Mathematical Models for Cellular Interactions in Development

II. Simple and Branching Filaments with Two-sided Inputs

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Continuing the presentation of a theory of growth models for filamentous organisms, the treatment is extended to cases where inputs are received by each cell from both directions along the filament, and the change of state and the output of a cell is determined by its present state and the two inputs it receives. Further symbolism is introduced to take care of branching filaments as well. Two entirely different models are constructed for a particular branching organism, resembling one of the red algae. These models are compared with reference to the number of states employed, and the presence or absence of instructions for unequal divisions and for inductive relationships among the cells. The importance of a morphogenetic control theory concerning these relationships is emphasized.

1. Introduction

The theory constructed in the preceding paper (Lindenmayer, 1968) could cope only with simple filaments, linear arrays of cells, with outputs by the cells transmitted only in one direction along the filament. Although there are developmental situations in which this simple theory can be useful, e.g. when a hormone-like auxin travels in an organ in one direction only, as auxin is known to behave in shoots of vascular plants, but in many more cases it is desirable to be able to carry out computations on the basis of two-directional input-output relationships. Such cases include not only filamentous organs, but also ring structures.

Ever since Turing (1952) proposed his famous morphogenetic models for shoot apices based on peaks and troughs of concentrations of morphogenetic substances which react with each other and diffuse around a ring, many developmental biologists have expressed interest in these kinds of explanatory hypotheses (e.g. Wardlaw, 1953), but no further use has been made of them. One of the reasons for this may be the mathematical complexity of dealing with simultaneous first- and second-order differential equations, as in Turing's approach. The advantage of the theory proposed in the present

papers is that only finite mathematics is used, and consequently it lends itself more readily to combinatorial manipulations, such as programming for digital computers, and the theoretical framework can be kept at a rudimentary level. At the same time results are obtainable which could be just as meaningful for morphogenetic considerations as those based on differential equations.

The present paper explores a theory for the growth of filaments under two-sided inputs, and extends it to branching filaments. The mathematical theory of sequential machines is being used throughout, as outlined in the previous paper. As a demonstration, individual models are constructed for a particular branching filamentous organism. The problem of equivalence among models yielding the same growth pattern is then introduced.

2. Theory B: Simple Filaments with Two-sided Inputs

The formal assumptions in this theory are partly identical to those in theory A of the previous paper, and these will be referred to by their original number. The assumptions which need to be modified will have a "B" prefix with the number that the corresponding assumption has in theory A. The first such modified statement replaces (A6), to read:
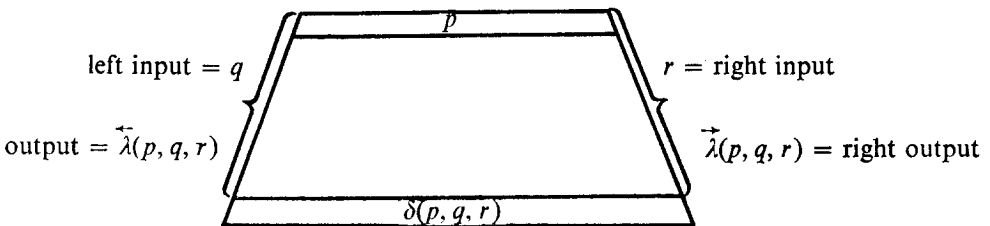
(B6) The δ, $\overrightarrow{\lambda}$ and $\overleftarrow{\lambda}$ functions are to be non-empty mappings from $S \times S \times S$ into S, with the restriction that the sequences inserted into the second and third places of the arguments of the functions must be of the same G-length.

The next-state and output functions have three variables in their arguments, the first for the present state, the second for the input from the left, and the third for the input from the right. Thus we have expressions like

$$\delta(p, q, r) = s \text{ or } \overrightarrow{\lambda}(p, q, r) = t \text{ or } \overleftarrow{\lambda}(p, q, r) = w,$$

in each of which the restriction placed on the functions requires that $g(q) = g(r)$.

We are postulating two different output functions, $\overrightarrow{\lambda}$ for the right output, and $\overleftarrow{\lambda}$ for the left output of a sequence under its inputs. The following diagram shows these relationships.

left input $= q$ p $r = $ right input

output $= \overleftarrow{\lambda}(p, q, r)$ $\overrightarrow{\lambda}(p, q, r) = $ right output

$\delta(p, q, r)$

The rules for concatenated input sequences are analogous to those in theory A.

(B7a) $\delta(p, u*w, v*z) = \delta(\delta(p, u, v), w, z)$

(B7b) $\overrightarrow{\lambda}(p, u*w, v*z) = \overrightarrow{\lambda}(p, u, v) * \overrightarrow{\lambda}(\delta(p, u, v), w, z)$

$\overleftarrow{\lambda}(p, u*w, v*z) = \overleftarrow{\lambda}(p, u, v) * \overleftarrow{\lambda}(\delta(p, u, v), w, z)$

for all p, u, v, w, z in S such that $g(u) = g(v)$ and $g(w) = g(z)$.

Unfortunately, the rules for concatenated state sequences cannot be given in analogous manner to (A7c) and (A7d). The problem is centered on the fact that if we try to provide a completely specified substitution for an expression like $\delta(p*q, u, v)$ we immediately discover that we are sucked into an infinite regress. This is because we would have to write something like the following

$$\delta(p*q,u,v) = \delta(p,u,\overleftarrow{\lambda}(q,\overrightarrow{\lambda}(p,\overleftarrow{\lambda}(q,\ldots)),v)) * \delta(q,\overrightarrow{\lambda}(p,u,\overleftarrow{\lambda}(q,\overrightarrow{\lambda}(p,\ldots)),v)),$$

where the "..." stands for an infinitely long expression of alternating left and right outputs. Yet, it is perfectly clear that computations with two-sided inputs can be carried out, or programmed for a computer, if it is done line-by-line. The difficulty lies only in trying to find general expressions for input and output sequences of any length. Thus, we shall avoid the above predicament by stating substitution rules only for unit-length inputs and outputs.

(B7c) For all p, u and v in G, and r and s in S,

$$\delta(s*p*r, u, v) = \delta(s, u, p) * \delta(p, \overrightarrow{\lambda}(s, u, p), \overleftarrow{\lambda}(r, p, v)) * \delta(r, p, v),$$

(B7d) $\overrightarrow{\lambda}(s*p*r, u, v) = \overrightarrow{\lambda}(r, p, v)$,

$\overleftarrow{\lambda}(s*p*r, u, v) = \overleftarrow{\lambda}(s, u, p)$.

The rules for empty sequences are similar to their counterparts in theory A.

(B8a) $\delta(e, p, q) = \overrightarrow{\lambda}(p, e, e) = \overleftarrow{\lambda}(p, e, e) = e$,

(B8b) $\delta(p, e, e) = \overrightarrow{\lambda}(e, p, q) = \overleftarrow{\lambda}(e, q, p) = p$,

for all p and q in S such that $g(p) = g(q)$.

As it turns out, the statements in this theory, that would correspond to (A9), are derivable from (B7d) and (B8b), thus we list them as parts of our first theorem in theory B.

(TB1) If p, u and v are in G, and r and s are in S, then

$$\overrightarrow{\lambda}(s*p, u, v) = \overleftarrow{\lambda}(p*r, u, v) = p.$$

Proof is by substituting e for r or s in (B7d). The significance of this theorem is that the right output of a non-empty sequence is the right-most component of that sequence, and its left output is its left-most component. Of course, if this is not the desired arrangement then the above assumptions need to be changed. A similar theorem can be obtained for state sequences, also by substituting e for r or s in (B7c).

(TB2) If p, u and v are in G, and r and s are in S, then

$$\delta(s*p, u, v) = \delta(s, u, p) * \delta(p, \overrightarrow{\lambda}(s, u, p), v), v)\text{ and}$$

$$\delta(p*r, u, v) = \delta(p, u, \overleftarrow{\lambda}(r, p, v)) * \delta(r, p, v).$$

The assumptions (B6), (B7a–d) and (B8a–b) are the only ones necessary to complete theory B, in addition to statements (A1) to (A5), and (A10) to (A13), except for a definition corresponding to (A11b) which can be readily added:

(B11b)   Generating $\overrightarrow{\lambda}$ and $\overleftarrow{\lambda}$ functions are $\overrightarrow{\lambda}$ and $\overleftarrow{\lambda}$ functions with arguments restricted to members of G.

Then, by (TB1), we have the statement that $\overrightarrow{\lambda}(p, u, v) = \overleftarrow{\lambda}(p, u, v) = p$ for all p, u and v in G. Thus generating $\overrightarrow{\lambda}$ and $\overleftarrow{\lambda}$ functions must be mappings from $G \times G \times G$ into G.

An interesting question is how theory A is related to theory B. First of all it can be noted that the transition from statements in one to those in the other may be accomplished by adopting the following transformation rule:

(AB1) We can assert in theory A that $\delta(p, q) = s$ and $\lambda(p, q) = t$ if and only if we can assert in theory B that $\delta(p, q, r) = s$ and $\overrightarrow{\lambda}(p, q, r) = t$ for every r such that $g(r) = g(q)$.

It is the case then that every statement in theory A is derivable in theory B. In particular, it can be shown that (A7c), which was that

$$\delta(q*p, r) = \delta(q, r) * \delta(p, \lambda(q, r)), \text{ for all } p, q \text{ and } r \text{ in } S,$$

is derivable from the transformed version of (B7c), namely that

$$\delta(s*p*r, u) = \delta(s, u) * \delta(p, \lambda(s, u)) * \delta(r, p), \text{ for all } p \text{ and } u \text{ in } G, \text{ and } s \text{ and } r \text{ in } S.$$

Similarly, (A7d) and (A9) are derivable from the transformed version of (B7d), provided that the other assumptions of theory A are available.

The reverse relationship, however, does not hold, i.e. not all statements in B can be derived from those in A. Clearly, theory B is a richer system in which many patterns can be expressed which cannot in theory A.

As an example for statements in theory B, a theorem is presented for the development of banded patterns under two-sided inputs.

(TB3) If $\vec{\lambda}(p, r, q) = r$ for every q such that $g(q) = g(r)$, and if $\delta(p, r, r) = p^m$, and if $m \neq 0$ and $n \neq 0$, then $\delta(p, r^n, r^n) = p^{mn}$.

This theorem is closely analogous to (TA13) in the preceding paper, and its proof follows essentially along the same lines.

The next theorem, on the other hand, has no counterpart in theory A. We introduce it by way of a concrete example. Figure 1 shows the computer expansion of the sequence 111 under left and right input sequences consisting of 1's. The generating δ function is presented in the form of two matrices, the first for present state 0, and the other for present state 1. The left inputs are in the vertical column on the left, and the right inputs are in the horizontal row on top, the rest of the matrix showing the next states for each triple combination of present state, left input and right input. The generating set $G = \{0, 1\}$.

Present state	0	Right input 0	1	Present state	1	Right input 0	1
Left input	0	0	1	Left input	1	1*1	1*1
	1	1	1		1	0	0

In Fig. 1 the left-most and right-most symbols in each row represent the environmental inputs, which are arbitrarily set rather than computed. The left column of the computed sequences can be seen to consist of alternating 1's and 0's, and no divisions take place in this column. Thus we can take this column and consider it to be the left environmental input sequence. Then we notice that in the column to its right there is a regularly repeated sequence of 1001 sequences. This is an indication that we are dealing with a repetition of certain patterns in every fourth row, as we have seen this to happen in Figs 3 and 4 of the previous paper. We make a new plot of Fig. 1, therefore, showing only every fourth row, with the inputs from row to row consisting of 1010 on the left and of 1111 on the right. This is shown in Fig. 2.

A certain kind of constant apical pattern is evident in Fig. 2. This, however, is unlike those in Figs 1 and 4 of the preceding paper, in that the apical pattern is only partially repeating because of influences from the right input encroaching on it. No expression similar to (TA10) is available for this behavior, but some other regularities can be pointed out.

Row
```
 1  11111

 2  10001
 3  11011

 4  101111
 5  1111001

 6  1000111
 7  11011101

 8  101110011
 9  11110011111

10  100011110001
11  1101110001011

12  1011100101111111
13  1111001111111000001

14  10001111000000100011
15  11011100010000111101111

16  1011100101111001110001111001
17  111100111111110001111001011100111

18  10001111000000101110001111111100111101
19  11011100010000111111001011100000011100011

20  101110010111100111000001111111001000011100010111111
21  111100111111110001111001000111100000011111001110010111111001

22  100011110000000101110001111101110010000111000011111001111111100000111
23  110111000100001111110010111000011100111110011100100110001111000000100011
01

24  10111001011110011100000111111100100111001111000011110011111111001011100010
000111101110011

25  111100111111110001111001000111000000111111110011110001001110001111000000011
111100101111001110001110011111

26  10001111000000101110001111101110010000111000000011110001011111110010111000
1000001110000001111111000111110010110011110001

27  1101110001000011111100101110001110011111100111001000001110001011111110000000
11111110010111100011100100001110000001011100011111111001111000101

28  1011100101111001110000011111110010011100111100001111001111110001110010111111
10000010000111000000111111100010111001111110011100100001111110010110000001111000
101111111

29  1111001111111000111100100011100000011111110011110001001110001111000010111
00111111100000100011110011100100001110000001011111100111100001111001111100111000
00111111100100001110001011111000001

30  100011110000001011100011111011001000011100000001111000101111111001011100
100111111100111100000010001111011100011110011111100111001000011111100000011110001
001111001110010000111110011100101111110000000100011
```

FIG. 1

Row	Left input	Right input
1	1010	11|__ 111 1
5		1100|__
9		11001111|__
13		11001111111000	00
17		1100111111100011110010	1110011
21		110011111110 00 11110010 0011100000011111|00111001011111100 __
25		110011111110 00 11110010 0011100000011111 11100111110001001111000
		11110000	00 01111111 0010111100111000 111001111
29		110011111110 00 11110010 0011100000011111 11100111110001001111000
		11110000 10 11100...

<div align="center">FIG. 2</div>

It is possible to show for this particular δ function that for all sequences r, if the G-length of r is 4, then $\overset{\leftarrow}{\lambda}(11, 1010, r) = 1001$, which was the regularly repeated sequence in the second computed column of Fig. 1. That this is so can be shown most easily by an incomplete calculation under an unknown right input of length 4:

$$
\begin{array}{c|c|c}
1 & 11 & r_1 \\
0 & 00 & r_2 \\
1 & 0.. & r_3 \\
0 & 1.. & r_4 \\
  & 11.. &
\end{array}
$$

Beside the fact that the first column has 1001 in its first four places, we also obtained the fact that there is an s such that $\delta(11, 1010, r) = 11*s$, for any r of length 4.

A theorem can now be formulated, asserting that whenever we have a p such as 11, a q such as 1010 and a t such as 1001 behaving as they do in the above example, any n repetition of q as the left input to p will result in a left output sequence of n-times repeated t, under any right input sequence whatever; and the next-state sequence, under these conditions will always begin with p.

(TB4) If, for every r such that $g(r) = g(q)$, $\overset{\leftarrow}{\lambda}(p, q, r) = t$ and $E![\delta(p, q, r) \leftarrow p]$, then for every non-negative integer n and every w such that $g(w) = n.g(q)$, it is the case that $\overset{\leftarrow}{\lambda}(p, q^n, w) = t^n$ and $E![\delta(p, q^n, w) \leftarrow p]$.

Proof is by mathematical induction and requires no lemmas.

That the type of right input influences the extent of self-replicating left portions in these arrays is illustrated by a comparison of Fig. 3 with Fig. 2. In Fig. 3 each new array is computed under a left input of 1010,

Row	Left input	Right input		
1	1010	11| 00 00		
5		11|1		
9		11|10		
13		11 00|0 10		
17		11 00 1|000111 10		
21		11 00 1 111111|1001 11100000010		
25		11 00 1 111111 0001|011100111111100000101 11000111110		
29		11 00 1 111111 0001 1110010001111011100101111110001111001011100		
		1 111101 1100 10000111000000010		

FIG. 3

as is the case in Fig. 2, but the right input in Fig. 3 consists of 0's rather than of 1's as in the other one. The self-replicating part is increasing at a much slower rate in Fig. 3 than in Fig. 2 (its right boundary is indicated by the stepwise line). It may be noticed that we have a set of successive self-replicating sequences, each longer than the previous one:

$$\delta(110, 1010, r_1) = 11001*s_1$$
$$\delta(11001, 1010, r_2) = 110011111*s_2$$

and so on. These sequences represent the minimum self-replicating left-hand portion we can obtain under any right input sequences, provided that the right input consists of repetitions of 1010.

3. Theory C: Branching Filaments

Branching filaments can be handled within the already available theoretical framework with the addition of only one more formal concept. Left and right brackets, [ ], will be used to delimit each branch, while the entire organism is described by a single linear array as before. The state symbols of each primary branch are enclosed in brackets and inserted into the array after the basal cell in the main filament, and, similarly, the symbols of each secondary branch are enclosed in brackets and inserted after its basal cell on the primary branch, and so on. If there are more than two branches on a basal cell, then their expressions simply follow consecutively after the state symbol of the basal cell. Relative positions of the branches to each other and to the main filament cannot be indicated in this system, in the sense that left and right branches cannot be distinguished.

Since with any desired number of branches we still have a single linear array, we can use the same concatenation operator $*$ and work with the δ and λ functions, as before, provided that we specify rules for dealing with the bracketed expressions. Such rules are presented now for two-sided inputs, those for one-sided inputs are easily derivable from them. In some of these rules a constant c must be invoked in order to provide environmental inputs at the tips of branches, for which the inputs would otherwise remain unknown or would have to be specified by other conventions.

(C1) $\delta(q*[p], u, v) = \delta(q, u, v) * [\delta(p, \overset{\rightarrow}{\lambda}(q, u, v), c^{g(u)})]$

(C2) $\delta([p]*r, u, v) = [\delta(p, u, c^{g(u)})] * \delta(r, u, v)$

(C3) $\overset{\rightarrow}{\lambda}(q*[p], u, v) = \overset{\rightarrow}{\lambda}(q, u, v)$

(C4) $\overset{\rightarrow}{\lambda}([p]*r, u, v) = \overset{\rightarrow}{\lambda}(r, u, v)$

(C5) $\overset{\leftarrow}{\lambda}(q*[p], u, v) = \overset{\leftarrow}{\lambda}(q, u, v)$

(C6) $\overset{\leftarrow}{\lambda}([p]*r, u, v) = \overset{\leftarrow}{\lambda}(r, u, v)$

for all p, q, r, u, v in S, and some c in G.

(C7) $[e] = e$

By substituting e for q or r in the above formulas we obtain:

(TC1) $\delta([p], u, v) = [\delta(p, u, c^{g(u)})]$

(TC2) $\overset{\rightarrow}{\lambda}([p], u, v) = u$

(TC3) $\overset{\leftarrow}{\lambda}([p], u, v) = v$, for all p, u, v in S.

Under the assumptions of theory C the basal cell of a primary branch receives inputs only from its two neighbors along the main filament, not from the adjacent cell on the branch, and similarly for all higher order branches. This is evident from (C1), where q may stand for the state of the basal cell of branch $[p]$. If it would be desirable for biological reasons to let the cells of the branches contribute to the input of the basal cells, in other words, to let each basal cell receive inputs from each of its three or more neighbors, then a somewhat more complex theory has to be constructed in which sets of inputs determine the next states and outputs.

4. Models for a Branching Filamentous Organism

Two models are presented which were constructed to simulate the development of a particular red alga, *Callithamnion roseum* Harvey. Detailed developmental descriptions are available for this organism (Konrad-Hawkins, 1964), certain aspects of which were followed in this exercise.

We plan to produce a developmental pattern with the following features: (a) the main filament should have at its base one to three cells which do not bear branches; (b) each successive cell above these on the main filament should bear one branch; (c) in all stages three or four cells below the tip of the main filament should have no branches; (d) each primary or higher order branch should repeat the pattern of the main filament. Certain important details of the growth of *C. roseum* are purposely omitted from this list of requirements. Most notably, while the position of the transverse walls in the filaments appears to have a significance in determining the branching points, this aspect has been ignored in these models. Actually, more complex models have been constructed which take wall characteristics into account, but these will be reported on at a later time.

Two entirely different δ functions are presented, both giving rise to essentially the same growth pattern. The first model has a generating set of nine symbols, the integers from 1 to 9, for the set of state sequences. The next state is specified independently from the input received. In other words, in the generating δ matrix the same next-state sequence should be entered under all nine inputs. This is shown in an abbreviated form in the following table:

<div align="center">Present states</div>

	1	2	3	4	5	6	7	8	9
Under any input $q \in G$	2*3	2	2*4	2*5	6*5	7	8	9*[3]	9

This table could also be expressed by a series of statements such as:
$$\{\delta(1, q)|q \in G\} = \{2*3\},$$
$$\{\delta(2, q)|q \in G\} = \{2\}, \text{ etc.}$$

If we adopted the following transformation rule
$$\delta_n(p) = q \text{ if and only if } \{\delta(p, r)|g(r) = n\} = \{q\},$$
then only the following concatenation and branching rules were needed:
$$\delta_n(p*q) = \delta_n(p) * \delta_n(q)$$
$$\delta_n([p]) = [\delta_n(p)].$$

This is the case of no inputs passing in either direction in the filament, and could be called "the theory of zero-sided inputs". It is embedded in theory A, just as theory A is embedded in theory B.

Making use of the above generating matrix, a sample calculation is carried out for 15 lines in Fig. 4, with a diagrammatic representation of the resulting organism shown in Fig. 5. Each cell in Fig. 5 has in it the symbol for the state in which the cell is in at line 15 of the calculation. The branches

Row

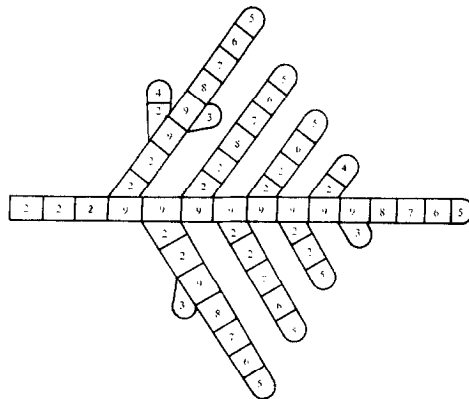|	
1	1|1
2	1|23
3	1|224
4	1|2225
5	1|22265
6	1|222765
7	1|2228765
8	1|2229 [3] 8765
9	1|2229 [24] 9 [3] 8765
10	1|2229 [225] 9 [24] 9 [3] 8765
11	1|2229 [2265] 9 [225] 9 [24] 9 [3] 8765
12	1|2229 [22765] 9 [2265] 9 [225] 9 [24] 9 [3] 8765
13	1|2229 [228765] 9 [22765] 9 [2265] 9 [225] 9 [24] 9 [3] 8765
14	1|2229 [229 [3] 8765] 9 [228765] 9 [22765] 9 [2265] 9 [225] 9 [24] 9 [3] 8765
15	|2229 [229 [24] 9 [3] 8765] 9 [229 [3] 8765] 9 [228765] 9 [22765] 9 [2265] 9 [225] 9 [24] 9 [3] 8765

FIG. 4

FIG. 5

are drawn alternately to the left and to the right of the filament that bears them; this is purely arbitrary as it has already been pointed out. It is clear that if we start the computation with a single cell in state 1 then the model fulfills the requirements stated at the beginning.

The second model has a generating set of only four members: $G = \{0, 1, 2, 3\}$, and two-sided inputs are assumed (theory B), as well as branching (theory C). The generating δ function is given as three matrices; 0 is used exclusively as an input symbol, thus no values are required for it in the δ function. The $\overrightarrow{\lambda}$ and $\overleftarrow{\lambda}$ generating functions are defined by (B11b), (TC2) and (TC3).

Present state		Right input					2	0	1	2	3		3	0	1	2	3
	1	0	1	2	3												
Left input	0	2	1	1	1		0	1*1	1	1	1		0	2	1	1	1
	1	2	2	1	1		1	1*1	2	2	2		1	1	2	3	3
	2	2	2	1	1		2	1*1	1	3	1		2	1	2	3	3
	3	1	2	3	3		3	1*1	3	3	3		3	1	3	3	1*[1]

A computation, beginning with a cell in state 1 under constant environmental inputs from both sides of 0's, is shown in Fig. 6. If we would start with a cell in state 2 or 3 instead, we would get the same results except for the first few lines. Figure 7 shows the diagrammatic view of the organism corresponding to line 28 of the calculation.

Row

1	0	10
2	0	20
3	0	110
4	0	120
5	0	1110
6	0	1220
7	0	12110
8	0	12220
9	0	123110
10	0	122220
11	0	1233110
12	0	1233220
13	0	12333110
14	0	1231 [1] 3220
15	0	1223 [2] 33110
16	0	1213 [11] 1 [1] 3220
17	0	1212 [22] 3 [2] 33110
18	0	1212 [311] 3 [11] 1 [1] 3220
19	0	1212 [222] 2 [22] 3 [2] 33110
20	0	1212 [3311] 1 [311] 3 [11] 1 [1] 3220
21	0	1212 [3322] 1 [222] 2 [22] 3 [2] 33110
22	0	1212 [33311] 1 [2311] 2 [311] 3 [11] 1 [1] 3220
23	0	1212 [31 [1] 322] 1 [2222] 2 [222] 2 [22] 3 [2] 33110
24	0	1212 [23 [2] 3311] 1 [23311] 2 [3311] 1 [311] 3 [11] 1 [1] 3220
25	0	1212 [13 [11] 1 [1] 322] 1 [23322] 2 [3322] 1 [222] 2 [22] 3 [2] 33110
26	0	1212 [12 [22] 3 [2] 3311] 1 [233311] 2 [33311] 1 [2311] 2 [311] 3 [11] 1 [1] 3220
27	0	1212 [12 [311] 3 [11] 1 [1] 322] 1 [231 [1] 322] 2 [31 [1] 322] 1 [2222] 2 [222] 2 [22] 3 [2] 33110
28		1212 [12 [222] 2 [22] 3 [2] 3311] 1 [223 [2] 3311] 2 [23 [2] 3311] 1 [23311] 2 [3311] 1 [311] 3[11] 1 [1] 322

FIG. 6

Comparing the growth patterns of these two models, we find a structural similarity between Figs 5 and 7. What we mean by this is that the origins and lengths of the branches are approximately the same in the two pictures. What this corresponds to in the original linear arrays from which these pictures were drawn is the distribution of the brackets along the arrays.
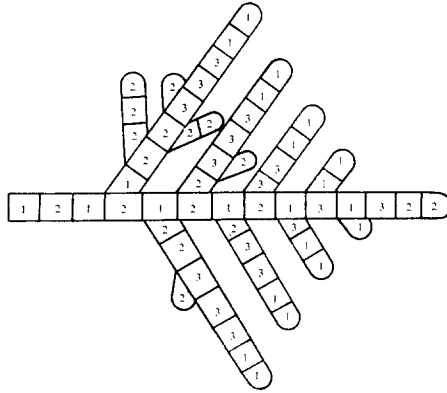

FIG. 7

Thus we have constructed two roughly similar growth models with respect to the distribution of the branches, but certainly not with respect to distribution of states along the filament. There is "branching equivalence" between the two δ,λ-functions, but no equivalence between the functions in the sense of Ginsburg (1962). In the latter sense, for each state in the first model there is a state in the second one such that the outputs under all inputs are identical for both states, and, similarly, for every state in the second model there is a state in the first one such that the outputs under all inputs are identical. This is certainly not the case for our models.
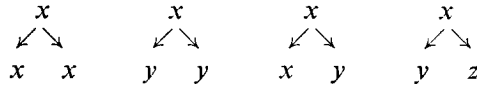
The most interesting aspect of the comparison of the two models is the presence or absence in them of unequal divisions and of induction processes among cells. This is discussed in the following section.

5. Discussion

The central problem in these papers is the relationship between the controls of cell division and cell induction, and morphogenesis. Before discussing what this theory tells us about this relationship, we have to make a few comments about the division and induction processes we are concerned with.

Cell division may be equal (equational) or unequal according to the respective states of the mother and daughter cells. As mentioned before, by

states we understand any physiological or morphological aspect of the cells which have a significant influence on the life of the cell. "Differentiation" is the usual term employed to designate a change in states. It has been stated (by H. Holzer in a lecture at the 1966 AIBS meetings) that differentiation is always accompanied by cell division. Holzer proposed that basically four types of cell divisions may be distinguished:

$$
\begin{array}{cccc}
x & x & x & x \\
\swarrow\searrow & \swarrow\searrow & \swarrow\searrow & \swarrow\searrow \\
x \quad x & y \quad y & x \quad y & y \quad z
\end{array}
$$

The first two are equal divisions, the last two are unequal. The last three give rise to differentiation. Whether or not Holzer's thesis on the connection of differentiation and division is correct, these concepts are worth further exploration.

Concerning induction processes, the following summary by Lang (1965) is useful: "(There are) the following principal cases of contagious differentiation: (1) the specific character of a differentiated cell or tissue is perpetuated by cell division, giving rise to cell or tissue lineages carrying this character; (2) the differentiating or differentiated cell or tissue induces *identical* or very similar differentiation in its neighborhood; this is known as homeogenetic induction; (3) a differentiated cell or tissue induces or modifies differentiation *of another type* in adjacent cells or tissues, this is called heterogenetic induction. ... It may be noted that one can also speak of *negative* homeo- or heterogenetic induction, i.e. differentiation of a cell or tissue may prevent differentiation of identical or of different cells and tissues in the same or in another tissue. ... An example is the (development of) stomatal pattern in dicot leaves."

The theories proposed here are able to cope with all of the division and induction cases mentioned. The first model in the previous section has several unequal divisions in its δ matrix, belonging to one of the two types given above, for instance

$$
\begin{array}{ccc}
3 & & 5 \\
\swarrow\searrow & \text{and} & \swarrow\searrow \\
2 \quad 4 & & 6 \quad 5
\end{array}
$$
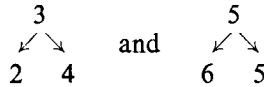
But this model has no inductive instructions. On the other hand, the second model has many inductive instructions, but no unequal divisions. In fact, it has division instructions of only the first type

$$
\begin{array}{c}
1 \\
\swarrow\searrow \\
1 \quad 1
\end{array}
$$

Among the inductive instructions of the second model there are some representing homeogenetic induction, like $\delta(1, 2, 1) = 2$ and $\delta(1, 3, 3) = 3$, and some heterogenetic induction, like $\delta(3, 1, 1) = 2$ and $\delta(2, 2, 3) = 1$. Negative induction is difficult to define, because how does one know whether a certain input prevented a change of state in a cell, or simply had no effect on that cell. If negative induction should only mean that the present state of a cell remains unchanged under an input from a cell in a similar or different state, then there are many examples for this in the second model. Thus $\delta(1, 2, 2) = 1$ could be regarded as a case for negative heterogenetic induction, and perhaps $\delta(3, 3, 2) = 3$ a case for negative homeogenetic induction.

The two models were constructed by many trials with as few individual states (members of the generating set) as possible. The first required nine states, while the second only three states plus one environmental input. So, having inductive instructions with two-sided inputs seems to be much more economical of number of states. Other models, not included here, were constructed with inductive instructions and one-sided inputs, and they seemed to require more individual states than the models with two-sided inputs, but less than those without inputs (which is the same as having only one individual input). An organism obviously has a choice of a very large number of different sets of hereditary instructions to reliably produce a certain structure which it needs for survival. Some of these instructions may specify the occurrence of equal or unequal divisions, others that of induction taking place with one or more sided inputs. Roughly speaking, the more inductive processes are specified and with inputs coming from more sides, the fewer states will be needed and fewer unequal divisions. Which of these alternatives is less costly for the organism is difficult to tell, but there may be an optimum number of states for a given developmental pattern, which requires the smallest total of induction and unequal division instructions taken together. Such optimization considerations may eventually lead us to more realistic models.

In view of the large number of possible models which give rise to similar morphogenetic patterns the most important problem is that of narrowing down the set of possibilities. This can be ultimately done on the basis of experimental evidence only. But a better theoretical understanding of equivalence relationships among models of different types would help considerably to sharpen the questions asked in the experiments.

While branching filaments, no matter how complicated, can be handled as linear, one-dimensional arrays, the growth of a shoot apex can be described only by a two-dimensional model, and the growth of a gastrula probably by one which is at least three-dimensional. The theoretical framework to cope with more than one-dimensional structures is not available yet.

Simplified approaches to morphogenesis in the shoot apex are, however, possible on the basis of one-dimensional models of rings (as in Turing's model, 1952) or of contact parastichies (as invoked by Plantefol, 1948). Primitive apices with tetrahedral apical cells can also be approached on this basis, since the tetrahedral cell and the sister cells of previous tetrahedral cells can be considered a filament. Further studies are planned on these and related subjects.

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