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Meta-dynamical adaptive systems and their applications to a fractal algorithm and a biological model

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Abstract

In this article, one defines two models of adaptive systems: the *meta-dynamical adaptive system* using the notion of Kalman dynamical systems and the *adaptive differential equations* using the notion of *variable dimension spaces*. This concept of variable dimension spaces relates the notion of spaces to the notion of dimensions. First, a computational model of the Douady's Rabbit fractal is obtained by using the meta-dynamical adaptive system concept. Then, we focus on a defense-attack biological model described by our two formalisms.

Keywords: dynamical systems, adaptive systems, biological systems, fractal algorithm.

MSC: 93A05; 37F50; 92D15; 92D25

1 Introduction

In the two last decades, there has been much interest in the study and formalization of complex adaptive systems (see [21] and [8]). Many different approaches have been proposed: artificial chemistries, evolutionary formalism,

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cellular automata. However, from a more theoretical viewpoint, few mathematical formalisms exist for adaptive systems. Though we may cite the chapter “Categorical System Theory” proposed by A.H. Louie in [18] who discuss the relationship between natural and formal systems, most of the studies are mainly simulation-based (see [8] and [9]). With the recent evolution of physics and biology, a general mathematical formalism for adaptive systems would be very useful. Actually, behind their apparent heterogeneity, most of the adaptive systems share one important feature: they are dynamical objects whose structures are sometimes modified by a top level automation-like rule. On the basis of this observation, we have built a two-level formalism that helps us to design an algorithm for fractals and a biological model of co-evolution in a bacterium-phage system.

The main goal of this article is to present a concept of adaptive systems, general enough to be used in different fields (mathematics, physics or biology) and to apply this framework to a fractal implementation and a biological system. Besides, a new concept of spaces is developed. Since the second part of the 19th century, various definitions of dimensions, in particular those developed by Cantor and Peano, have appeared (see [14]). These new definitions lead to the concept of a fractal model and with it, a global view of spaces (see [13]). In order to study adaptive systems, we will use a sort of “adaptive” space called *variable dimension space* whose dimension changes. This new kind of space brings the notion of space and the notion of dimension together.

The paper is organized as follows. In section 2, a very general adaptive system concept called *meta-dynamical adaptive system* is given by using an extension of Kalman systems. Section 3 is dedicated to the Douady’s Rabbit fractal implemented as a meta-dynamical adaptive system. In section 4, the concept of variable dimension space leads to a special model of adaptive system: the *adaptive differential equation*. Finally, we use our concepts of adaptive systems to describe a biological example of a defense-attack model in section 5.

2 Meta-dynamical adaptive system

It is possible to give a general definition of adaptive systems by using the concept of *meta-dynamical adaptive system* developed by one of the author during his Ph.D. ([2, 4]). But, in order to be able to present our formal approach, we will have a look at the main ideas behind the formalization of the concept of dynamical system by Kalman in [12]. The aim of Kalman’s approach is to show that some very common mathematical structures plus a few axioms can provide a very general framework where the notion of dynamical systems (of all kinds) is captured. Time is modelled as an ordered subset of the reals (to cover both the continuous and discrete paradigms). The important objects are the state set (the variables characterizing the system) and the transition function. The transition function defines the trajectory in the state set starting from an initial state. Only a few axioms are required to characterize these objects and allow them to form a “dynamical system”. Among the more important ones are

direction of time, consistency, composition property and causality. Let us recall the fundamental definition of Kalman (see [12]).

A *dynamical system respecting Kalman axioms* is defined by the following axioms:

1. There is a given time set T , a state set X , a set of input values U , a set of acceptable input functions $\Omega = \{\omega : T \rightarrow U\}$, a set of output values Y , and a set of output functions $\Gamma = \{\gamma : T \rightarrow Y\}$,
2. (Direction of time) T is an ordered subset of the reals¹,
3. The input space Ω satisfies the following conditions:
 - (a) (Nontriviality) Ω is nonempty,
 - (b) (Concatenation of inputs) An input segment $\omega_{]t_1, t_2]}$ is $\omega \in \Omega$ restricted to $]t_1, t_2] \cap T$. If $\omega, \omega' \in \Omega$ and $t_1 < t_2 < t_3$, there is an $\omega'' \in \Omega$ such that $\omega''_{]t_1, t_2]} = \omega_{]t_1, t_2]}$ and $\omega''_{]t_2, t_3]} = \omega'_{]t_2, t_3]}$,
4. There is given a state-transition function

$$\varphi : T \times T \times X \times \Omega \rightarrow X.$$

whose value is the state $x(t) = \varphi(t, \tau, x_\tau, \omega) \in X$ resulting at time $t \in T$ from the initial state $x_\tau = x(\tau) \in X$ at initial time $\tau \in T$ under the action of the input $\omega \in \Omega$. φ has the following properties:

- (a) (Direction of time) φ is defined for all $t \geq \tau$ but not necessarily for all $t < \tau$.
- (b) (Consistency) $\varphi(t, t, x, \omega) = x$ for all $t \in T$, all $x \in X$ and all $\omega \in \Omega$.
- (c) (Composition property) For any $t_1 < t_2 < t_3$, we have

$$\varphi(t_3, t_1, x, \omega) = \varphi(t_3, t_2, \varphi(t_2, t_1, x, \omega), \omega)$$

for all $x \in X$ and all $\omega \in \Omega$.

- (d) (Causality) If $\omega, \omega' \in \Omega$ and $\omega_{] \tau, t]} = \omega'_{] \tau, t]}$ then

$$\varphi(t, \tau, x, \omega) = \varphi(t, \tau, x, \omega').$$

5. There is given a readout map $\eta : T \times X \rightarrow Y$ which defines the output $y(t) = \eta(t, x(t))$. The map $] \tau, t[\rightarrow Y$ given by $\sigma \mapsto \eta(\sigma, \varphi(\sigma, \tau, x, \omega))$, $\sigma \in] \tau, t[$ is an output segment, that is, the restriction $\gamma_{] \tau, t]}$ of some $\gamma \in \Gamma$ to $] \tau, t[$.

A dynamical system is referred as $\Sigma = \{T, X, U, \Omega, Y, \Gamma, \varphi, \eta\}$.

Now, inspired by the definition of dynamical systems of Kalman, we propose a formalization of our meta-dynamical adaptive system.

¹Such a general definition could include exotic sets such as fractal cantor sets, for instance, in practice, the sets used are part of \mathbb{R} or \mathbb{N} .

Definition 1 A meta-dynamical adaptive system \mathcal{M} is a composite mathematical concept defined by the following axioms:

1. **The dynamical level:** the suitably indexed set

$$\Sigma_{i,j} = \{T_0, X_i, U, \Omega, Y, \Gamma, \varphi_{i,j}\}$$

is a dynamical system respecting Kalman axioms for all $(i, j) \in I \times J$ where $\{\varphi_{i,j}\}_{j \in J}$ are transition functions on state set X_i :

$$\varphi_{i,j} : T_0 \times T_0 \times X_i \times \Omega \rightarrow X_i.$$

2. **The meta-dynamical level:** let $X = \bigcup_{i \in I} X_i$ be the set of all the possible states of the system and $D = \{\varphi_{i,j}\}_{(i,j) \in I \times J}$ be the set of all possible transition functions, then there exists a meta-dynamical time T_1 and a meta-dynamical rule²

$$\Phi : T_1 \times X \times D \rightarrow X \times D$$

such that:

- (a) (Temporal hierarchy) $T_1 \subseteq T_0$,
- (b) (Coherence states/transitions) If $\Phi(t, x_1, \varphi_{i_1, j_1}) = (x_2, \varphi_{i_2, j_2})$ for $t \in T_1$, then $x_1 \in X_{i_1} \Rightarrow x_2 \in X_{i_2}$.

If $t \in T_1$ and $\Phi(t, x, \varphi) = (x, \varphi)$, Φ is said to be mute at (t, x, φ) else (t, x, φ) is a commutation point.

3. **Evolution rule between dynamical and meta-dynamical levels:** let $x_t = \varphi(t, t_1, x_1, \omega)$ with ω an input function, there exists a “meta”-transition function

$$\Psi : T_1 \times T_1 \times X \times D \times \Omega \rightarrow X \times D$$

such that:

- (a) (Dynamical phase) If Φ is mute on (t, x_t, φ) for all $t \in [t_1, t_2] \cap T_1$, then Ψ is defined between t_1 and t_2 and
 - i. if $t_2 \notin T_1$, then

$$\Psi(t_2, t_1, x_1, \varphi, \omega) = (x_{t_2}, \varphi),$$

- ii. else $t_2 \in T_1$ and

$$\Psi(t_2, t_1, x_1, \varphi, \omega) = \Phi(x_{t_2}, \varphi).$$

²It is possible to consider input values at the metadynamical level, then Φ is defined as follows

$$\Phi : T_1 \times X \times D \times \Omega_1 \rightarrow X \times D$$

where $\Omega_1 = \{\omega : T_1 \rightarrow U_1\}$ is the set of acceptable “meta”-input functions.

- (b) (Concatenation rule) If there exists $t_2 \in]t_1, t_3[$ such that Ψ is defined between t_1 and t_2 and between t_2 and t_3 then Ψ is defined between t_1 and t_3 and

$$\Psi(t_3, t_1, x_1, \varphi, \omega) = \Psi(t_3, t_2, \Psi(t_2, t_1, x_1, \varphi, \omega), \omega).$$

- (c) (Stopping rule) Ψ is defined between t_1 and t_2 if, respecting previous axioms, there is only a finite number of commutation points in $[t_1, t_2]$.

The meta-dynamical rule in point 2) can operate at instants for which the system is defined and not necessarily at all of them (see point 2.(a)); actually a higher level is usually slower. Moreover, as the meta-dynamical rule can change the state and the transition function, we have to consider that both match well: the resulting state has to belong to the state set on which the new transition function operates (point 2.(b)). In point 3. we describe how dynamics and the meta-dynamical rule combine together to make the system change with time.

To take up notions mainly used in social science, our dynamical rule can be seen as a heterarchical level and our meta-dynamical level as a hierarchical level. Let us recall that a *heterarchy* is a network of elements which share the same “horizontal” position level in a *hierarchy*. Each level in a hierarchical system is composed of a heterarchy which contains its constituent elements (see [11]).

Remark 2 In the second case of (3.a), when $t_2 \in T_1$, we deliberately consider that $(t_2, \Phi(x_{t_2}, \varphi))$ is mute. We do not consider the case where the meta-dynamics would “rebound” and have several commutations at the same time. If the system has several commutations, it is always possible to consider this set of commutation as one, with the final state of the last commutation (provided that, we know from 3.(c) that the number of commutations is finite). Axiom 3.(c) is to avoid Zeno-style system with an infinite number of commutations in a finite amount of time (e.g. with a quantity $x(t) = \sin\left(\frac{2\pi}{1-t}\right)$ with a commutation each time $x(t) = 0$ on $[1 - \epsilon, 1 + \epsilon]$).

Remark 3 The index set J is associated with the change of dynamics in the same state space. We recognize here the framework of hybrid systems (see [22]).

Remark 4 It is also important to differentiate between the continuous or discrete dynamics and the continuous or discrete meta-dynamics because the confusion is easy. The first case is well known. The second one shows the difference between a meta-dynamical time T_1 which is continuous (see section 3) and a meta-dynamical time which is discrete (see section 5).

Example 5 On Fig. 1, we can see a meta-dynamical system in action. At $t_5 = t_c$, we pass from a 2-dimensional state set to a 3-dimensional one. The dynamics are continuous, so $T_0 = [t_0, t_{end}]$ and the meta-dynamical time set T_1 is discrete: $T_1 = \{t_1, t_2, t_3, \dots, t_8\}$. Since the meta-dynamics is mute on t_1, t_2 ,

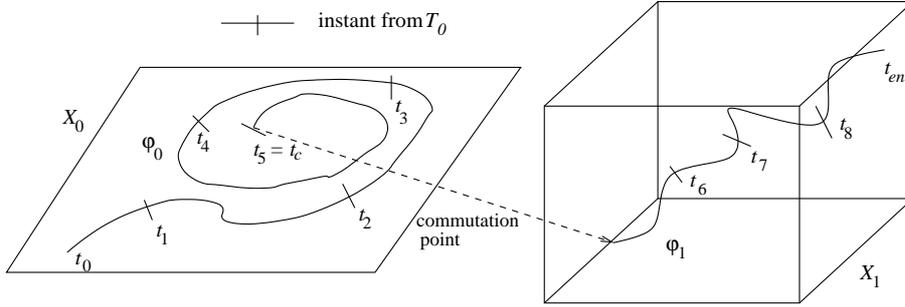


Figure 1: Illustration of some axioms of a metadynamical system

t_3 and t_4 , the evolution from t_0 to t_5 is a purely dynamical phase, ended by a commutation (Axiom 3.(a)). Evolution from t_5 to t_{end} is also purely dynamical (the meta-dynamics is mute on t_6 , t_7 and t_8 . The junction between the two of them is made by using the concatenation rule. As there is only one commutation, the system is defined.

Now, it is possible to expand some classical notions of dynamical system, as the notion of trajectory.

Definition 6 Let \mathcal{M} be a meta-dynamical adaptive system with the meta-transition function Ψ , if for $t \in T_1$,

$$\Psi(t, t_0, x_0, \varphi_0, \omega) = \bar{\Phi}(x_t, \varphi_t)$$

with $x_t \in X_t$ then (X_t, φ_t) is a meta-state of \mathcal{M} in t .

The sequence $(X_{t_i}, \varphi_{t_i})_{0 \leq i \leq n, 0 \leq n \leq +\infty}$ of meta-state of \mathcal{M} such that for all $t \in [t_i, t_{i+1}[$, $(X_t, \varphi_t) = (X_{t_i}, \varphi_{t_i})$ and $(X_{t_i}, \varphi_{t_i}) \neq (X_{t_{i+1}}, \varphi_{t_{i+1}})$ is called meta-orbit of \mathcal{M} .

If $n < +\infty$, (X_{t_n}, φ_{t_n}) is said to be an absorbent meta-state.

The sequence $(t_i, X_{t_i}, \varphi_{t_i})_{0 \leq i \leq n, 0 \leq n \leq +\infty}$ satisfying the same conditions is called a trajectory of \mathcal{M} .

One can extend definition 1 to stochastic systems.

Definition 7 Let us consider the dynamical rule of definition 1 with the following meta-dynamical rule

$$p\bar{\Phi} : T_1 \times X \times D \rightarrow (X \times D \rightarrow [0, 1])$$

where $p\bar{\Phi}$ is a probability distribution on $X \times D$ which represents the probability

$$p\bar{\Phi}(t, x, \varphi) \cdot (x_f, \varphi_f)$$

that (x, φ) becomes (x_f, φ_f) at t . The stochastic evolution rule between dynamical and meta-dynamical levels is given by

$$p\Psi : T_1 \times T_1 \times X \times D \times \Omega \rightarrow (X \times D \rightarrow [0, 1])$$

where $p\Psi$ is a probability distribution on $X \times D$ which represents the probability

$$p\Psi(t_1, t_2, x, \varphi, \omega) \cdot (x_f, \varphi_f)$$

that (x, φ) becomes (x_f, φ_f) between t_1 and t_2 with the input function ω . The properties of $p\Phi$ and $p\Psi$ are the same as Φ and Ψ given in 1. Such a system is called a stochastic meta-dynamical adaptive system.

The interest of definition 7 is its generality. It is for example well adapted to model a large number of complex adaptive systems, in particular the biological model we develop in section 5.

3 Algorithm for the Douady's Rabbit fractal

The goal of this example is to give an algorithm based on definition 1 allowing to describe the Douady's Rabbit Fractal. In this example, the set I and thus the family $\{X_i\}_{i \in I}$ of definition 1 is not countable. The Riemann Sphere \mathbb{S}^2 is mapped one-to-one onto the extended complex plane $\mathbb{C}_\infty = \mathbb{C} \cup \{\infty\}$ by stereographic projection. Let us recall some definitions. Let $\mathbb{K} = \mathbb{R}$ or \mathbb{C} and \mathcal{B} be the unit ball of \mathbb{K} . If $f : \mathbb{K} \rightarrow \mathbb{K}$ is a function, $x \in X$ is *periodic* of period $n \in \mathbb{N}$ if $f^n(x) = x$ and for all $k \in \{1, \dots, n-1\}$, $f^k(x) \neq x$. For x periodic of period n , the *cycle* $\mathcal{O}(x)$ is the set

$$\mathcal{O}(x) = \{x, f(x), \dots, f^{n-1}(x)\}$$

and its cardinal is n . Moreover, if f is differentiable at x , x is *stable*, *quasi stable* or *unstable* if $|(f^n)'(x)| < 1$, $|(f^n)'(x)| = 1$ or $|(f^n)'(x)| > 1$. If x is stable, x is *attractive* if there exists an interval V strictly containing x so that for all $x \in V$

$$f^n(x') \xrightarrow[n \rightarrow +\infty]{} x.$$

Now, let us recall the definition of the Julia set (see [1]). Let R be a non-constant rational function on \mathbb{S}^2 . The *Fatou set* of R is the maximal open subset of \mathbb{S}^2 on which $\{R^n\}_{n \in \mathbb{N}}$ is equicontinuous where $R^n = R \circ \dots \circ R$. The *Julia set* J_R of R is the complement of the Fatou set on \mathbb{S}^2 . The *filled in Julia set* K_R of a function R is all the points which are not attracted to the super-attracting fixed point at infinity, that is

$$K_R = \{z \in \mathbb{C} : R^n(z) \rightarrow \infty\}.$$

This closed set includes the Julia set as its boundary, $J_R = \partial K_R$. The *escape set* I_R of a function R is all the points that "escape" to infinity, that is

$$I_R = \{z \in \mathbb{C}_\infty : R^n(z) \rightarrow \infty\}.$$

If R is a polynomial of degree 2, J_R is called a quadratic Julia set. The following result can be found in [6]: if P is a polynomial of degree $d \geq 2$, then J_P is closed

and dense within itself.

Here, we are interested in quadratic Julia sets with

$$P_c(z) = z^2 + c \quad (1)$$

where $c \in \mathbb{C}$. For small values of c , the Julia set is distorted by varying degrees from the unit circle, in these cases the Julia set has an infinite length. For large values of c , the Julia set becomes an infinite set of totally disconnected points, often said to be dust like (in the sense of Cantor). In the quadratic case there are only these two possible -connected and disconnected- types. The *Mandelbrot set* is the space containing the value c for which the associated Julia set is connected. It is generated by the quadratic sequence

$$\begin{cases} z_{n+1} = z_n^2 + c \\ z_0 = c \end{cases} \quad (2)$$

A complex point $z = a + ib \in \mathbb{C}$ will be denoted by $(a; b)$. The Douady's Rabbit fractal is a Mandelbrot set with $c = (-\frac{3}{2} + \frac{1}{2}(a + b); \frac{\sqrt{3}}{2}(a - b))$ where $a = \sqrt[3]{\frac{25 + \sqrt{621}}{54}}$ and $b = \sqrt[3]{\frac{25 - \sqrt{621}}{54}}$, so $c \simeq (-0.12256; 0.744862)$ (see [7]). As the points get closer to the Douady's Rabbit fractal, the speed of convergence becomes slower. With the choice of c , $(c^2 + c)^2 + c = 0$ so the origin is an attractive cycle³ of period 3 of P_c

$$\mathcal{O}(0) = \{0, c, c^2 + c\}.$$

The boundary points move chaotically. Thus, the idea is to change the points by using the speed of convergence as an adaptive value. The principle of our algorithm is to have a set of points evolved to the fractal boundary. For this, one gives a weight to each point. This weight varies with a dynamics which "rewards" the most adapted points (the points which are less attracted by limit values) and "penalizes" the least interesting ones. When the most efficient points reach a certain threshold, they are allowed to be multiplied in their neighborhood. The least efficient points disappear when they reach a minimal threshold. This system of thresholds which changes the dynamical structure is our meta-dynamics.

Dynamical level (DL): with the formalism of definition 1, we have $T_0 = \mathbb{N}$. The index set I is the set of all finite sets of points of \mathbb{C} (so i is a set of points

³Let $\mathbb{K} = \mathbb{R}$ or \mathbb{C} , $f : \mathbb{K} \rightarrow \mathbb{K}$ be function, $x \in X$ is *periodic* of period $n \in \mathbb{N}$ if $f^n(x) = x$ and for all $k \in \{1, \dots, n - 1\}$, $f^k(x) \neq x$. For x periodic of period n , the *cycle* $\mathcal{O}(x)$ is the set

$$\mathcal{O}(x) = \{x, f(x), \dots, f^{n-1}(x)\}$$

and its cardinal is n . Moreover, if f is differentiable at x , x is *stable*, *quasi stable* or *unstable* if $|(f^n)'(x)| < 1$, $|(f^n)'(x)| = 1$ or $|(f^n)'(x)| > 1$. If x is stable, x is *attractive* if there exists an interval V strictly containing x so that for all $x \in V$

$$f^n(x) \xrightarrow{n \rightarrow +\infty} x.$$

of \mathbb{C} and I is not countable). For all $i \in I$, $X_i = \mathbb{N}^{card(i)}$ is the set of the point weights of i . At each given point $z \in \mathbb{C}$, we attach a selective value

$$\begin{aligned} \mu_n : \mathbb{C} &\rightarrow \mathbb{R}^+ \\ z &\mapsto \min \left\{ |P_c^n(z)|, |P_c^n(z) - c|, |P_c^n(z) - c^2 - c|, \frac{1}{|P_c^n(z)|} \right\} \end{aligned}$$

$\{0, c, c^2 + c\}$ is the attractive cycle of period 3, $\frac{1}{P_c^n(z)}$ is referring to the attraction to the infinity seeing that $P_c^n(z) \xrightarrow{n \rightarrow +\infty} \infty$ is equivalent to $\frac{1}{P_c^n(z)} \xrightarrow{n \rightarrow +\infty} 0$. One increases the weight of the points which are close to the boundary. In order to do this, we organize a ‘‘competition’’ by comparing their mutual slowness of convergence. So, the weights of the points $z \in i$ are given by

$$\begin{aligned} \omega_z(t+1) &= \omega_z(t) + \sum_{q \in i, q \neq z} \delta(z, q) \text{ with } \delta(z, q) = \begin{cases} 1 & \text{if } \mu_t(z) > \mu_t(q) \\ 0 & \text{if } \mu_t(z) = \mu_t(q) \\ -1 & \text{if } \mu_t(z) < \mu_t(q) \end{cases} \\ \omega_z(0) &= 0 \end{aligned}$$

where $t \in \mathbb{N}$. Using the notation of section 2, we have the following transition function

$$\varphi_i(t+1, t, \{\omega_z(t)\}_{z \in i}) = \{\omega_z(t+1)\}_{z \in i}$$

for all $t \in \mathbb{N}$. For each state space there is only one associated transition function, so the use of the index set J is unnecessary.

Meta-dynamical level (ML): with the formalism of definition 1, we have $T_1 = k\mathbb{N}$. When the weight of a point reach an upper threshold $M > 0$, the point is allowed to give birth to a new point, randomly in its neighborhood. When the weight of a point reaches a lower threshold $m < 0$, the point is removed. This can be modelled by the meta-dynamical rule

$$\Phi \left(t, \{\omega_z(t)\}_{z \in i(n)}, \varphi_{i(n)} \right) = \left(\{\omega_{z'}(t)\}_{z' \in i(n+1)}, \varphi_{i(n+1)} \right)$$

where

$$\begin{aligned} i(n+1) &= \{z + \varrho\epsilon : \varrho \text{ is a random point in } \mathcal{B}, z \in i(n) \text{ and } \omega_z(t) > M\} \cup \\ &\{z \in i(n) : \omega_z(t) \geq m\} \end{aligned}$$

such that $\epsilon > 0$ given. The weight of the reproduced point is shared between itself $\omega_z(t)$ and the new neighbouring point $\omega_{z+\varrho\epsilon}(t)$. The other weights are kept equal. Let us sum up the evolution rule:

$$\dots \rightarrow \varphi_{i(n)}(t) \xrightarrow{\text{DL}} \varphi_{i(n)}(t+1) \xrightarrow{\text{DL}} \dots \xrightarrow{\text{DL}} \varphi_{i(n)}(t+k) \xrightarrow{\text{ML}} \varphi_{i(n+1)}(t+k) \rightarrow \dots$$

As the time increases, the selective value becomes more and more accurate, i.e. $i(n)$ tends to a set of points belonging to the Julia space J_{P_c} or to the empty set when $n \rightarrow +\infty$. This is an interesting point because the calculations are concentrated on the fractal boundary. In a lot of classical algorithms, the

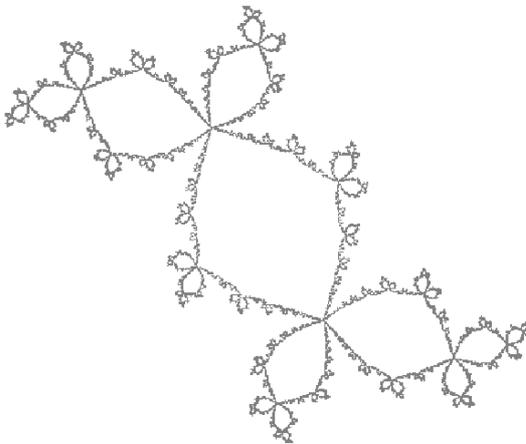


Figure 2: The Douady's Rabbit fractal

calculation time is squandered for points in the interior $\overset{\circ}{K}_{P_c}$ (see [16]). Indeed, this meta-dynamical adaptive system produces a cloud of points which gather round the Julia space J_{P_c} called the Douady's Rabbit fractal (see Fig. 2).

Though we have developed this algorithm in the setting of Julia sets, the same framework can be used to explore many complex frontiers, for example other fractal structures where the boundary properties are largely unknown. Indeed, this kind of algorithm is really interesting because the calculation is concentrated on a specific region.

4 Adaptive differential equations

First, let us recall the classical notion of Hausdorff fractal dimension (see [17]). Let \mathcal{E} be a subspace of a metric space \mathcal{M} and ρ a positive number, one defines \mathcal{R}_ρ as the set of all coverings $(\mathcal{B}_i, \rho_i)_i$ of \mathcal{E} by balls \mathcal{B}_i with diameter $0 < \rho_i < \rho$. For each positive number α , one denotes:

$$H_\rho^\alpha(\mathcal{E}) = \inf \left\{ \sum_i \rho_i^\alpha : (\mathcal{B}_i, \rho_i)_i \in \mathcal{R}_\rho \right\}.$$

$H^\alpha(\mathcal{E}) = \lim_{\rho \rightarrow 0} H_\rho^\alpha(\mathcal{E})$ is called the α -dimensional Hausdorff measure of \mathcal{E} and belongs to $[0, +\infty]$. Then, let

$$\dim(\mathcal{E}) = \inf \{ \alpha > 0 : H^\alpha(\mathcal{E}) = 0 \},$$

it is the Hausdorff dimension of \mathcal{E} . On the one hand, the Hausdorff dimension is defined for all metric spaces. On the other hand, in the case of a classical space (non fractal), it is identical to its topological dimension (for example the Hausdorff dimension of \mathbb{R}^n is n). In the case of a simple linear fractal, such

as fractals with internal homothetia obtained by an homothetic iteration with constant ratio, the Hausdorff dimension is equal to the homothetic dimension $dim_h(\mathcal{E})$ given by:

$$dim_h(\mathcal{E}) = \frac{\ln(n)}{\ln(k)} = \log_k(n)$$

where n is the number of subsets obtained during the homothetic process of reduction with ratio $\frac{1}{k}$ (see [5]). For more information on dimension theory the reader may refer to [19] or [10].

The variable dimension space is defined as follows:

Definition 8 Let \mathcal{M} be a metric space and Λ a parameter space. One defines two maps $d : \Lambda \rightarrow [0, +\infty]$, $\lambda \mapsto d(\lambda)$ and $F : \Lambda \rightarrow 2^{\mathcal{M}}$ where $F(\lambda)$ verifies $dim F(\lambda) = d(\lambda)$ and $2^{\mathcal{M}}$ is the family of non-empty subsets of \mathcal{M} . $F(\Lambda)$ is a set of variable dimension spaces. If $F(\Lambda)$ is a totally ordered set for the inclusion, one calls (F, d) a variable dimension space. d is the dimension function and $d(F(\lambda)) \leq d(\mathcal{M})$ for all $\lambda \in \Lambda$. If Λ is a topological space then F is a set valued function and we may take account of the regularity of d . The variable dimension space (F, d) is continuous if d is continuous. Moreover, if Λ is an ordered space then (F, d) is increasing (respectively decreasing) if d is increasing (respectively decreasing).

To illustrate these definitions, we can consider the following example:

Example 9 Let $\frac{1}{4} \leq \lambda \leq \frac{1}{2}$, one defines four similarities from the family K^c of the compact subset of the square $c = [0, 1]^2$ with value in K^c by

- $s_{1,\lambda}(x) = \lambda x$,
- $s_{2,\lambda}(x) = \lambda \begin{pmatrix} \frac{1}{2} - \lambda & -\sqrt{\lambda - \frac{1}{4}} \\ \sqrt{\lambda - \frac{1}{4}} & \frac{1}{2} - \lambda \end{pmatrix} x + \begin{pmatrix} \lambda \\ 0 \end{pmatrix}$,
- $s_{3,\lambda}(x) = \lambda \begin{pmatrix} \frac{1}{2} - \lambda & \sqrt{\lambda - \frac{1}{4}} \\ -\sqrt{\lambda - \frac{1}{4}} & \frac{1}{2} - \lambda \end{pmatrix} x + \begin{pmatrix} \frac{1}{2} \\ \sqrt{\lambda - \frac{1}{4}} \end{pmatrix}$ and
- $s_{4,\lambda}(x) = \lambda x + \begin{pmatrix} 1 - \lambda \\ 0 \end{pmatrix}$.

Then, one defines the function $\Omega_\lambda : K^c \rightarrow K^c$, $x \mapsto s_{1,\lambda}(x) \cup s_{2,\lambda}(x) \cup s_{3,\lambda}(x) \cup s_{4,\lambda}(x)$.

Ω_λ being contracting, one defines $F(\lambda)$ as the fixed point⁴ of this function for the Hausdorff distance. In [13], one may find the following result: the dimension

⁴To prove this, one uses two classical results: the family of subsets of a Banach space endowed with the Hausdorff distance is also a Banach space and if the similarities are contracting in K^2 , then the function Ω_λ is also contracting in K^c with the Hausdorff distance [20].

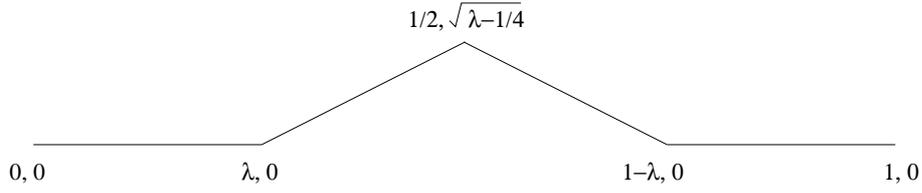


Figure 3: Van Koch snowflake generator

of $F(\lambda)$ is $d(\lambda) = \frac{\ln 4}{\ln(\frac{4}{\lambda})}$. So, (F, d) is a continuous increasing variable dimension space on $\Lambda = [\frac{1}{4}, \frac{1}{2}]$. A similar construction allows us to turn continuously a n -dimension space into a $(n+1)$ -dimension space.

An interesting application of the above concept arises when the variable dimension space is the state space of the solutions of a differential equation over a period of time. The union of the solutions then “moves” on a variable dimension space. We talk about an adaptive differential equation.

Definition 10 Let X be a Banach space of finite dimension called the possible state space. Consider

1. a subdivision $\{t_i\}_{i \in \mathbb{N}}$ of \mathbb{R}_+ ,
2. an application $d : \mathbb{R}_+ \times X \rightarrow \mathbb{N}$, $(t, y) \mapsto d(t, y)$ such that $d(0, y)$ is given,
3. an application $g : \mathbb{R}_+ \times \mathbb{R}^{\dim(X)} \rightarrow \mathbb{R}^{\dim(X)}$,

such that one has the system

$$\begin{cases} \dot{x}_i(t) = f_i(t, x_i(t)), t \in [t_i, t_{i+1}[, x_i(t) \in \mathbb{R}^{d(t_i, y_i)}, i \in \mathbb{N} \\ x_i(t_i) = g(t_i, y_i) \end{cases} \quad (3)$$

where $y_0 = x_0(0)$, $y_i = \lim_{t \rightarrow t_i^-} x_{i-1}(t)$ for $i \in \mathbb{N}^*$, $\dot{x}_i(\cdot)$ is the right derivative of $x_i(\cdot)$ and

$$\{f_i\}_{i \in \mathbb{N}} : [t_i, t_{i+1}[\times \mathbb{R}^{d(t_i, y_i)} \rightarrow \mathbb{R}^{d(t_i, y_i)}$$

is a family of applications. Such a system is called an adaptive differential equation. A trajectory of the system (3) is a family

$$x(t) = \{x_i(t) : t \in [t_i, t_{i+1}[]\}_{i \in \mathbb{N}}.$$

One may notice that $\dim(g(t_i, y_i)) = d(t_i, y_i)$. This concept of adaptive differential equation is not a succession of ordinary differential equations because the initial condition of each system i depends on the system $i-1$. The ordinary differential equations represent a case where d is constant.

The adaptive differential equation is a reductive approach of the meta-dynamical adaptive system to a system described by a differential equation whose meta-dynamics is discrete and where $\dim X < +\infty$.

5 Application to a biological model

Here, we want to model the influence of the bacterium-phage interaction on the co-evolution of the populations of bacteria and phages. In the following we will need the definition of the Hamming distance. Let $n \in \mathbb{N}$, the *Hamming distance* is the function $d_H : \{0, 1\}^n \rightarrow \mathbb{N}$ defined by

$$d_H(s_1, s_2) = \sum_{k=0}^{n_c} |s_i^k - s_j^k|$$

where $s_1, s_2 \in \{0, 1\}^n$. d_H represents the number of differing bits between the two binary strings $s_1 = s_1^1 s_1^2 \dots s_1^n$ and $s_2 = s_2^1 s_2^2 \dots s_2^n$.

The attack of a bacteria population by phages is assumed to be done by the lysis process: a phage hangs on the surface of a bacterium cell, injects its DNA in it and then forces the bacterium to yield its own replicas inside the cell. When the cell is full, it bursts, releasing a huge quantity of copies of the infecting phage. The efficiency of the attack (i.e. the probability of success of the infection), depends on the couple bacterium-phage. One of the other characteristics of bacterial and phages populations are their high variabilities. They frequently mutate, creating new populations with new properties. Such a system has two dynamics to be taken into account: the dynamics of the populations of bacteria and phages and the meta-dynamics of evolution geared by mutations and extinctions. It is without any doubt a model which is not in the scope of the classical theory of dynamical systems, but our formalism applies well to it.

Dynamical level: it is made up of a set of ordinary differential equations. Let us consider the following system

$$\{S, \{B_i\}_{0 \leq i \leq n_b}, \{P_j, I_{1,j}, I_{2,j}, I_{3,j}\}_{0 \leq j \leq n_p}\}, \quad (4)$$

with S the concentration of nutrient, B_i the different bacteria strains with $0 \leq i \leq n_b$ and P_j and $I_{k,j}$ the different phages strains with $0 \leq j \leq n_p$. To each population B_i and P_j is associated a binary string $s_i^b \in \{0, 1\}^n$ and $s_j^p \in \{0, 1\}^n$. These binary strings code for the properties of attack (for the phages) or defence (for the bacteria) facing the infection (see [2] for the biological discussion). The populations are then characterized by the different concentrations and the two lists of bit strings. The set L of all the pairs of lists is taken as our second index (the one called J in definition 1).

The model is described by a modified version of Mosekilde equations (see [15]). This set of ordinary differential equations describes the interactions of bacterial populations B_i and phage populations P_j in a chemostat. B_i and P_j also symbolize the concentration of these populations and S the concentration of the nutrient. The process of infection of bacteria by phages is modelled by three infection stages $I_{1,j}$, $I_{2,j}$ and $I_{3,j}$. One associates with the ecosystem (4) the state space $X_{1+n_b+4n_p} = \mathbb{R}_+^{1+n_b+4n_p}$. Over a period of time without appearance or disappearance of any strain of bacteria or phages, the dynamical

evolution of the system (4) is modelled by the evolution of the concentrations of S , the different bacteria B_i and phages P_j , and three infection stages $I_{k,j}$. With the formalism of definition 1, that means that $T_0 = \mathbb{R}$ and for a fixed $l \in L$ the transition function $\varphi_{1+n_b+4n_p,l}$ is the integration of the following set of differential equations

$$\left\{ \begin{array}{l} \frac{dB_i}{dt} = \frac{\nu SB_i}{\kappa+S} - B_i \sum_{j=1}^{n_p} \alpha \omega_{ij} P_j - \rho B_i \\ \frac{dI_{1,j}}{dt} = P_j \sum_{i=1}^{n_b} \alpha \omega_{ij} B_i - 3 \frac{I_{1,j}}{\tau} - \rho I_{1,j} \\ \frac{dI_{2,j}}{dt} = \frac{3}{\tau} (I_{1,j} - I_{2,j}) - \rho I_{2,j} \\ \frac{dI_{3,j}}{dt} = \frac{3}{\tau} (I_{2,j} - I_{3,j}) - \rho I_{3,j} \\ \frac{dP_j}{dt} = 3 \frac{\beta I_{3,j}}{\tau} - P_j \left(\sum_{i=1}^{n_b} \alpha B_i + \sum_{j=1}^{n_p} \sum_{k=1}^3 \alpha I_{k,j} \right) - \rho P_j \\ \frac{dS}{dt} = \rho(\sigma - S) - \sum_{i=1}^{n_b} \frac{\nu \gamma S B_i}{\kappa+S} \end{array} \right. \quad (5)$$

with $0 \leq i \leq n_b$, $0 \leq j \leq n_p$, ρ the rate of dilution ($\rho = 0.0045 \text{ min}^{-1}$), κ and ν respectively the saturation term and the growth from the Monod equation ($\kappa = 10 \mu\text{g.ml}^{-1}$, $\nu = 0.024 \text{ min}^{-1}$), α the theoretical adsorption constant depending on phage and bacterium size ($\alpha = 10^{-9} \text{ ml. min}^{-1}$), τ a time constant ($\tau = 30 \text{ min}$), β the number of copies of phage j released during the burst of the infected bacterial cell ($\beta = 100$), σ the continuous supply of substrate ($\sigma = 10 \mu\text{g.ml}^{-1}$), γ the amount of nutrient consumed in each cellular division ($\gamma = 0.01 \text{ ng}$) and finally ω_{ij} the probability of infection of B_i by P_j which depends on the similarity between bit string s_i^b (attached to bacterium population B_i) and s_j^p (attached to phage population P_j) as follows

$$\omega_{ij} = \left(1 - \frac{d_H(s_i^b, s_j^p)}{n_c} \right)^2$$

with n_c the size of the binary string.

Here, we are not interested in the identification of the biological dynamical level which can be found in [2]. With the given size of a binary string n_c , there exists a finite number of possible dynamical systems, here differential equations. Indeed, the number of possible different populations of bacteria is equal to the number of parts of the set of binary strings of size n_c . So, there are $2^{2^{n_c}}$ possible populations of bacteria. For the same reason, one deduces that the possible number of populations of phages is the same and thus the total number of possible state spaces is $2^{2^{n_c}} \times 2^{2^{n_c}} = 2^{2^{n_c}+1}$. So, with the notation of definition 1, it means that $\text{card}(J) = 2^{2^{n_c}+1}$. If we take for example $n_c = 10$, one has $2^{1025} \simeq 3.6 \times 10^{308}$ possible state spaces. Theoretically, one can consider a 3.6×10^{308} dimensional space to embed the system (5). Nevertheless, when it comes to numerical simulations, such a big system is impossible to deal with.

One thus understands the need of an adaptive system to describe the system (5).

Meta-dynamical level (meta-dynamical adaptive system point of view): this is the main difference with the model of Mosekilde given in [15, Chapter A] which is not evolutive.

Proposition 11 *Consider a small interval of time Δt , the adaptive changes of the system (4) are given by the following mechanisms*

$$p\Psi(t + \Delta t, t, \delta, \varphi_{2+n_b+4n_p, l_1}) \cdot (\theta_1, \dots, \theta_k, \varphi_{1+k_\delta+n_b+4n_p, l_2}) = e^{-\lambda(t)} \frac{\lambda(t)^k}{k!} \quad (6)$$

and

$$\Psi(t + \Delta t, t, \delta, \varphi_{2+n_b+4n_p, l_1}, m_\delta) = \varphi_{2-\epsilon_\delta+n_b+4n_p, l_2} \quad (7)$$

where

1. formula (6) is the probability that the species δ (a bacterium B or a phage P) gives birth to $k \geq 1$ mutante strains $\theta_1, \dots, \theta_k$ on $[t, t + \Delta t[$ with $\lambda(t) = \frac{\delta(t)}{\delta_e} p_e$, p_e the probability that a small group of mutant species of size δ_e gradually replacing the species of the parent population δ . $\varphi_{i,j}$ is the function defined by equations (5) for $j = l_1, l_2$ and $k_\delta = k$ if δ is a bacterium and $k_\delta = 4k$ if δ is a phage,
2. formula (7) gives the determinist rule of the extinction of the species δ which depends on a given threshold m_δ , $\epsilon_\delta = 1$ if δ is a bacterium and $\epsilon_\delta = 4$ if δ is a phage.

$p\Psi$ is the stochastic transition function of definition 7 which governs the meta-dynamical rule of the appearance. Ψ is the transition function of definition 1 which governs the meta-dynamical rule of the extinction.

Proof. Consider the probability $p_{B_i}(t, k)$ that the population B_i gives birth to k mutante strain on $[t, t + \Delta t[$ and the probability p_e that a small group of mutante bacteria of size B_e is gradually replacing the bacteria of the parent population B_i . Such a reasoning gives a binomial probability for

$$p_{B_i}(t, k) = C_{n(t)}^k p_e^k (1 - p_e)^{n(t)-k}$$

with $n(t) = \frac{B_i(t)}{B_e}$. When $n(t)$ is large, one may approximate the binomial probability by the Poisson probability

$$p_{B_i}(t, k) \simeq e^{-\lambda(t)} \frac{\lambda(t)^k}{k!} \quad (8)$$

with $\lambda(t) = \frac{B_i(t)}{B_e} p_e$. Suppose that the birth of all the populations to a Hamming distance of one (only one bit is different) is equiprobable. The birth of a mutant strain results in the change of a group of bacteria (which is a part of a parent population) of size B_e , in a population group with new characteristics. If this

population group already exists, the mutant population is added to it. The same mechanism governs the modelling of the phage mutation. For the extension, there exists a threshold m_δ below which the extinction of the population is certain. Every population under a given threshold (different for bacteria m_B and phages m_P) is removed from the system. Thus, the extinction is deterministic. ■

We have defined the macroscopic birth of a mutant population as an event occurring on an interval $[t, t + \Delta t[$. There exists a time set T_1 where the system (5) commutes. This commutation depends on the state of the system (5) and on the coefficient p_B et p_P respectively coefficient of the Poisson law of the bacterium and the phage. In order to simplify the model and to make it computable, one may suppose that

$$T_1 = t_0 + i\Delta t$$

even if in practice, the mutations have no reasons to be periodically defined. This allows to define, with the previous notations, the meta-dynamical rule

$$p\Phi(t_0 + i\Delta t, \delta, \varphi_{2+n_b+4n_p, l_1}) \cdot (\theta_1, \dots, \theta_k, \varphi_{1+k_\delta+n_b+4n_p, l_2}) = e^{-\lambda(t)} \frac{\lambda(t)^k}{k!}$$

$$\Phi(t_0 + i\Delta t, \delta, \varphi_{2+n_b+4n_p, 1}, m_\delta) = \varphi_{2-\epsilon_\delta+n_b+4n_p, 2}.$$

Then, at each step Δt there are four possible commutations:

- birth of a new bacterial strain: a variable B_{n_b+1} is added, the dimension of the system (5) increases by one,
- birth of a new phagical strain: four variables are added: P_{n_p+1} , I_{1, n_p+1} , I_{2, n_p+1} and I_{3, n_p+1} , the dimension of the system (5) increases by four,
- extinction of a bacterial strain: the concerned variable is removed, the dimension of the system (5) decreases by one,
- extinction of phagical strain: variables of the concerned phage are removed, the dimension of the system (5) decreases by four.

The different possible state spaces resulting from a commutation are given on figure 4.

If more than one event occurs at each moment $t \in T_1$, one composes the possible change of state spaces (for example, the extinction of a phage combined with the birth of a bacterial strain decreases the dimension of the system (5) by $4 - 1 = 3$).

Meta-dynamical level (adaptive differential equation point of view): we have described the biological model as a stochastic meta-dynamical adaptive system by using definition 7. This modelling corresponds to a stochastic view of the system (4) where the space of all stochastic realizations is infinite. There exists a family of points $\{t_i\}_{i \in \mathbb{N}}$ where the system (5) commutes. We have supposed that this commutation is given by $t_i = t_0 + i\Delta t$. Then, at each

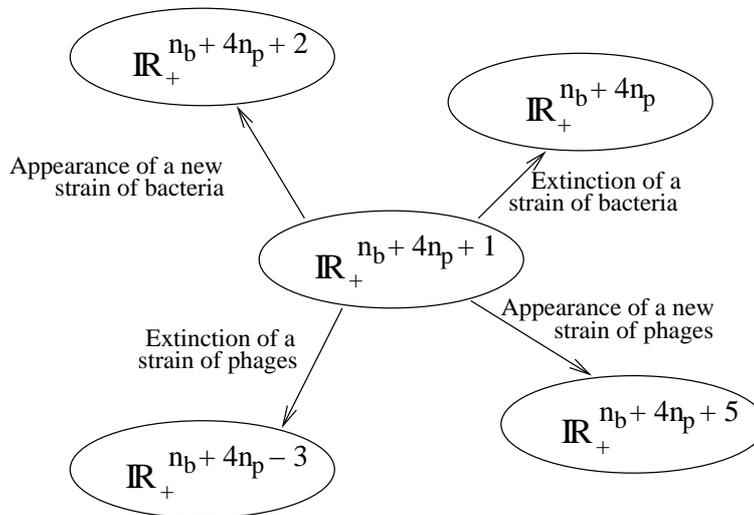


Figure 4: Evolution of the state space with n_b and n_p respectively the number of bacterial and phage strains before the transition.

step Δt the system may commute. To see a possible evolution of the system (4), we choose a stochastic realization at each point t_i (only for the appearance of a strain because the extinction of a strain is deterministic) $g(t_i, y_i)$ where $y_i = \lim_{t \rightarrow t_i^-} x_{i-1}(t)$ with $x_{i-1}(t)$ the solution of the system (5) on $[t_{i-1}, t_i[$. It describes the deterministic evolution of the system (4). By extension, for us a *stochastic realization* is a function

$$g : \mathbb{R}_+ \times \mathbb{R}^{\dim(X)} \rightarrow \mathbb{R}^{\dim(X)}$$

defined at least on $\{(t_i, y_i)\}_{i \in \mathbb{N}}$. For a given realization g , the system (4) may be modelled by an adaptive differential equation whose equations are given by the system (5). This modelling belongs to the variable dimensional space $\mathbb{R}_+^{n_b + 4n_p + 1}$ where $n_b + 4n_p + 1$ depends on g and follows the rule given on figure 4. A detailed study of this biological model with implementation can be found in [3].

In this example, one sees that the framework of the adaptive differential equations corresponds to the case of a transition function defined by a set of differential equations and a meta-dynamical time reduced to a discrete subset of \mathbb{R} .

6 Conclusion

We started our research with a biological system whose dynamics changes in different dimensions. Seeing that there was no mathematical framework to describe such a system, we have developed a mathematical tool following Kalman's

dynamical system called meta-dynamical adaptive system which was appropriate to give a constructive algorithm for some fractals. It was also adapted to describe and analyze our biological system. However, we have found our tool too general and we decided to develop a special tool for differential equations. The new system called “adaptive differential equation” is not a succession of differential equations because the initial condition of each system depends on the previous system and gives the new dimension of the following system. This model allows to describe a system of changing differential equations, in particular the stochastic realization of a stochastic meta-dynamical adaptive system. The last tool we use is the “variable dimension space”. This new kind of space links the notion of space and dimension in a changing dynamics. We think that our work will contribute to understand the huge number of complex systems where the space of exploration is too big to be investigated with classical means.

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