## THE FIBONACCI SEQUENCE ENCOUNTERED IN NERVE PHYSIOLOGY

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The pulses travelling along the nerve fibres originate in local currents of Sodium- and Potassium-ions, across the membranes which surround the fibres. The Sodium-current is switched on and off by small amounts of Calcium-ions. In order to model the operation of  $Ca^{2+}$ , assume that the  $Na^+$ -current flows through identical trans-membrane pores, each made up of a string of  $n Na^+$ -binding sites. Also,  $Ca^{2+}$  can enter the pores, occupy-ing two sites per ion, or, one site when entering the pore (cf. Fig. 2). Thus, a pore may momentarily look like Fig. 1.

	2 0 1 2	
Fig. 1	A pore in one of its possible states (0: empty site; $1 : Na^+$ ; $2 : Ca^{2+}$ )	)

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	2 2 0		
	2 2 1		
	2 0 2 1		
	2 2 0 1	1021	
	2 2 10		
	2 2 1111		
	2 1 0 1		
	2 1 1 0		
	2 1 1 1		
	2 0 1 1 1		
	2 110111		
	2 11 10 11		
	2 11 11 111		
			<b>E</b> 0
	1111111	111110	FIG. 2

Fig. 2 Graph for 5-site pore-process; only states with at most one vacant site.

Assume, further, that the particles can jump, in a stochastic manner, into a neighbouring empty site, without being able to overtake each other. During this process, Sodium may enter and leave the pores on either side, whereas Calcium may enter and leave at the left-hand side only. Thus, Calcium ions within a pore block the Sodium-current through this pore.

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This model reproduces the relevant outcome of experiments (publication in preparation).

Where and how do the Fibonacci numbers come in?

Let the stochastic process described above be Markoffean. Then, the process is conveniently pictured by a graph, with its points representing the finite number of possible states of a pore, given by its occupation by 0, 1, 2 (cf. Fig. 1), and its edges representing the allowed transitions between states. Alongside one has a set of homogeneous linear differential equations of the first order, describing the time development of the states' probabilities. These are, in essence, the forward-aquations of the Markoff-process.

For the time-stationary case, these equations are conveniently solved by graph-theoretical methods (T. L. Hill, *J. Theor. Biol.* (1966), 10, 442–459). Therefore, the graph needs careful investigation.

First, consider only pores with at most one site vacant. Under feasible physical conditions, these states can be shown to be the only relevant ones: only their probabilities differ appreciably from zero. Then, the graph boils down to a single cycle (along which  $Na^{\tau}$  is transported), and a large tree growing out of the cycle (cf. Fig. 2).

Note that the tree is made up of two types of subgraphs: each type ends in full pores, between which a vacancy travels from right to left (or vice versa). One specimen for each case is indicated by heavy edges, in Fig. 2.

It can be shown, that, in order to calculate the probabilities of the full-pore-states of the tree, one can throw out the one-vacancy-pores, too, ending up, in the case of Fig. 2, with the tree of Fig. 3.



Fig 3 Tree of full pores, corresponding to the tree in Fig. 2

From the general structure of the graph of Fig. 2, one infers that the tree of full-pore-states within the tree of the graph corresponding to *n*-site-pores ( $n = 2, 3, 4, \dots$ ), has the form of Fig. 4.

Counting the number of points, N(n), at level n, one finds

 $N(n) = F_n$  (n = 2, 3, 4, ...),

the Fibonacci sequence with  $F_1 = F_2 = 1$ . The tree of Fig. 4 is, indeed, the graph of Fibonacci's original rabbit family. This fact is based on the  $Ca^{2+}$  entering the pore, from the left, in two steps (cf. Fig. 2), as the ion has two legs, i.e., elementary charges.

Lanthanum<sup>3+</sup> is known, in its effect on the  $Na^+$ -current in nerve, as a super Calcium. If an analogous model is made, so that  $La^{3+}$ , instead of  $Ca^{2+}$ , switches the  $Na^+$ -current; and if  $La^{3+}$  enters the pores in three steps, then the graph corresponding to Fig. 4 is seen to have the structure of Fig. 5. Now the number  $N^{3+}(n)$  of points on level n (n = 2, 3, 4, ...) is given by



Fig. 4 Structure of full-pore-tree for *n*-sites-pores

etc.





This can obviously be generalized.

For the membrane model maker, these findings have already been useful.

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