end{aligned}$$

This function $(Tf)(x)$ is continuous on the interval $[x_{n-1}, x_n]$ for $n = 1, 2, \cdots, N$. So what is left to demonstrate is that $(Tf)(x)$ is continuous at each of the points $x_1, x_2, \cdots, x_{N-1}$. At each of these points, the value of $(Tf)(x)$ is apparently defined in two different ways. For $n \in \{1, 2, \cdots, N-1\}$ we have that

$$\begin{aligned}(Tf)(x_n) &= c_{n+1} l_{n+1}^{-1}(x_n) + d_{n+1} \cdot f(l_{n+1}^{-1}(x_n)) + f_{n+1} \\ &= c_{n+1} x_0 + d_{n+1} \cdot f(x_0) + f_{n+1} = y_n\end{aligned}$$

and also that

$$\begin{aligned}(Tf)(x_n) &= c_n l_n^{-1}(x_n) + d_n \cdot f(l_n^{-1}(x_n)) + f_n \\ &= c_n x_N + d_n \cdot f(x_N) + f_n = y_n,\end{aligned}$$

so both methods of evaluation lead to the same result. Therefore, we conclude that T does indeed take $\mathcal{F}$ into $\mathcal{F}$.

Now we are going to show that T is a contraction mapping on the metric space $(\mathcal{F}, d)$. Let $f, g \in \mathcal{F}$. Let $n \in \{1, 2, \cdots, N\}$ and $x \in [x_{n-1}, x_n]$. Then

$$|(Tf)(x) - (Tg)(x)| = |d_n| \cdot |f(l_n^{-1}(x)) - g(l_n^{-1}(x))| \leq |d_n| \cdot d(f, g).$$

It follows that

$$d(Tf, Tg) \leq \delta \cdot d(f, g) \quad \text{where} \quad \delta = \max\{|d_n| \ : \ n = 1, 2, \cdots, N\} < 1.$$

Then, we conclude that $T : \mathcal{F} \to \mathcal{F}$ is a contraction mapping. By the Contraction Mapping Theorem we know that T possesses a unique fixed point in $\mathcal{F}$. That is, there exists a unique function $f \in \mathcal{F}$ such that

$$(Tf)(x) = f(x) \quad \text{for all } x \in [x_0, x_N].$$

Moreover, this function f passes through the interpolation points.

Finally, let $\tilde{G}$ denote the graph of f. Notice that the equations that define T can be rewritten as

$$(Tf)(a_n x + e_n) = c_n x + d_n f(x) + f_n \quad \text{for} \quad x \in [x_0, x_N] \quad \text{and for} \quad n = 1, 2, \cdots, N,$$

which implies that

$$\tilde{G} = \bigcup_{n=1}^{N} w_n(\tilde{G}).$$

But $\tilde{G}$ is a nonempty compact subset of $\mathbb{R}^2$. By Theorem 3.1, there is only one nonempty compact set G, the attractor of the IFS, which obeys the latter equation. Therefore, it follows that $\tilde{G} = G$. This completes the proof. □

Remark. Why do both of theorems above have the restriction that N is greater than 1? Well, if we look at any hyperbolic IFS of the form $\{\mathbb{R}^2;\ w_1(x, y)\}$, then by definition, w_1 is a contraction mapping and the attractor of the IFS is a single point. But for $N = 1$, the curve we are attempting to interpolate has two interpolation points. Hence the attempt will fail.

Now, we are able to define what is called fractal interpolation functions.

Definition 3.2. *The function $f(x)$ whose graph is the attractor of an IFS as described in Theorems 3.1 and 3.2 above, is called a* ***fractal interpolation function*** *corresponding to the data $\{(x_i, y_i) : i = 1, 2, \cdots, N\}$.*

Example 1. In Figure 11 below, we can see an example of a sequence of iterates $\{T^n f_0 : \ n = 0, 1, 2, 3, \cdots\}$ obtained by repeated application of the contraction mapping T introduced in the proof of Theorem 3.2. The initial function $f_0(x)$ is linear, and the sequence $\{f_{n+1}(x) = (Tf_n)(x)\}$ converges to the fractal interpolation function f, which is the fixed point of T.

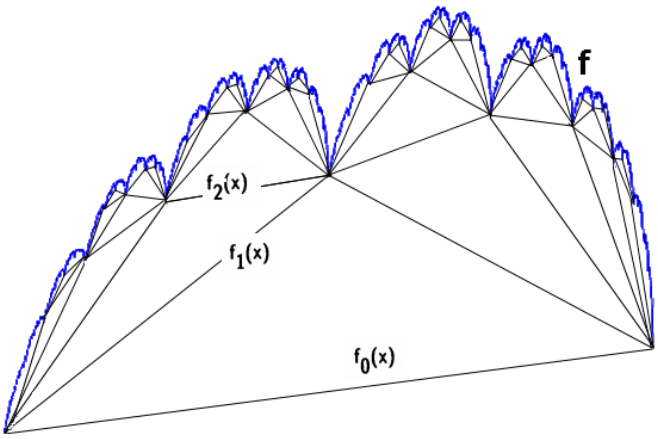

Figure 11: Example of a Fractal Interpolation Function. The graph is made by running program A.2, see details in Appendix.

At this point, in view of the proof of Theorem 3.2, we may wonder why going to the trouble of establishing that there is a metric such that the IFS is contractive. After all, we could simply use the contraction mapping T to construct fractal interpolation functions. The answer has two main parts.
The first one is that, in this way, we are able to apply the theory of hyperbolic IFS, seen in Chapter 2, to fractal interpolation functions. In particular, this means that we can use IFS algorithms to construct fractal interpolation functions, that we can use the Collage Theorem to find fractal interpolation functions which approximate given data, and that we can use the Hausdorff metric to discuss the accuracy of approximation of experimental data by a fractal interpolation function.
The second one is that we can provide a common language for the description of an important class of functions and sets by treating fractal interpolation functions as attractors of IFS of affine transformations. This common language is what is known as IFS code.

One consequence of the fact that the IFS $\{\mathbb{R};\ w_n :\ n = 1, 2, \cdots, N\}$ associated with a set of data $\{(x_n, y_n) : n = 1, 2, \cdots, N\}$ is hyperbolic is that any set $A_0 \in \mathcal{H}(\mathbb{R}^2)$ leads to a Cauchy sequence of sets $\{A_n\}$ that converges to G in the Hausdorff metric. As in Chapter 2, we can define $W : \mathcal{H}(\mathbb{R}^2) \to \mathcal{H}(\mathbb{R}^2)$ by

$$W(B) = \bigcup_{n=1}^{N} w_n(B) \quad \text{for all} \quad B \in \mathcal{H}(\mathbb{R}^2).$$

Then $\{A_n = W^n(A_0)\}$ is a Cauchy sequence of sets which converges to G in the Hausdorff metric. Moreover, if A_0 is the graph of a function $f_0 \in \mathcal{F}$ then A_n is the graph of $T^n f_0$.

3.3 The Fractal Dimension of Fractal Interpolation Functions

As we said at the beginning of the chapter, fractal interpolation functions have a fractal character allowing us to compute the fractal dimension of their graphs. In order to do this, we will use the theorem presented below.

Theorem 3.3. *Let $N > 1$ be a positive integer. Let $\{(x_n, y_n) \in \mathbb{R}^2 : n = 1, 2, \cdots, N\}$ be a set of data, and let $\{\mathbb{R}^2;\ w_n :\ n = 1, 2, \cdots, N\}$ be an IFS associated with the data, where*

$$w_n \begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} a_n & 0 \\ c_n & d_n \end{pmatrix} \cdot \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} e_n \\ f_n \end{pmatrix} \quad for \quad n = 1, 2, \cdots, N.$$

The vertical scaling factors d_n obey $0 \leq d_n < 1$, and the constants a_n, c_n, e_n and f_n are given by equations (3.1), (3.2), (3.3) and (3.4) for $n = 1, 2, \cdots, N$. Let G denote the attractor of the IFS, so that G is the graph of a fractal interpolation function associated with the data. If

$$\sum_{n=1}^{N} |d_n| > 1$$

and the interpolation points do not all lie on a single straight line, then the fractal dimension of G is the unique real solution D of

$$\sum_{n=1}^{N} |d_n| a_n^{D-1} = 1.$$

Otherwise the fractal dimension of G is 1.

Remark. Let's see how to compute the fractal dimension of a fractal interpolation function in case where the interpolation points are equidistant.

Let $x_i = x_0 + \frac{i}{N}(x_N - x_0)$ for $i = 1, 2, \cdots, N$. It follows that $a_n = \frac{1}{N}$ for $n = 1, 2, \cdots, N$. Hence if $\sum_{n=1}^{N} |d_n| > 1$, then by Theorem 3.3 the fractal dimension D of the interpolation function obeys

$$\sum_{n=1}^{N} |d_n| (\frac{1}{N})^{D-1} = (\frac{1}{N})^{D-1} \sum_{n=1}^{N} |d_n| = 1.$$

Therefore, we have

$$D = 1 + \frac{\log \sum_{n=1}^{N} |d_n|}{\log N}.$$

Notice that $\sum_{n=1}^{N} |d_n| < N$. Then the fractal dimension of a fractal interpolation function is less than 2. However, we can make it arbitrarily close to 2 by selecting

the respective vertical scaling factors close to 1 (or to -1). On the other hand, since $\sum_{n=1}^{N} |d_n| > 1$ the fractal dimension is greater than 1. Again, by selecting d_n close to 0 we can vary it down to 1.

Finally, observe that the fractal dimension does not depend on the selected interpolation points (unless these are collinear). It only depends on the selection of the vertical scaling factors.

Let's see an example.

Example 2. Let $\Delta = \{(0, 10), (0.5, 13), (1, 11)\}$ be a set of data, and let $\{\mathbb{R}^2;\ w_1, w_2\}$ be an IFS associated with Δ such that

$$w_1 \begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} a_1 & 0 \\ c_1 & d_1 \end{pmatrix} \cdot \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} e_1 \\ f_1 \end{pmatrix} = \begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} 0.5 & 0 \\ 2.5 & 0.5 \end{pmatrix} \cdot \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} 0 \\ 5 \end{pmatrix},$$

$$w_2 \begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} a_2 & 0 \\ c_2 & d_2 \end{pmatrix} \cdot \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} e_2 \\ f_2 \end{pmatrix} = \begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} 0.5 & 0 \\ -2.7 & 0.7 \end{pmatrix} \cdot \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} 0.5 \\ 6 \end{pmatrix}.$$

The vertical scaling factors are $d_1 = 0.5$ and $d_2 = 0.7$, satisfying that $0 \leq d_1, d_2 < 1$. Moreover, the constants a_n, c_n, e_n and f_n are given by equations (3.1), (3.2), (3.3) and (3.4) for $n = 1, 2$. Let G denote the attractor of the IFS, so that G is the graph of a fractal interpolation function associated with the data. Then, since

$$\sum_{n=1}^{2} |d_n| = |d_1| + |d_2| = 0.5 + 0.7 = 1.2 > 1$$

and the interpolation points do not all lie on a single straight line, by Theorem 3.3 we have that the fractal dimension of G is the unique real solution D of

$$\sum_{n=1}^{2} |d_n| a_n^{D-1} = 1.$$

That is

$$|0.5| \cdot (0.5)^{D-1} + |0.7| \cdot (0.5)^{D-1} = 1 \iff (0.5)^{D-1} \cdot (0.5+0.7) = 1 \iff (0.5)^{D-1} = 1/1.2$$

$$\iff (D-1) \cdot \log(0.5) = \log(1/1.2) \iff D = 1 + \frac{\log(1/1.2)}{\log(0.5)} = 1.263.$$

Therefore, the fractal dimension of G is 1.263.

At this point, we could ask whether the fractal dimension of the graph G computed using the Box Counting Theorem would be the same as the one just obtained

($D = 1.263$) by means of Theorem 3.3. To verify that, we would need to construct the fractal interpolation function associated with Δ (i.e. the attractor of the IFS $\{\mathbb{R}^2;\ w_1, w_2\}$), plot its graph, and then apply the Box Counting Theorem to compute its fractal dimension.

In order to do this test, I have created a Matlab program so that, given a data set and the vertical scaling factors d_n, it constructs a fractal interpolation function passing through the interpolation points. This function is, as well, the attractor of the IFS $\{\mathbb{R}^2;\ w_1, w_2\}$. The Matlab implementation is based on an algorithm for computing fractals from IFS, known as Deterministic Algorithm. You can see how it works, as well as the code of the program, in the section of Appendix A.2. The program also computes and returns the values of the constants a_n, c_n, e_n and f_n according to equations (3.1), (3.2), (3.3) and (3.4) for $n = 1, 2$.

The result of running this program is the graph in Figure 12 below.

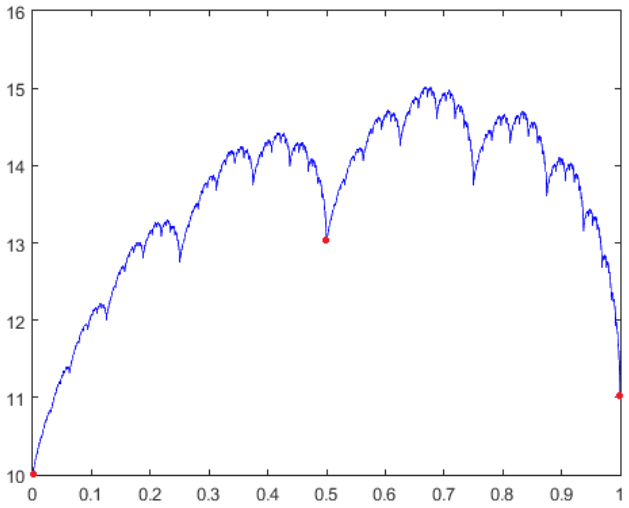

Figure 12: Graph G of the Fractal Interpolation Function related to the data Δ.

To obtain this graph, we have applied the Deterministic Algorithm a total of 10 times. In Figure 13 below, you can see the produced graphs given after 1, 2, 3, 4, 5 and 6 iterations respectively. First image is showing the three interpolation points $\Delta = \{(0, 10), (0.5, 13), (1, 11)\}$. In addition, we can see how the graphs are closer to G in each iteration.

As we have seen in Example 1 before, G can be also be obtained by repeated application of the contraction mapping T defined in Theorem 3.2.

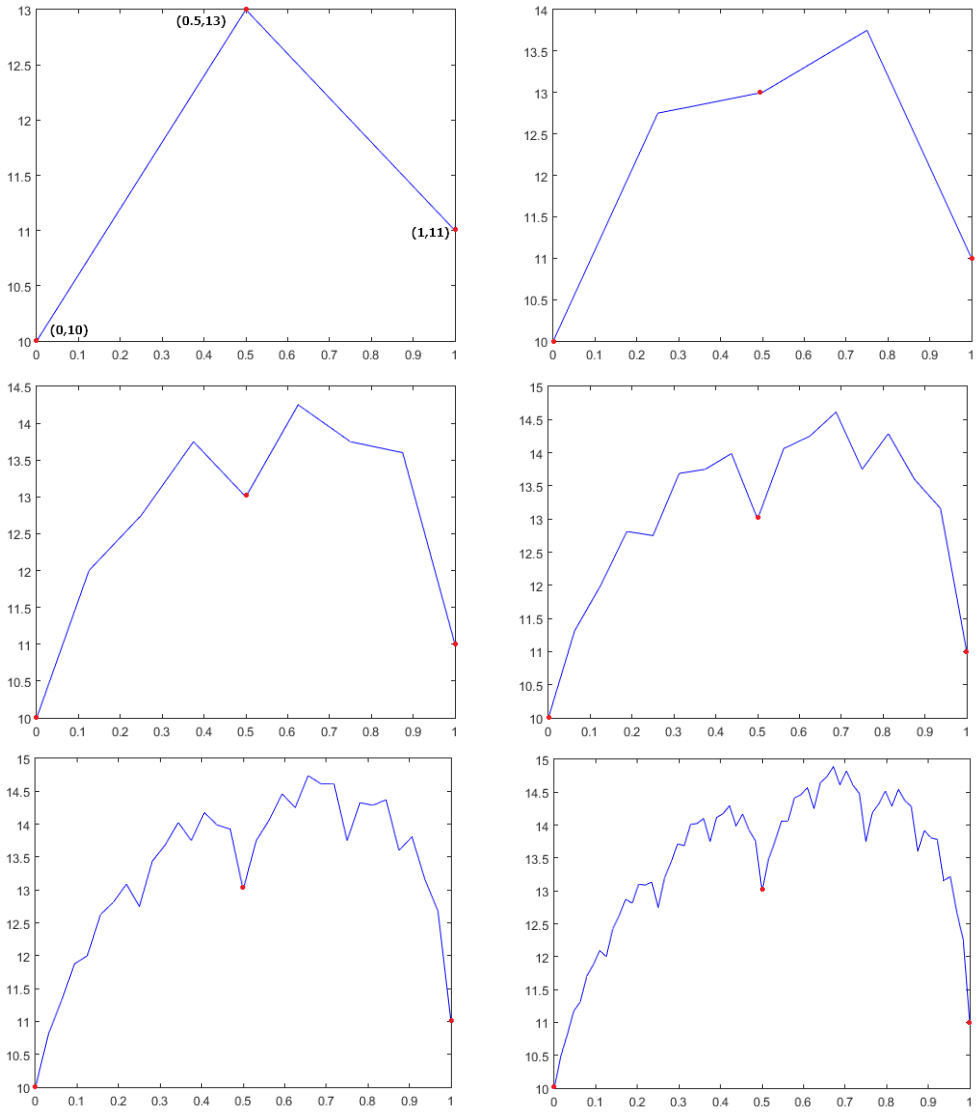

Figure 13: Produced graphs after 1,2,3,4,5 and 6 iterations of the Deterministic Algorithm respectively.

Finally, the program also computes the fractal dimension of the graph of this fractal interpolation function using the Box Counting Theorem. As before, you can see the details in the section of Appendix A.2. The result, however, is that $D = 1.297$ is the dimension of the graph G. Recall that the result obtained by Theorem 3.3 is that $D = 1.263$, being 0.034 the difference between them. Hence, we can say that the results obtained by our test fit well with the theoretical ones. Therefore, we conclude that our test is effective for calculating the fractal dimension of the graph of a fractal interpolation function.

To end with this example, let's verify that the vertical scaling factor, d_n, determine the fractal dimension of the attractor of the IFS.

For instance, if we take $d_1 = 0.2$ and $d_2 = -0.1$, since

$$\sum_{n=1}^{2} |d_n| = |d_1| + |d_2| = 0.2 + 0.1 = 0.3 < 1$$

the fractal dimension of G is 1.

On the other hand, if we take the vertical scaling factors $d_1 = 0.8$ and $d_2 = -0.9$, since

$$\sum_{n=1}^{2} |d_n| = |d_1| + |d_2| = 0.8 + 0.9 = 1.7 > 1$$

and the interpolation points do not all lie on a single straight line, by Theorem 3.3 we have that the fractal dimension of G is the unique real solution D of

$$\sum_{n=1}^{2} |d_n| a_n^{D-1} = 1.$$

That is

$$|0.8|\cdot(0.5)^{D-1}+|-0.9|\cdot(0.5)^{D-1} = 1 \iff (0.5)^{D-1}\cdot(0.8+0.9) = 1 \iff (0.5)^{D-1} = 1/1.7$$

$$\iff (D-1)\cdot\log(0.5) = \log(1/1.7) \iff D = 1 + \frac{\log(1/1.7)}{\log(0.5)} = 1.766.$$

Therefore, the fractal dimension of G is 1.766.

As we can observe, if we take vertical scaling factors near to 1 or -1, the fractal dimension is close to 2. On the contrary, if we take them around 0 the fractal dimension is close to 1.

4 Natural Fractals: Tumors

We have seen in previous chapters the concept of *artificial fractal*, as well as how to construct it from IFS and how to calculate its fractal dimension by means of the Box Counting Theorem. We have also studied the fractal interpolation functions and how are they related to all this. But now, what remains to be studied is the concept of natural fractal.

As we have previously said, a **natural fractal** is a real object that presents self-similarity for only a range of scales. In fact, in nature we cannot proceed *ad infinitum*. Hence, this mathematical object will be only an accurate model within this particular range. Examples of natural fractals can be the contour of bone fissures, wrinkles, the brain, the retina or tumors contour as well.

In this chapter we are going to focus on tumors, and we are going to study their roughness using the so-called local width function, their growing dynamics by means of the critical exponents, and their fractal dimension from these two concepts.

4.1 Dynamic Scaling of Growing Interfaces and Tumor Growth

A **tumor** is a swelling of a part of the body, generally without inflammation, caused by an abnormal growth of tissue, whether benign or malignant. We refer to it as a *tumor developing in vivo*, while tumor cell lines growing in petri dishes for experimental studies are called *tumor developing in vitro*. Along this section, we are going to use scaling techniques to analyze the fractal nature of the growing interfaces or fronts of both types of tumors.

What determines the growth dynamic behavior of a tumor is the morphology of its contour. The tumor or cell colony contour is the tumor-host interface, i.e., it is where tumor cells proliferation and spread in host tissues take place. This contour presents scale invariance, what gives it a fractal character. In particular, tumor interfaces are an example of self-affine objects which are "intermediate" between fractal objects and none-fractal objects. This means that when we make a scale change that is the same in all directions, they change morphology. But when the scale change is different for each direction, they behave like fractal objects in that they appear the same before and after the transformation. This dynamic behavior provides us the information needed to study the tumor growth dynamic. However, it is really complicated to obtain a description of the tumor contour due to its high degree of complexity. That is why we will need a dynamic scaling analysis to help us to determine the fractal character, and subsequently the growth dynamic, of tumor interfaces.

Let's start with the dynamic scaling analysis. **Dynamic scaling** is an heuristic discipline that studies the geometrical features of growing interfaces using different

concepts from the theory of stochastic processes and fractal geometry. One of the most important features is *roughness*, since it is one of the factors that determine the tumor growth dynamic. In fact, roughness usually increases as the tumor grows, thus it is established a relation between them. In an informal way, we could define roughness as a useful quantitative measurement of the irregularity of an interface such as that of a tumor or cell colony contour. However, it is formally described through some universal quantities, known as *critical exponents*. The dynamic scaling analysis is what will determine these exponents, which in turn they will establish the growth dynamic of tumors. To perform this analysis, we first need to study the tumor interface by means of the local width function.

Let's start with a physical quantity that presents scale invariance properties, that is the *mean tumor radius* (see Figure 14). It is defined as follows

$$\bar{h}(t) = \frac{1}{N}\sum_{i=1}^{N} h(i,t),$$

where N is the number of points of the tumor interface, and $h(i,t)$ are the distances from these points i to the center of the tumor mass.

Now, the local fluctuations of the interface around its mean radius (i.e. the interface width) are measured by a function known as **local width function**. This function depends on both time and position, and it generally describes the process of roughening of an interface. The local width function is defined as the root mean square of the deviations of an interface about its mean value, and it is a function of the arc length $l \subset [0, 2\pi]$ and the time t. That is

$$w(l,t) = \left\{ \frac{1}{n}\sum_{i=1}^{n} (h_l(i,t) - \bar{h}_l(t))^2 \right\}^{1/2},$$

where n is the number of points of the tumor interface in the interval l, $h_l(i,t)$ are the distances from these points $i \in l$ to the center of the tumor mass, and $\bar{h}_l(t)$ the mean tumor radius in l (see Figure 14).

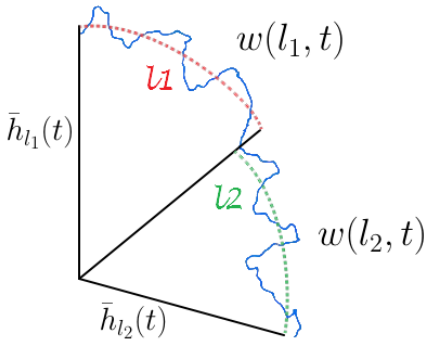

Figure 14: Interface width of a tumor or cell colony border. The local width functions $w(l_1,t)$ and $w(l_2,t)$ are calculated for sectors with an arc length l_1 and l_2 respectively. Source [3].

The roughening process of an interface develops both in time and in space, and it is described by the so-called **critical exponents**. Usually, the interfaces become more and more rough as time goes by until, in some cases, they reach saturation and stay always of the same roughness. This increase in roughness implies that the fluctuations around the mean tumor radius increase as well, i.e, implies an increment of the interface width. Therefore, since these fluctuations are measured by the local width function, it is giving a description of the tumor growth process. This dynamic process is divided in two different stages, let's study what happens at each stage.

Stage 1: Initially, the tumor grows exponentially as a power of time. At the same time, the interface becomes increasingly rougher, making that the interface width increases as a power of time as well. This stage is described by the power law

$$w(l,t) \sim t^{\beta} \quad \text{for} \quad t \ll t_s. \tag{4.1}$$

The exponent β is called the **growth exponent**, and it describes the development of the interface width with time.

Stage 2: These local fluctuations cannot grow indefinitely, therefore, there must exist a point at which these fluctuations saturate. This critical time is called the saturation time, t_s, and it is when the tumor changes its growth behavior. The tumor passes from grow exponentially to do it radially, as a power of the system size L. In this case, the roughness of the interface remains the same and it is the tumor mass the one that grows. In this case, the power law describing this stage is

$$w(L,t) \sim L^{\alpha} \quad \text{and} \quad w(l,t) \sim l^{\alpha_{loc}} \quad \text{for} \quad t \gg t_s. \tag{4.2}$$

The exponent α is called the **global roughness exponent**, and it quantifies the roughness of the saturated interface at system size scale L. At small scale of the system, the critical exponent characterizing this roughness is the **local roughness exponent** α_{loc}.

Now, the saturation time, t_s, at which the interfaces crosses over from one behavior to another depends on the system size, providing a new critical exponent. That is,

$$t_s \sim L^{z} \tag{4.3}$$

where z is called the **dynamic exponent**. This exponent is related to the correlation time of the interface. Its physical meaning is related to the celerity by which the information about points growing on the interface is transmitted across the interface.

Finally, let's show that the three critical exponents α, β and z are not independent.

Let A, B, C be constants. On the one hand, by (4.1) we have that

$$w(L,t) \simeq A \cdot t^{\beta} \quad \text{for} \quad t \ll t_s \Longrightarrow w(L,t) \simeq A \cdot t_s^{\beta} \cdot \left(\frac{t}{t_s}\right)^{\beta} \quad \text{for} \quad \frac{t}{t_s} \ll 1$$

$$\Longrightarrow w(L,t) \simeq A \cdot t_s^{\beta} \cdot f(u) \quad \text{for} \quad u \ll 1,$$

where $f(u) \simeq u^{\beta}$. On the other hand, by (4.2) we have that

$$w(L,t) \simeq B \cdot L^{\alpha} \quad \text{for} \quad t \gg t_s \Longrightarrow w(L,t) \simeq L^{\alpha} \cdot f(u) \quad \text{for} \quad u \gg 1,$$

where $f(u) \simeq B$ is a constant. Hence,

$$w(L,t) \simeq L^{\alpha} \cdot f\left(\frac{t}{t_s}\right) \quad \text{with} \quad f(u) = \begin{cases} \frac{A \cdot t_s^{\beta}}{L^{\alpha}} \cdot u^{\beta} & \text{if} \quad u \ll 1 \\ \\ B & \text{if} \quad u \gg 1 \end{cases}, \tag{4.4}$$

being $\frac{A \cdot t_s^{\beta}}{L^{\alpha}}$ and B asymptotic constants.

This function $f(u)$ defined above is called the **scaling function**. Now, by (4.3) we have that $t_s \simeq C \cdot L^z$. Then, if we evaluate the scaling function f at the crossover point $u = 1$, we obtain the following relation

$$\frac{A \cdot t_s^{\beta}}{L^{\alpha}} = B \Longrightarrow A \cdot (C \cdot L^z)^{\beta} = B \cdot L^{\alpha} \Longrightarrow A \cdot C^{\beta} \cdot L^{z\beta} = B \cdot L^{\alpha} \Longrightarrow z\beta \simeq \alpha \Longrightarrow z \simeq \alpha/\beta.$$

Therefore, the scaling law $z = \alpha/\beta$ is valid for any growth process that obeys the scaling relation (4.4).

To sum up, we have seen over this section that the dynamic of the growth process of a tumor or cell colony can be fully described by the four critical exponents determined by the scaling analysis. Recall that the exponents α and α_{loc} are related to the border's shape, the exponent β is related to the development over time of the contours, and that z is the dynamic exponents that relates α and β. According to (4.1), (4.2) and (4.3), we have the following relations

$$w(L,t) \sim t^{\beta} \; for \; t \ll t_s \Longrightarrow \beta \simeq \frac{log(w(L,t))}{log(t)},$$

$$w(L,t) \sim L^{\alpha} \; for \; t \gg t_s \Longrightarrow \alpha \simeq \frac{log(w(L,t))}{log(L)},$$

$$w(l,t) \sim l^{\alpha_{loc}} \; for \; t \gg t_s \Longrightarrow \alpha_{loc} \simeq \frac{log(w(l,t))}{log(l)},$$

$$z \simeq \frac{\alpha}{\beta} \Longrightarrow z \simeq \frac{log(t)}{log(L)}.$$

In conclusion, both cell colonies and tumors present exactly the same growth dynamic, which is described by means of the local width function as follows

$$w(l,t) = \begin{cases} t^{\beta} & \text{if} \quad t \ll t_s \\ \\ l^{\alpha} & \text{if} \quad t \gg t_s \end{cases}.$$

This growth dynamic corresponds to the *molecular beam epitaxy* (MBE) universality class. MBE is a method for thin-film deposition of single crystals, whose main feature is the roughening of growing interfaces. Its growth dynamic is characterized by a linear growth rate, the constraint of cell proliferation to the colony/tumor border, and surface diffusion of cells at the growing edge.

Studies and experiments, as the ones in [3], show the following features about tumor growth dynamics:

1. Cell diffusion at the colony or tumor border: It was observed that tumors in vivo and in vitro present surface diffusion, that is, their cells move along the tumor/colony border unable to get away from it.

2. Cell proliferation mainly restricted to the colony or tumor border: Experiments have shown a relationship between the ability to proliferate and spatial distribution within the colony or tumor. In particular, a clear tendency toward the restriction of cell proliferation to the edge of the colony or tumor was seen, as well as an inhibition in the innermost areas.

3. Linear growth rate: For both types of tumors, it was observed that tumor radius grows linearly with time. The growth rate of colonies was obtained by plotting the variation of the mean radius as a function of time. In vivo tumor growth rate could not be measured this way. However, the restriction of cell proliferation to the tumor contour mathematically implies that it is linear.

These proved that tumor growth dynamic corresponds to the MBE universality class both for tumors in vivo and in vitro.

4.2 Fractal Dimension

What remains to be studied is the fractal dimension of the natural fractals, in particular, of tumors. In an strict sense, we can only compute accurately the fractal dimension for very specific mathematical objects. Hence, we need a method to estimate the fractal dimension of a tumor based on its fractal characteristics. That is, a method using all the concepts studied so far in this chapter.

As we have seen before, in vivo and in vitro tumor interfaces present a self-similar character. However, dynamic scaling deals with interfaces that roughen in time but remain graph (i.e. can be described by means of continuous functions) showing self-affinity as well. In this case, the interface scales as

$$h(x,t) \sim b^{-\alpha} h(bx,t), \tag{4.5}$$

where α is called the Hölder or self-affine exponent, and corresponds to the local roughness exponent studied before. Hence, the function $h(x,t)$, which describes the tumor or colony contour, is a Hölder continuous non differentiable function, so it behaves like fractal function. Therefore, if $\Delta(l) \equiv |h(x_1) - h(x_2)|$ is the height difference between two points separated by a distance $l \equiv |x_1 - x_2|$ for a fixed time

t, we have that

$$\Delta \simeq l^{\alpha_{loc}}. \tag{4.6}$$

In addition to the roughness exponent α_{loc}, it is possible to associate a fractal dimension D to the function $h(x,t)$. Consider that this self-affine function is defined on the interval $[0,1]$ which we cover with boxes of size l. We first divide the horizontal domain of the function into N_s segments, so the width of each one is $l = 1/N_s$. In a horizontal interval of size l, the height changes according to (4.3), so we require $\Delta/l \simeq l^{\alpha_{loc}-1}$ boxes of size $l \times l$ to cover the function. Since we need $l^{\alpha_{loc}-1}$ boxes to cover the variation in one segment, for N_s segments the total number of boxes required is

$$N(l) \simeq N_s \times l^{\alpha_{loc}-1} \simeq l^{\alpha_{loc}-2} \quad \text{for} \quad \Delta \ll l.$$

Thus, since $N(l) \simeq l^{-D}$ as we saw in Chapter 2, we have that

$$D \simeq 2 - \alpha_{loc}. \tag{4.7}$$

For $\Delta \gg l$ the number of boxes required to cover the function scales as $N(l) \simeq 1/l$, and therefore $D \simeq 1$.

We conclude that the fractal dimension of tumors and natural fractals can be estimated, in general, by means of the formula $D \simeq 2 - \alpha_{loc}$.

4.3 Real Example

Finally, we are going to study the real case of a tumor using the experimental data in [3]. What we are going to do is performing a test to compute the fractal dimension of the tumor shown in Figure 15, and then calculate the local roughness exponent α_{loc} with the formula $D \simeq 2 - \alpha_{loc}$. Finally, we will compare our results to the ones obtained in [3] by the experts.

To carry out this test I have created a Matlab program so that, given a bitmap image file of a tumor contour, it computes its fractal dimension using the Box Counting Theorem. You can see in detail how the program works, as well as its code, in the section of Appendix A.3. I wasn't able to compute neither the width function nor the roughness exponents from that bitmap image file, since the tumor contour has concavities. That is why I am using the aforementioned formula to do it.

Let's consider the C6 cell line studied in [3]. The contours of this tumor in vitro, shown in Figure 15, were measured at intervals of 24 hours. We are taking for this test the black, the dark blue, and the orange ones (see Figure 16).

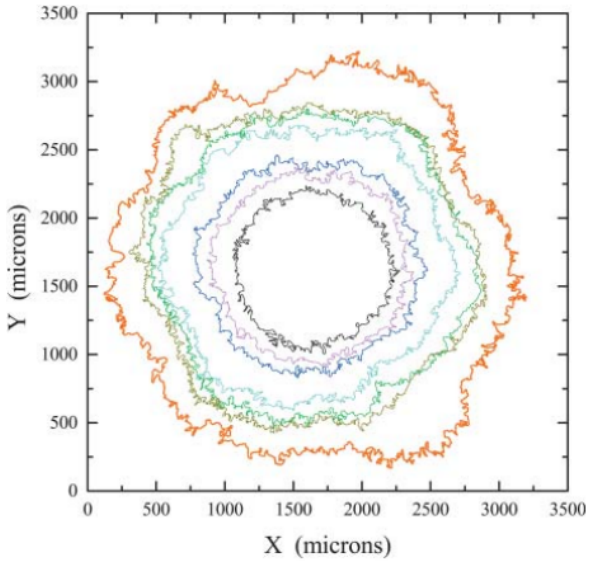

Figure 15: Cell colony contours. Contours of a C6 cell line at different culture times. Source [3]

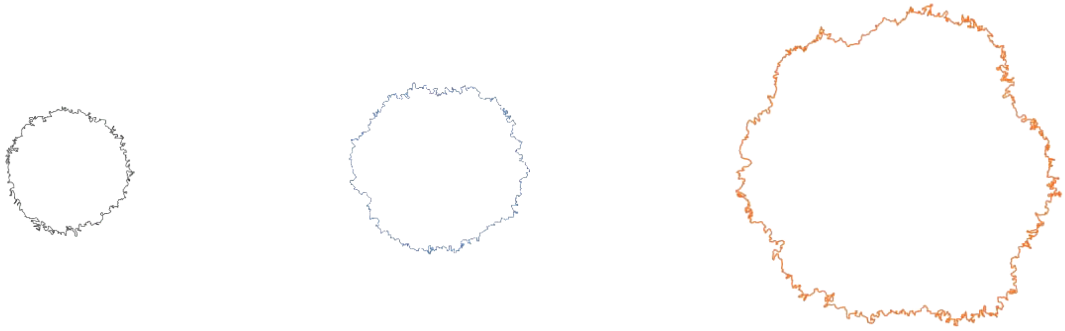

Figure 16: Contours of a C6 cell line at intervals of 24, 72 and 168 hours respectively.

According to [3], the tumor has a fractal dimension $D = 1.21 \pm 0.03$, a local roughness exponent $\alpha_{loc} = 0.91 \pm 0.05$, and a global roughness exponent $\alpha = 1.49 \pm 0.15$. Let's compare these experimental results with the ones obtained from our test.

Let's start with the black contour, where $t = 24h$. If we run program A.3 we obtain that the fractal dimension of this tumor contour is $D = 1.29$. Therefore, according to (4.7), we have that

$$D \simeq 2 - \alpha_{loc} \Longrightarrow \alpha_{loc} = 2 - D = 2 - 1.29 = 0.71.$$

Let's continue with the blue contour, where $t = 72h$. If we run program A.3 we obtain that the fractal dimension of this tumor contour is $D = 1.32$. Then, according to (4.7), we have that

$$D \simeq 2 - \alpha_{loc} \Longrightarrow \alpha_{loc} = 2 - D = 2 - 1.32 = 0.68.$$

Let's finish with the orange contour, where $t = 168h$. If we run program A.3 we obtain that the fractal dimension of this tumor contour is $D = 1.49$. Thus, according to (4.7) once more, we have that

$$D \simeq 2 - \alpha_{loc} \Longrightarrow \alpha_{loc} = 2 - D = 2 - 1.49 = 0.51.$$

As we can see, the results of our test are close to the ones in [3], specially for the black contour. On the other hand, we can also observe that the fractal dimension of this tumor contours increases as time goes by. That is, the fractal dimension of the black contour is smaller than the one for the blue contour, which in turn is smaller than the one of the orange contour. Therefore, we could say that the tumor is growing according to our test.

Regarding the local roughness exponents, we can say that they fit well enough with the one in [3] ($\alpha_{loc} = 0.91 \pm 0.05$), specially the local roughness exponent of the black contour again. We can observe as well, how the roughness of the contour changes as the tumor grows. Since it is decreasing, we could think that the tumor is reaching the saturation point in which the roughness remains "constant". However, we would need more information and studies to confirm that.

We finally conclude that our test works quite good for computing the fractal dimension of a tumor. Furthermore, the local roughness exponents computed using this fractal dimension and the formula (4.7), fit sufficiently well to the results obtained in [3].

5 Conclusions

The aim of this project was to study fractal geometry in order to apply it to the study of tumors. When I started this project, I was not fully aware of the significance and the complexity of fractal geometry. Even now, after 50 pages, I don't see the limits of this discipline.

I started this work by studying elementary concepts such as metric spaces, affine transformations or contraction mappings. These concepts led me to the Iteration Function Systems, and then to the fractal dimension. It was here, and due to the Box Counting Theorem, that I realized that fractal dimension would be a very important matter to develop it in detail along the project.

And that is what I did, since Chapter 3 was focus on the fractal interpolation functions and their fractal dimension. Moreover, I created a program so that, given a data set and the vertical scaling factors, it constructs a fractal interpolation functions passing through the interpolation points and then computes the box counting dimension of its graph. This program helped me to understand the relation of these functions with fractals, as well as its application to fields such as Economy (stock market).

Finally, with Chapter 4, I have learned how to apply the theoretical concepts about fractals to the problems of the real world. In particular, I have observed the utility of the fractal geometry in an issue as important as the tumor growth. During my research I have learned how to describe the tumor growth dynamics by means of the critical exponents, which are no more than a description of the tumor contour (again fractal). However, from here a set of mathematical models based on stochastic partial differential equations can be developed to describe completely tumor growth. This work would be, without any doubt, a very interesting project.

Throughout this process of research and work, I have learn that fractal geometry is a very powerful tool that can be used, among others, to describe processes as sophisticated as the tumor growth. Therefore, my conclusion is that not only lives can be saved with a white coat and a scalpel, but also with a paper and a pen.

References

[1] Barnsley, M.F.: *Fractals Everywhere*, Academic Press INC., London, 1988.

[2] Barabási, A.L.; Stanley, H.E.: *Fractal Concepts in Surface Growth*, Cambridge University Press, Cambridge, 1995.

[3] Brú, A.; Albertos, S.; Subiza, J.L.; López, J.; Brú, I.: The Universal Dynamics of Tumor Growth, *Biophysical Journal*, 85: 2948-2961, November 2003.

[4] Brú, A.; Pastor, J.M.; Fernaud, I.; Brú, I.; Melle, S.; Berenguer, C.: Super-Rough Dynamics on Tumor Growth, *Physical Review Letters*, 81(18): 4008-4011, 2 November 1998.

[5] Das Sarma, S.; Ghaisas, S.V.; Kim, J.M.: Kinetic super-roughening and anomalous dynamic scaling in nonequilibrium growth models, *Physical Review E*, 49(1): 122-125, January 1994.

[6] Brú, A.; Casero, D.; De Franciscis, S.; Herrero, M.A.: Fractal analysis and tumor growth, *Mathematical and Computer Modelling*, 47: 546-559, 2008.

[7] Brú, A.; Fernaud, I.; Pastor, J.; Melle, S.; Brú, I.; Berenguer, C.; Fernaud, M.J.: Non-linear Dynamics in Tumoral Processes, *Anales de Física, Monografías RSEF*, 10: 1-2, 1998.

6 Appendix: Programs

6.1 A.1

This Matlab program firstly computes and returns the values of the constants a_n, c_n, e_n and f_n, for $n = 1, 2$, according to equations (3.1), (3.2), (3.3) and (3.4) of Chapter 3. Then, it constructs a fractal interpolation function passing through the interpolation points. The input is the data set $\Delta = \{(0, 0), (30, 50), (60, 40), (100, 10)\}$, the vertical scaling factors $d_1 = 0.5$, $d_2 = -0.5$ and $d_3 = 0.23$, and the number of mappings, $N = 3$.

This program is based on an algorithm for computing fractals from IFS, known as Deterministic Algorithm. This algorithm is based on the idea of directly computing a sequence of sets $\{A_n = W^n(A_0)\}$ starting from an initial set A_0.

```
% THE FRACTAL DIMENSION OF FRACTAL INTERPOLATION FUNCTIONS

% 1. FRACTAL INTERPOLATION FUNCTION
% Data set
X = [0 30 60 100];
Y = [0 50 40 10];

% N is the number of mappings and N+1 the number of points
N = 3;
points = N+1;

% Vertical scaling factors
d = [0.5 -0.5 0.23];

% Calculate the shear transformations from the data set and the vertical
% scaling factors
a = [];
c = [];
e = [];
f = [];
for n=1:N
    den = X(4)-X(1);
    a = [a, (X(n+1)-X(n))/den];
    c = [c, (Y(n+1)-Y(n)-d(n)*(Y(4)-Y(1)))/den];
    e = [e,(X(4)*X(n)-X(1)*X(n+1))/den];
    f = [f, (X(4)*Y(n)-X(1)*Y(n+1)-d(n)*(X(4)*Y(1)-X(1)*Y(4)))/den];
end
```

```
% Iteration Points
% IP is a (N+1)x2 matrix representing the interpolation points
% D is a Nx1 matrix representing the vertical scaling factors

IP = [0 0; 30 50; 60 40; 100 10];
D = [0.5; -0.5; 0.23];
A_0 = IP;

% Deterministic Algorithm
% The algorithm computes and returns N^(steps+1)+1 points representing the
% attractor of the FIF

for i = 1:5
    l=1;
    for j=1:N
        for k=1:points-1
            P(l,1)=a(j)*A_0(k,1)+e(j);
            P(l,2)=c(j)*A_0(k,1)+D(j)*A_0(k,2)+f(j);
            l=l+1;
        end
    end
    P(l,1)=A_0(points,1);
    P(l,2)=A_0(points,2);
    points=l;
    A_0=P;
end
figure
plot(A_0(1:size(A_0,1),1),A_0(1:size(A_0,1),2),'b');
```

6.2 A.2

This Matlab program is the same as the above (A.1), unlike that, in addition to the fractal interpolation function, it also computes the fractal dimension of its graph.

In this case, the input for the first part of the program is the data set $\Delta = \{(0, 10), (0.5, 13), (1, 11)\}$, the vertical scaling factors $d_1 = 0.5$ and $d_2 = 0.7$, and the number of mappings, $N = 2$. For the second part, where it computes the fractal dimension of the graph of the fractal interpolation function just created, the input is the image of the output of the first part in bitmap format.

```
% THE FRACTAL DIMENSION OF FRACTAL INTERPOLATION FUNCTIONS

% 1. FRACTAL INTERPOLATION FUNCTION
% Data set
X = [0 0.5 1];
Y = [10 13 11];

% N is the number of mappings and N+1 the number of points
N = 2;
points = N+1;

% Vertical scaling factors
d = [0.5 0.7];

% Calculate the shear transformations from the data set and the vertical
% scaling factors
a = [];
c = [];
e = [];
f = [];
for n=1:N
    den = X(3)-X(1);
    a = [a, (X(n+1)-X(n))/den];
    c = [c, (Y(n+1)-Y(n)-d(n)*(Y(3)-Y(1)))/den];
    e = [e,(X(3)*X(n)-X(1)*X(n+1))/den];
    f = [f, (X(3)*Y(n)-X(1)*Y(n+1)-d(n)*(X(3)*Y(1)-X(1)*Y(3)))/den];
end
```

```
% Iteration Points
% IP is a (N+1)x2 matrix representing the interpolation points
% D is a Nx1 matrix representing the vertical scaling factors

IP = [0 10; 0.5 13; 1 11];
D = [0.5; 0.7];
A_0 = IP;

% Deterministic Algorithm
% The algorithm computes and returns N^(steps+1)+1 points representing the
% attractor of the FIF

for i = 1:10
    l=1;
    for j=1:N
        for k=1:points-1
            P(l,1)=a(j)*A_0(k,1)+e(j);
            P(l,2)=c(j)*A_0(k,1)+D(j)*A_0(k,2)+f(j);
            l=l+1;
        end
    end
    P(l,1)=A_0(points,1);
    P(l,2)=A_0(points,2);
    points=l;
    A_0=P;
end
figure
plot(A_0(1:size(A_0,1),1),A_0(1:size(A_0,1),2),'b');
```

```
% 2. FRACTAL DIMESION
% Open the image and convert it to grey scale
M = imread('FIF3.bmp');
M = rgb2gray(M);

% Convert the image to black and white
M=im2bw(M, 0.9);
figure
imshow(M);

% Save the number of rows and columns of pixels of the image
[height,width] = size(M);

% Compute the fractal dimension by Box Counting
D = [];
num_boxes = [];
length = [];
partition = 0;
boxes = 0;

for n=1:10
    boxes = 0;
    partition = (width/2^n);
    for k=0:partition:(width-partition)
        for m=0:partition:(width-partition)
            G = find(~M(k+1:k+partition,m+1:m+partition));
            if size(G)~= 0
                boxes = boxes + 1;
            else
            end
        end
    end
    num_boxes = [num_boxes, boxes];
    length = [length, 2^n];
    D = [D, log(num_boxes(end))/log(2^n)];
end
FRACTAL_DIMENSION = D(10);
```

6.3 A.3

This last Matlab program computes the fractal dimension of three different contours of the image shown in Figure 15. To select each one of these contours, I have used the program "GIMP". The results are shown in the image of Figure 16. It also computes the local roughness exponent using the formula (4.7) of chapter 4.

The input of the program is each one of the contours in a bitmap image file ('tumor_orange.bmp', 'tumor_blue.bmp', and 'tumor_black,bmp').

```
% Open the image and convert it to grey scale
M = imread('tumor_orange.bmp');
M = rgb2gray(M);

% Convert the image to black and white
level_orange = 0.8;
level_blue = 0.99;
level_black = 0.7;
M=im2bw(M, level_orange);
imshow(M);

% Save the number of rows and columns of pixels of the image
[height,width] = size(M);

% Compute the fractal dimension by Box Counting
D = [];
num_boxes = [];
length = [];
partition = 0;
boxes = 0;
```

```
for n=1:10
    boxes = 0;
    partition = (width/2^n);
    for k=0:partition:(width-partition)
        for m=0:partition:(width-partition)
            G = find(~M(k+1:k+partition,m+1:m+partition));
            if size(G)~= 0
                boxes = boxes + 1;
            else
            end
        end
    end
    num_boxes = [num_boxes, boxes];
    length = [length, 2^n];
    D = [D, log(num_boxes(end))/log(2^n)];
end
D;
FRACTAL_DIMENSION = D(10);

figure
plot(log(length),log(num_boxes),'color', [1 .5 0]);
title('Fractal Dimension');
xlabel ('log(length)');
ylabel('log(number of boxes)');

% Local Roughness exponent according to the formula (4.7)
alpha = 2 - D(10);
LOCAL_ROUGHNESS_EXPONENT = alpha;
```