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PHYSICAL TIME GROWTH FUNCTIONS ASSOCIATED WITH DEVELOPMENTAL MODELS OPERATING IN PHYSIOLOGICAL TIME

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"Physiological time varies -in rate does it? and if so, in what sense?- from one organism to another, and from one stage to another in the development of a single one."

P.B. Medawar.

Physical time growth functions associated with developmental models operating in physiological time *)

by

P.M.B. Vitányi

ABSTRACT

The theory of growth functions as developed on the basis of Lindenmayer systems (also called developmental models) seems unable to account for several phenomena occurring in developmental biology. If, however, we drop the assumption that changes (=rewriting of strings) in the system occur at unit time intervals, we can describe phenomena like progressive dissipation of growth energy, biological rhythms, changes in environmental conditions which influence the growth rate etc., in the model. Thus we derive a hybrid model by assuming discrete cells and instantaneous cell division but continuous time. The number of past rewritings then corresponds to physiological time and the total time consumed to physical time. It is shown how, e.g., exponential growth in physiological time may lead to a logistic growth curve in physical time and, similarly, linear growth in physiological time to monomolecular growth in physical time. Both physical time growth functions are examples of sigmoïdal growth curves, generally occurring in developmental biology, hitherto unattainable in the theory of growth functions of L systems. Some extensions of the model are discussed and an interpretation in terms of table Lindenmayer systems with a computable control word is given. The strength of the results seems to lie in the fact that the model relates stereotype elemental (cellular) behavior to empirically observed overall growth curves.

KEYWORDS & PHRASES: *Lindenmayer systems, biological development, growth functions, physiological time, sigmoidal growth.*

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*) This report will be submitted for publication elsewhere.

1. INTRODUCTION

In about 1968 Lindenmayer proposed automata theoretic models for growth and development of (filamentous) multicellular organisms. These models (named L systems after their originator) have caused much activity from the side of mathematicians and formal language theorists (see e.g. HERMAN and ROZENBERG [1975], ROZENBERG and SALOMAA [1974], LINDENMAYER and ROZENBERG [1976]) but have not yet been adopted to a great extend by workers in the field of developmental biology. An exception can be found in LÜCK and LÜCK [1976]. One reason for this lack of interest might be that the mathematical questions considered in L system theory have no interest, or even interpretation, for the biologist. A fundamental difficulty may be that the basic assumptions of the model are such that it is not adequate at all to model certain biological phenomena. This can be remedied by adding features ad hoc, which in fact is mostly done in biological applications of the theory. As a consequence, the mathematical fabric which has been woven on the firm fundaments of the basic assumptions than comes apart and for a large part does not hold for the featured model.

SZILARD [1971] initiated the study of growth functions of Lindenmayer's developmental models. Under the restriction that there is no interaction amongst cells this leads to a nice closed form solution for growth functions: a combination of exponential and polynomial terms (see section 2). However, the model can not account for empirically derived growth functions such as the logistic one $A/(1+Be^{-kt})$ or the monomolecular one $A(1-Be^{-kt})$ (cf. MEDAWAR [1945]). Even the introduction of cell interaction does not help us out. In the first place we get quite unlikely flows of messages through the organism (see e.g. HERMAN and ROZENBERG [1975]) which are more suitable to electronic computers and in fact give the organism the computing power of one. In the second place, we are still not able to obtain growth which, always increasing the size of the organism, tends towards stability in the limit. The slowest increasing growth we can obtain by allowing cell interaction is logarithmic and thus cannot account for the asymptotic behavior of sigmoïdal growth functions like the logistic and monomolecular ones.

Apart from this it can be argued that, for instance, purely exponential growth such as met in the theory of L systems, does not reflect biological reality: in a short time the organism would fill the universe! However, it has been shown that under continuous culture conditions bacteria and monocellular algae can easily be kept under exponential growth as can filamentous algae, Lück (private communication). Of course, if the culture medium remains unaltered in time, as is eventually the case, there will be a sigmoïdal growth curve. Mostly, growth curves of higher plants show this form. Sometimes, there is also a very long, nearly linear, median phase. Lianes grow like that. In any case, that real growth normally stops somehow is not necessarily related to food constraints but can also be the result of higher hierarchical processes such as flowering. Actually, in the last decades serious experimental workers seem only to consider the first so-called exponential phase.

Growth functions as occurring in developmental biology have a purely empirical origin. The size of an organism is plotted graphically against its age. The resulting curve is expressed, as accurately as need be, by means of an algebraïc equation. No biological significance is attributed to the exact form it takes. The growth function's chief function is to facilitate the analysis of the curve of growth (MEDAWAR [1945]).

In this paper we attempt to clarify what in our view are some of the shortcomings of the otherwise quite appealing model of Lindenmayer and how to overcome them. As examples we show how to derive logistic and monomolecular growth curves.

In biology, as opposed to the usual automata theoretic approaches, we meet the problem of environment. In an organism each cell has an environment (apart from the adjacent cells) which is going to influence its behavior, c.q. division rate. In algae this is the surrounding water from which it draws its food. In larger plants the environment consists of the outside world and inside the organism e.g. the vessels which transport nutricients. Furthermore, growth inhibitors, temperature and, for all we know, the phases of the moon will influence the growth rate of the organism. Of course, every one of these exogenous influences may occasion changes in endogenous parameters. Apart from this, e.g. the following empirical generalisations are mentioned by MEDAWAR [1945].

(i) Size is a monotonic increasing function of age.

(ii) Usually, what results from growth is itself capable of growing.

(iii) Under the actual conditions of development living tissue progressively loses power to reproduce itself at the rate it was formed.

In automata theory we are dealing with abstractions which are not subject to physical constraints, and identical cells do identical things at all times. In actual organisms, differences in environment in space and time are going to create differences in cell behavior such as division rates etc. So even if we assume that a cell is essentially an autonomous unit, changes and divisions do not occur at unit time intervals, but division times are governed by environmental parameters, like concentration and accessibility of nutricients, growth inhibitors, enzymes, temperature, light. It will come as no surprise that this is corroborated by experimental evidence.

The biologist observed very little real differences in cell types/ states (e.g. cells with distinct stereotype behavior). Erickson in his experiments with growth in corn cobs essentially distinguishes between cells in the core and those in the surrounding tissue only, and insists that all cells in one of these areas behave more or less alike. The Lücks, experimenting on algae, distinguish between four cell types (according to ancestry). Under changing environmental conditions they observe changes in size and division times only (private communication).

To account for differences in cell behavior induced by time or extracellular agents, the automata theorist is inclined to postulate a very large number of cell states. In doing so, he makes no distinction between the autonomous properties of cells and changes in division times due to extracellular agents. We can overcome this difficulty by assuming but a few different cell types and taking intervals between changes in the model as a variable quantity. We shall call the elapsed time *physical* or *real* time and the number of times the model has undergone changes *physiological* time. This is in agreement with biological terminology. To quote MEDAWAR [1945].

..."Growth is more rapid earlier in life than later, and if the time intervals are equal in length -are days for example- the approximation

will correspondingly be less efficient at the beginning than at the end. The length of the choosen interval should evidently bear some relation to the work done by the organism in its life span; to the organism's "physiological age" in fact... (Physiological time is biology's claim to be considered at least as obscure to the lay mind as theoretical physics. The organism it is argued, dispenses a Time of its own making by a just measure of the work done...)"

We want to show that the underlying model of L systems, even without cellular interactions, gains in adequacy and explaining power if we treat the time intervals between changes of cell states and division as a function of elapsed time, environmental parameters, and possibly the number of previous changes. Hence we consider L systems operating in physiological time and their associated physical or real time growth functions. Later on we solve some examples yielding well known growth curves. In the last section we formulate some extensions of the model on which the automata theorist might want to turn lose his bag of tricks, and show some relations with so-called table L systems.

2. LINDENMAYER SYSTEMS AND GROWTH FUNCTIONS

A *deterministic context free Lindenmayer system (DOL system)* is a triple $G = \langle W, \delta, w \rangle$ where W is a finite nonempty *alphabet*, δ is a *homomorphism* from W^* into W^* and $w \in WW^*$ is the *initial string*.

The alphabet W symbolizes the set of different cell states (cell types with distinct stereotype behavior or appearance), δ describes the transition of a cell from one state to another or the division of a cell in a string of cells, and the initial string symbolizes the (filamentous) organism we deal with initially. An element (string) of W^* symbolizes a linear array of cells.

We define the composition of i copies of δ by $\delta^0(v) = v$ and $\delta^i(v) = \delta(\delta^{i-1}(v))$ for each string $v \in W^*$ and all $i > 0$. The sequence produced by G is $S(G) = w, \delta(w), \delta^2(w), \ldots, \delta^i(w), \ldots$ where $\delta^i(w)$ symbolizes the stage the organism is in after i string rewritings (or physiological time steps). The *growth function* of G is defined as $f_G(i) = \lg(\delta^i(w))$, i.e., the *length* of $\delta^i(w)$ (the number of occurrences of letters in $\delta^i(w)$).

We can derive a closed form solution for f_G as follows, cf. PAZ and SALOMAA [1973] and SALOMAA [1973].

Associate wich each element v of W^* its *Parikh vector* $\bar{v}$, i.e., the row vector $(i_1,i_2,\ldots,i_n)$ where i_j denotes the number of occurrences of a_j in v, $1 \leq j \leq n$, for $W = \{a_1,a_2,\ldots,a_n\}$. The *growth matrix* M_G of G is the $n \times n$ matrix of which the j-th row consists of $\overline{\delta(a_j)}$. It is easy to see that $\overline{\delta^i(w)} = \bar{w} M_G^i$ and

$$(1) \qquad f_G(i) = \bar{w} M_G^i \eta$$

where $\eta = (1,1,\ldots,1)^T$: the n dimensional unit vector. (T denotes transposition.) Now $f_G(i)$ is the number of cells in the organism after i rewritings. If we want $f_G(i)$ to denote the length or weight of the organism after i rewritings, and different cell types have different lengths/weigths we only have to choose η in $\mathbb{R}_+^n$ ($\mathbb{R}_+$ denotes the set of positive real numbers) such that the j-th element of η is the length/weight of a cell (type) a_j. This causes no difficulties with the now following theory and was done by POLLUL and SCHÜT [1975].

According to the Cayley-Hamilton theorem, M_G must satisfy its own characteristic equation: $p(x) = \det(M_G - Ix) = 0$, where 0 denotes the n x n matrix with zero entries. For each $i \geq n$, after multiplication with M_G^{i-n}, left multiplication with $\bar{w}$ and right multiplication with η, the following homogeneous linear difference equation with constant coefficients holds

$$(2) \qquad f_G(i) = \sum_{j=1}^{n} b_j f_G(i-j), \quad i \geq n,$$

where $p(x) = \sum_{j=0}^{n} b_j x^{n-j}, b_0 = 1$, is the characteristic polynomial of M_G. From known facts concerning such difference equations it follows that the closed form solution of f_G is given by

$$(3) \qquad f_G(i) = \sum_{j=1}^{r} p_j(i) c_j^i,$$

where the c_i's are the r distinct roots of the characteristic equation $p(x) = 0$ of M_G, $p_j(i)$ is a polynomial in i of degree one less than the

multiplicity of the root c_j, $1 \leq j \leq n$. The constant coefficients of the terms of the polynomials $p_1(i), p_2(i), \ldots, p_r(i)$ are determined from $f_G(s)$, $f_G(s+1), \ldots, f_G(n)$ where s is the multiplicity of the zero root in $p(x) = 0$. (Remember that $f_G(i) = \lg(\delta^i(w))$ gives us the initial values of f_G.) For a more leisure introduction to the needed concepts in L system theory see e.g. HERMAN and VITÁNYI [1976].

Now imagine that the clock which governs the discrete time rewriting of the string of cells does not tick at unit time intervals (keeping physiological time) but rather at variable time intervals related with the changes in time of the influences exerted by environmental and internal parameters and maybe related with the number of previous rewritings, thus keeping real time. The time interval between the occurrences of the i-th and the i+1 th elements of S(G) is given by $t(i+1) - t(i)$ for some function $t: \mathbb{R}_+ \to \mathbb{R}_+$. Then the size (c.q. weight, number of cells) of the organism modeled is given by $L_G(t(i)) = f_G(i)$, or $L_G(t) = f_G(i(t))$ where $i = t^{-1}$, i.e., $i: \mathbb{R}_+ \to \mathbb{R}_+$ is the *function inverse* of $t: \mathbb{R}_+ \to \mathbb{R}_+$. (t has an inverse since it is strictly increasing.) i(t) gives the number of rewritings which have occurred op to time t as a function of the real time elapsed. It seems reasonable to assume that, e.g., the time delay between two consecutive stages (rewritings) of an organism, is connected with the concentrations of nutricients it has access to and waste products and growth inhibitors it secretes. Such concentrations will be related to the organism's size and history in that environment. So the fundamental relation is

$$L_G(t) = f_G(i(t)) \tag{4}$$

where $i: \mathbb{R}_+ \to \mathbb{R}_+$ is the physiological time as a function of the real time and $t: \mathbb{R}_+ \to \mathbb{R}_+$ is the real time as as function of the physiological time. The function i is found by describing in e.g. differential equations the relations between t, $L_G(t)$, the influences of environmental parameters which are not influenced by the organism such as temperature, day and night cyclus; the influences of environmental parameters which are influenced by the organism such as food concentration. To take a simple example where we do not ascribe a physical meaning to t(i): suppose

that $f_G(i) = 2^i$ and $t(i) = i^2$. Then $i(t) = \sqrt{t}$ and $L_G(t) = 2^{\sqrt{t}}$, a real time growth function of the so-called subexponential growth type.

Note that one assumption we have made is that the relative changes of time intervals in between the rewriting of a letter does not depend on the letter or its position in the string.

By some examples we show that we can derive by the above method well known biological growth functions. The problem of constructing real time growth functions for an organism modeled in physiological time by a DOL system consists in finding a plausible set of physical constraints (e.g. a set of differential equations), solving $i(t)$, and by substituting in $f_G(i)$ solving $L_G(t)$.

3. REAL TIME GROWTH FUNCTIONS OF LINDENMAYER SYSTEMS OPERATING IN PHYSIOLOGICAL TIME

In this section we investigate some examples of growth behavior we are liable to meet according to the theory developed above. We shall be concerned with algae-like organisms which (I) reside in a closed environment containing an initial amount of food stuff, (II) are subject to periodic speeding up and slowing down of division rates (i.e., some sort of biological rithm), and (III) (I) and (II) together.

(I) ORGANISMS IN A CLOSED INVIRONMENT CONTAINING AN INITIAL AMOUNT OF NUTRICIENTS.

Suppose we have (fig 1) a (filamentous) organism residing in a trough filled with water from which it draws its food. We shall assume that (i) the organism uses no food to maintain itself but only to grow; (ii) it excretes no waste products etc. which inhibit its growth; (iii) at all times the concentration of food throughout the trough is uniform; (iv). No parameters influence the growth except the concentration of food.

Let $a(t)$ be the concentration of nutricients at time t. Assume that for $a(t) \geq a_0$ the environment is optimal and the organism grows according to the modeling DOL system, i.e., physiological time and real time are the same. After some time, say t_0 time units, the food level has been depleted

to a_0 and the growth rate starts slowing down. Since the surface of the filamentous organism is proportional to its length (or the amount of cells it is made up off), i.e., the value of f_G, we choose our differential equations as follows.

$$\frac{da(t)}{dt} = - c_1 f_G(t) a(t) \tag{5}$$

where c_1 is the nutricient absorbtion constant pro unit of organism. This yields

$$a(t) = a(0) e^{-\int_0^t c_1 f_G(x) dx} \tag{6}$$

and substituting $a(t_0) = a_0$ yields t_0. From t_0 onwards the division times of cells grow larger because there is a food shortage and for $t \geq t_0$ we have

$$\frac{da(t)}{dt} = - c_1 L_G(t) a(t) \tag{7}$$

$$\frac{dt(i)}{di} = g(a(t)) \tag{8}$$

$$L_G(t) = f_G(i(t)) \tag{9}$$

for some function g yet to be choosen. Since t is the inverse function of i (8) leads to

$$\frac{di(t)}{dt} = 1/g(a(t)) \tag{10}$$

Considering everything in phase-space (7) and (10) give

$$\frac{da}{di} = -c_1 f_G(i) a g(a) \tag{11}$$

and hence (with some abuse of notation)

$$\int_{a=a_0}^{a(i)} \frac{1}{ag(a)} da = - c_1 \int_{i=t_0}^{i} f_G(i) di. \tag{12}$$

At this point we might wonder whether it is necessary to give a(t) a strong and explicit interpretation as food concentration. The fact that real growth normally stops somehow is not necessarily connected with exhaustive constraints but can also be the result of higher integrated processes such as flowering. See LÜCK [1966] for a discussion about largely independent levels of organization in a plant's hierarchical make up. Therefore, perhaps, it would be better to give a(t) a more mathematical purpose than too restricted biological significance. For instance, integration constants may always enter into a(t).

EXAMPLE 1.: *the logistic growth curve.*
Assume that $f_G(i) = 2^i$ and $g(a) = c_2/a$
$t \leq t_0$. According to (6).

$$a_0 = a(0)e^{-\int_0^{t_0} c_1 2^t dt}$$

which yields

$$t_0 = \log_2 \left(1 + \frac{\ln 2}{c_1} \ln \frac{a(0)}{a_0}\right) .$$

Substituting f_G and g in (12) yields

$$\frac{1}{c_2} (a(i) - a_0) = - c_1 \frac{1}{\ln 2} (2^i - 2^{t_0}).$$

Substitute $a(i) = c_2 \frac{di}{dt}$ and we have to solve i in

$$\frac{di}{dt} = \frac{a_0}{c_2} - \frac{c_1}{\ln 2} (2^i - 2^{t_0}) \tag{13}$$

via separation of i and t

$$\int_{i=t_0}^{i} \frac{1}{A+B2^i} di = \int_{t=t_0}^{t} dt \tag{14}$$

with

$$A = \frac{a_0 \ln 2 + c_1 c_2 2^{t_0}}{c_2 \ln 2}$$

$$B = \frac{-c_1}{\ln 2}$$

which yields, after substitution of $y = 2^i$

$$(15) \qquad \int_{y=2^{t_0}}^{y} \frac{1}{A\, y \ln 2}\, dy - \int_{y=2^{t_0}}^{y} \frac{B}{A \ln 2\ (A+By)}\, dy = \int_{t=t_0}^{t} dt.$$

Solving i in (15) we obtain

$$(16) \qquad i(t) = \frac{1}{\ln 2} \cdot \ln\left(\frac{GA}{1-GB}\right) \quad \text{with} \quad G = \frac{2^{t_0} e^{A\,(t-t_0)\ln 2}}{A + B\,2^{t_0}}$$

Substituting $i(t)$ in $f_G(i) = 2^i$:

$$L_G(t) = 2^{i(t)}$$

$$= \frac{-A/B}{1-1/BG}$$

$$= \frac{\frac{a_0 \ln 2}{c_1 c_2} + 2^{t_0}}{1 + \frac{a_0 \ln 2}{c_1 c_2^2\, 2^{t_0}}\, e^{-\left(\frac{a_0 \ln 2}{c_2} + 2^{t_0} c_1\right)(t-t_0)}}$$

which is of the form $\frac{X}{1+Ye^{-kt}}$: the *logistic* or autocatalytic curve.

For $t=t_0$ we obtain: $L_G(t_0) = 2^{t_0} = 1 + \frac{\ln 2}{c_1} \ln\left(\frac{a(0)}{a_0}\right)$

For $t \to \infty$ we obtain: $L_G \max = 2^{t_0} + \frac{a \ln 2}{c_1 c_2}$

$$= 1 + \frac{\ln 2}{c_1} \ln\left(\frac{a(0)}{a_0}\right) + \frac{a_0 \ln 2}{c_1 c_2}$$

This yields the growth curve depicted in figure 2 in which for $t \le t_0$: $L_G(t) = f_1(t) = 2^t$ and for $t \ge t_0$: $L_G(t) = f_2(t) =$ the above logistic growth function. The only parameters involved are c_1, c_2, $a(0)$ and a_0.

EXAMPLE 2. Assume that $f_G(t) = t+1$ and $g(a) = c_2/a$

Then, according to (6) we can solve t_0 from

$$a_0 = a(0)e^{-\int_0^{t_0} c_1(t+1)dt}$$

which yields $t_0 = -1 \pm \sqrt{1 + \frac{2}{c_1} \ln \frac{a(0)}{a_0}}$

and since $\frac{a(0)}{a_0}$ is greater than 1 for $t_0 > 0$, clearly

$$t_0 = -1 + \sqrt{1 + \frac{2}{c_1} \ln \frac{a(0)}{a_0}}$$

and

$$L_G(t_0) = f_G(t_0) = \sqrt{1 + \frac{2}{c_1} \frac{a(0)}{a_0}}$$

From (12) we see that

$$a(i) - a_0 = \frac{c_1 c_2}{2} ((t_0+1)^2 - (i+1)^2)$$

$$= \frac{c_1 c_2}{2} (L_G(t_0)^2 - (i+1)^2)$$

Substituting $a(i) = c_2 \frac{di}{dt}$ we get

$$\frac{di}{dt} = \frac{a_0}{c_2} + \frac{c_1}{2} (t_0+1)^2 - \frac{c_1}{2} (i+1)^2$$

and

$$\int_{i=t_0}^{i} \frac{di}{A - B(i+1)^2} = \int_{t=t_0}^{t} dt$$

with

$$A = \frac{a_0}{c_2} + \frac{c_2}{c_1} (t_0+1)^2$$

$$B = \frac{c_1}{2}$$

which yields

$$t = t_0 - \frac{1}{2\sqrt{AB}} \ln \frac{\sqrt{A/B} + (t_0+1)}{\sqrt{A/B} - (t_0+1)} + \frac{1}{2\sqrt{AB}} \ln \frac{\sqrt{A/B} + (i+1)}{\sqrt{A/B} - (i+1)}$$

Setting

$$t_0 - \frac{1}{2\sqrt{AB}} \ln \frac{\sqrt{A/B}+(t_0+1)}{\sqrt{A/B}-(t_0+1)} \quad \text{to } Z$$

$\frac{1}{2\sqrt{AB}}$ to Y and $\sqrt{A/B}$ to X we have, after some computation

$$L_G(t) = f_G(i(t)) = i(t)+1$$

$$= X\left(1 - \frac{2}{1+e^{-Z/Y} \cdot e^{t/Y}}\right)$$

and

$$L_G \max = \lim_{t\to\infty} L_G(t) = X = \sqrt{\frac{2a_0}{c_1 c_2} + L_G(t_0)^2}.$$

The growth curve looks like figure 3:

$t < t_0$: $L_G(t) = f_1(t) = t+1$:linear

$t \geq t_0$: $L_G(t) = f_2(t) = X(1-2(1+e^{-Z/Y} \cdot e^{t/Y})^{-1})$

$t >> t_0$: $L_G(t) \approx X(1-2e^{+Z/Y} e^{-t/Y})$: the *monomolecular* growth curve

where $$t_0 = -1 + \sqrt{1 + \frac{2}{c_1} \ln \frac{a(0)}{a_0}}$$

$$L_G(t_0) = \sqrt{1 + \frac{2}{c_1} \ln \frac{a(0)}{a_0}}$$

$$L_G \max = \sqrt{\frac{2a_0}{c_1 c_2} + L_G(t_0)^2} = \sqrt{\frac{2a_0}{c_1 c_2} + \frac{2}{c_1} \ln \frac{a(0)}{a_0} + 1}.$$

Hence we see that between the two extremes of unbounded DOL growth, viz. exponential and linear, the chosen set of differential equations, which depict the depletion of food, always yields a sigmoïdal growth curve. Therefore, all unbounded DOL growth functions yield a sigmoïdal growth curve under these conditions.

(II) ORGANISMS WITH A PERIODICAL CHANGE OF DIVISION RATE.

In biology we meet a phenomenon called biological rhythms. Examples are circadian rhythms, flowerescence etc. Such phenomena might be connected with the hierarchical organisation of multicellular organisms, changes from daylight to night etc. According to the observations of the Lücks (private communication) the algae they observe show the following growth behavior. Under optimal conditions the algae behave in essence like a rather simple DOL system, LÜCK [1974], where each transition takes place after a unit time interval of 48 hours.

However, each fifth time interval the organism alternatively skips the required transition or executes two consecutive transitions in one time interval. Thus, after each period of ten time intervals the organism reaches the stage we would expect from the DOL model, but in between it periodically speeds up and slows down its growth rate. According to the discussion in section 2 this means that

$$L_G(t) = f_G(i(t))$$

where i(t) is the function inverse of

$$t(i) = \begin{cases} i \text{ for} & 0 \leq i \bmod 10 < 5 \\ i+1 \text{ for} & 5 \leq i \bmod 10 \leq 9 \end{cases} .$$

Therefore,

$$i(t) = \begin{cases} t \text{ for} & 0 \leq t \bmod 10 < 5 \\ t-1 \text{ for} & 5 \leq t \bmod 10 \leq 9 \end{cases} .$$

Suppose $f_G(i) = 2^{i/5}$ then $L_G(t) = 2^{i(t)/5}$ and the growth curve is as depicted in figure 4.

(III) COMBINATION OF (I) AND (II).

A combination of (I) and (II), i.e., an organism residing in a closed environment and showing periodic speed ups and slowing downs of growth rate is found by

$$L_G(t) = f_G(i(i'(t)))$$

where i' is a function as found in (I) and i' a function as found in (II). The resulting growth curve looks like figure 5, where we assume that the periodicity is independent of the organism's interaction with the environment.

4. SOME POSSIBLE EXTENSIONS AND AN INTERPRETATION IN TERMS OF TABLE L SYSTEMS

The assumption that the relation between physiological time and real time is the same for all cell types in the organism can be relaxed, and we obtain in general that a is rewritten as $f(t,a) \in \{a,\delta(a)\}$, $a \in W$ and $t \in \mathbb{N}$. Then the growth matrix at time t is

$$M_G(t) = \begin{pmatrix} \overline{f(t,a_1)} \\ \overline{f(t,a_2)} \\ \vdots \\ \overline{f(t,a_n)} \end{pmatrix}$$

where $\overline{f(t,a_i)}$ will be $\overline{a_i}$ or $\overline{\delta(a_i)}$ depending on t. (In our previous approach this would mean that $M_G(t)$ is either the unity matrix E or M_G depending on t.) The above approach is useful to express different division times of different cell types without having to introduce different cell states to account for distinct delays in division rates. We could even go farther, and use the DTOL model. A *DTOL system* (deterministic interaction-less table L system) is a triple $G = \langle W,\{\delta_1,\delta_2,\ldots,\delta_k\},w\rangle$ such that for all

i, $1 \leq i \leq k$, $G_i = \langle W, \delta_i, w \rangle$ is a DOL system. A *controlword* u is an element of $\{1,2,\ldots,k\}^*$. A word v is said to *derive* a word v' in G under the controlword $u = i_1 i_2 \ldots i_\ell$ if

$$v' = \delta_{i_\ell} \delta_{i_{\ell-1}} \ldots \delta_{i_2} \delta_{i_1} (v).$$

Now we define, for $A = \{M_G(t) \mid t \in \mathbb{N}\}$ (A is finite) a DTOL system

$$G = \langle W, \{\delta_1, \delta_2, \ldots, \delta_k\}, w \rangle$$

where k is the number of elements in A and each *table* δ_i corresponds to the distinct elements of A for which it is the associated set of rewriting rules, i.e., $A = \{M_{G_1}, M_{G_2}, \ldots, M_{G_k}\}$

$$M_{G_i} = \left(\begin{array}{c} \overline{\delta_i(a_1)} \\ \overline{\delta_i(a_2)} \\ \vdots \\ \overline{\delta_i(a_n)} \end{array} \right)$$

Where $W = \{a_1, a_2, \ldots, a_n\}$, $1 \leq i \leq k$. Now a computable function $h: \mathbb{N} \to \{1,2,\ldots,k\}$ is defined which has as its argument the real time t and is composed from functions which compute from the relevant parameters which table $\delta_{i_{h(t)}}$ is applicable at time t. Then the word sequence

$$S_h(G) = w, \delta_{i_{h(1)}}(w), \delta_{i_{h(2)}} \delta_{i_{h(1)}}(w), \ldots, \delta_{i_{h(t)}} \delta_{i_{h(t-1)}} \ldots \delta_{i_{h(1)}}(w), \ldots$$

gives us the required developmental history of the modeled organism and the lengths of the successive elements of $S_h(G)$ give us the real time growth function.

EXAMPLE. Suppose we have $G = \langle \{a\}, \delta(a) = a^2, a \rangle$ and $f(i) = 2^i$. If $t = i^2$ then $L_G(t) = 2^{\sqrt{t}}$

The present approach would model the organism as follows.

$$G' = \langle\{a\},\{\delta_1(a) = a, \delta_2(a) = a^2\},a\rangle$$

Hence $M_{G_1} = (1)$ and $M_{G_2} = (2)$

$$h(t) = \begin{cases} 2 \text{ if } t \text{ is a square} \\ 1 \text{ if } t \text{ is not a square} \end{cases}$$

which yields $L_G(t) = 2^{\lfloor\sqrt{t}\rfloor}$.

We might note here that the approach taken in section 3 always leads to DTOL systems with *two* tables: if the physiological L system was $G = \langle W,\delta,w\rangle$ then the associated DTOL system will be $G' = \langle W,\{\delta_1,\delta_2\},w\rangle$ where δ_1 is the identify function and $\delta_2 = \delta$. The associated function

$$h(t) = \begin{cases} 2 & \text{if } t = t(i) \text{ for some } i \in \mathbb{N} \\ 1 & \text{if } t \neq t(i) \text{ for all } i \in \mathbb{N}. \end{cases}$$

As a further extension of the ideas presented above we could, e.g., make the choice of table, for rewriting a letter at time t, depend on the geometric position in the string of that occurrence of the letter. For instance, the tip of a root grows while the basal part does not. In this case, as in this section in general, not only the derived string sequence could be different from that of the underlying DOL system, but also the set of derived strings could differ from that of the underlying DOL system which does not happen with the approach in section 3.

5. FINAL REMARKS

Although the paper is concerned with L systems, i.e., models for filamentous organisms such as algae, the same method should be applicable to more-dimensional growth as well. First find a, preferably interaction-less, model of how the organism grows in physiological time (the essential cell ancestry and division pattern) and than try to find the functional

relation between physiological time and real time. The advantages of such a procedure are that we have both a (qualitative) fundamental physiological time model and that the transition from one type of growth to another, e.g. from exponential to logistic, does not require changing the model but is a consequence of the functional relation between physiological and real time which governs the quantitative aspects of the matter

Among experimentalists it is considered that the over-all approximations like exponential, logistic etc. growth curves have nothing to do with elemental (cellular) behavior. Furthermore, usually only the initial exponential stage is studied; the later stages of growth are more or less neglected. We have tried to establish a relation between elemental behavior and the over-all growth curve and we have introduced as a most significant state of a growing organism, or of the history of a growing organism, the stage at which the growth ceases to be exponential and becomes sigmoïdal: at time t_0.

The presented ideas should not be of interest solely for people working with algae but for every experimentalist who tries to fit theoretical growth functions to observed data.

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REFERENCES

DOUCET, P.G., (1976), *Studies on L systems*, Ph.D. thesis University of Utrecht, Utrecht, The Netherlands.

HERMAN, G.T. & G. ROSENBERG, (1975), *Developmental systems and Languages*, North Holland, Amsterdam.

HERMAN, G.T. & P.B.M. VITÁNYI (1976), *Growth Functions associated with biological development*, American Mathematical Monthly 83, 1-15.

LINDENMAYER, A, (1968), *Mathematical models for cellular interactions in development*, Parts I and II, J. Theoret. Biol. 18, 280-315.

LINDENMAYER, A. & G. ROZENBERG, (1976), *Automata, Languages, Development*. North Holland, Amsterdam.

LÜCK, H.B., (1966), *Sur la traduction morphogénétique de la cinétique cellulaire pendant la croissance des entre-noeuds de Tradescantia Fluminensis Vell.*, Bulletin de la Société Botanique de France, 220-225.

LÜCK, H.B., (1974), *On growth of Algae: elementary behavior rules as a foundation of morphogenetics*. In: Proc. Biologically Motivated Automata Theory, 77-80, IEEE publication, New York.

LÜCK,J. & H.B. LÜCK, (1976), *Cell number and cell size in filamentous organisms in relation to ancestrally and positionally dependent generation times*. In: LINDENMAYER and ROZENBERG [1976], 109-124.

MEDAWAR, P.B., (1945), *Size, shape and age*. In: Essays on Growth and Form (W.E. le Gros Clark and P.B. Medawar eds.) Oxford.

PAZ, A. & A. SALOMAA, (1973), *Integral sequential word functions and growth equivalence of Lindenmayer systems*, Information and Control, 23, 313-343.

POLLUL, W. & D. SCHÜTT, (1975), *Characterization of growth in deterministic Lindenmayer systems*, Indagationes Mathematicae, 37, 183-188.

ROZENBERG, G. & A. SALOMAA, (1974), *L systems*. Lecture Notes in Computer Science 15, Springer Verlag, Heidelberg.

SALOMAA, A., (1973), *On exponential growth in Lindenmayer systems*, Indagationes Mathematicae, 35, 23-30.

SZILARD, A., (1971), *Growth functions of Lindenmayer systems*, Comp. Science Dept., Univ. of Western Ontario, Tech. Rept. no. 4.

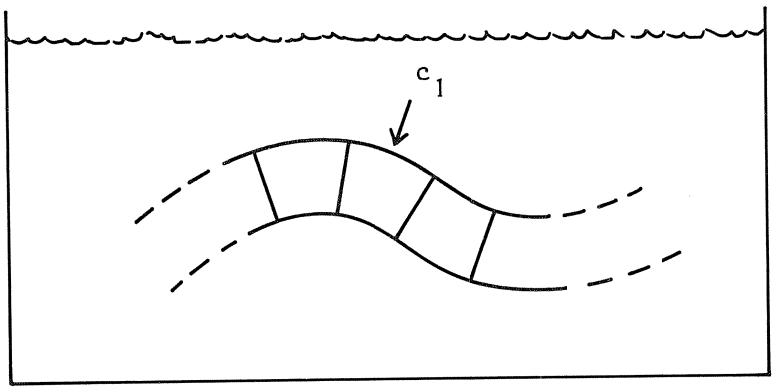

Figure 1.

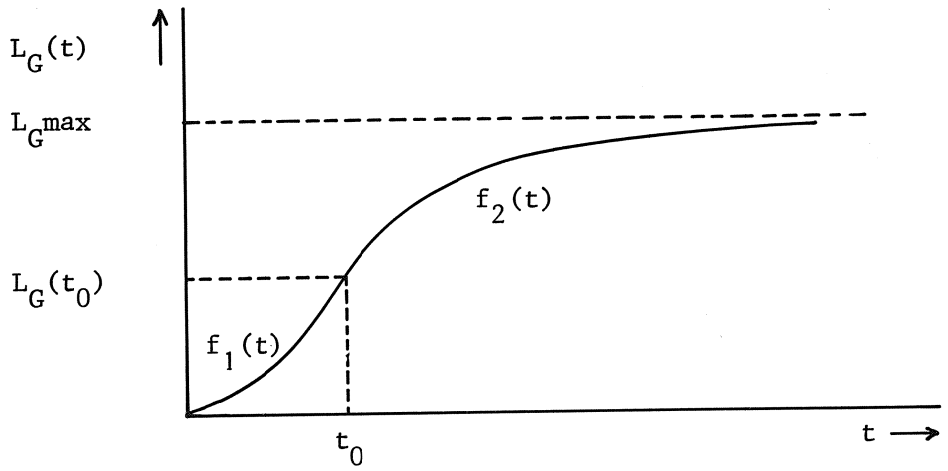

Figure 2.

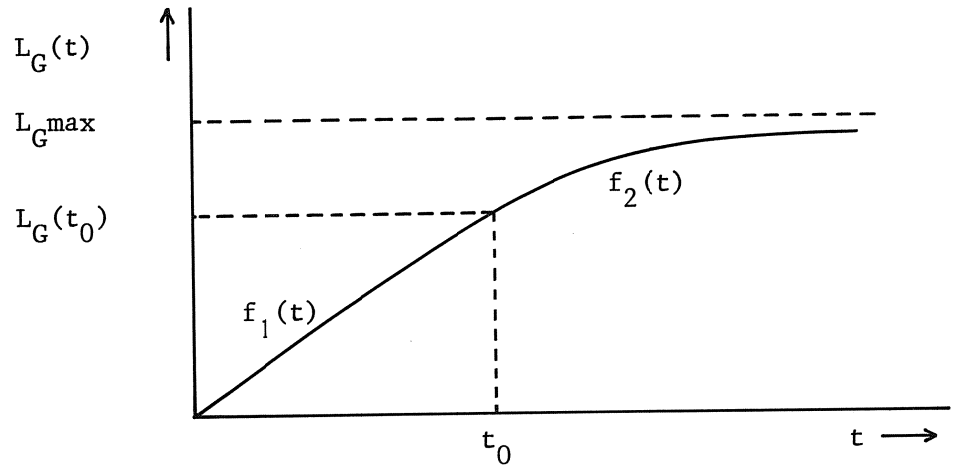

Figure 3.

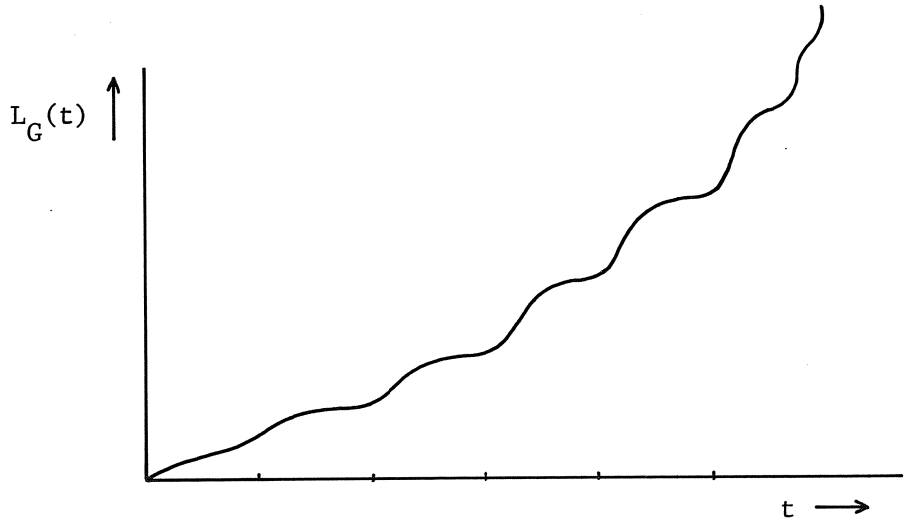

Figure 4.

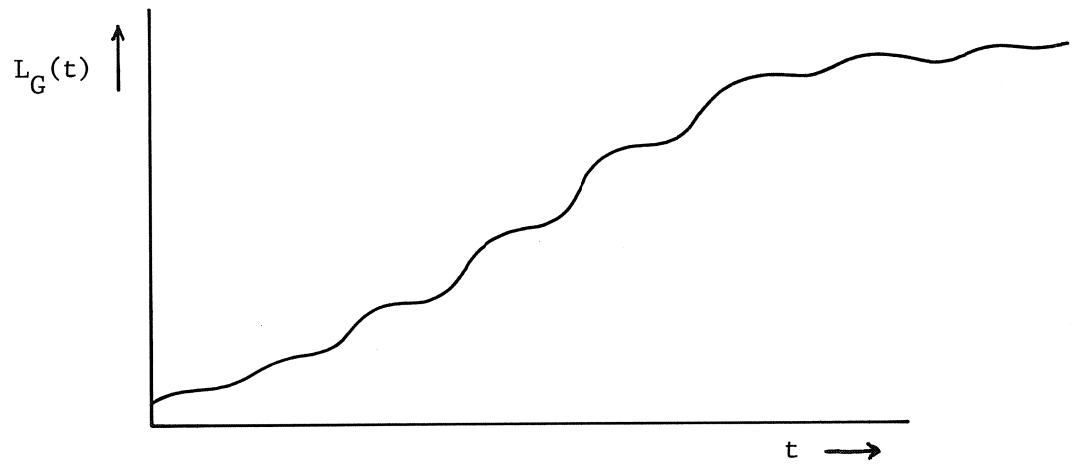

Figure 5.