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Submitted on 1 Jan 1987

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On the approach of the stationary state in Kauffman’s random Boolean network

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(Reçu le 8 septembre 1986, accepté le 9 octobre 1986)

Résumé. — Le modèle de Kauffman est un réseau booléen qui a k connexions aléatoires par nœud et qui évolue de façon déterministe suivant une règle aléatoire figée. Pour un système de N nœuds, nous considérons un intervalle de temps 0 ≤ t ≤ tN, tel que \( \lim_{N \to \infty} t_N = \infty \). Nous montrons (i) que le recouvrement moyen entre deux états initiaux arbitraires obéit exactement à l’équation de l’approximation de « recuit » de Derrida et Pomeau, (ii) que pour k ≤ 2 chaque état converge faiblement vers un état de point fixe. De plus, (iii) nous obtenons des limites supérieures sur les corrections dues aux effets de taille finie. Enfin, (iv) nous calculons exactement le recouvrement de paire comme fonction du temps pour k = 1 et le comparons aux résultats précédents.

Abstract. — Kauffman’s model is a Boolean network having k quenched random connections per node, and evolving deterministically in time according to a quenched random rule. For a systems of N nodes we consider a time domain 0 ≤ t ≤ tN, with \( \lim_{N \to \infty} t_N = \infty \). It is shown (i) that in this limit the average overlap between two arbitrary initial states rigorously obeys an equation first derived by Derrida and Pomeau, and (ii) that for k ≤ 2 each state evolves, in a weak sense, to a fixed point state. Also, (iii) upper bounds on the finite size corrections are obtained. Lastly, (iv) for k = 1 the exact time-dependent pair overlap is found and compared to the results (i)-(iii).

1. Introduction.

Kauffman’s model [1] describes the deterministic time evolution of a system of N Boolean (or « spin ») variables \( s_1(t), s_2(t), ..., s_N(t) \), each capable of taking either of the two values +1 and −1. The spins may change of value only at the discrete times \( t = 0, 1, 2, ... \). The value \( s_i(t) \) of the spin at the site (or « node ») \( i \) is determined by the set of values at the previous instant of time, \( t - 1 \), of the \( k \) ancestor spins at the ancestor sites \( i_1, i_2, ..., i_k \), according to a transformation

\[
s_i(t) = r_i\left(s_{i_1}(t-1), ..., s_{i_k}(t-1)\right).
\]

(1.1)

Here the indices \( i_j \) are \( Nk \) independent random variables taking the values 1, ..., \( N \) with equal probability. They are quenched, i.e., chosen once for all in a given realization of the model. Similarly, the \( r_i \) are \( N \) independent random functions; each takes the value +1 or −1 with equal probability for every set of values of its arguments. They are also quenched. Finally, \( k \) is a parameter of the model (we may fix it at any of the values 1, 2, ..., \( N \)).

The Kauffman model is one example of a quenched network of Boolean automata [2, 3]. Models of this type were introduced to describe regulatory systems of great complexity, such as encountered for example in biology. They constitute a new class of very difficult but interesting problems in statistical mechanics. An important question which one would like to answer is how to characterize the stationary states (i.e. the limit cycles) of such Boolean networks. How many cycles are there for a given transformation, what is their length, what are their stability properties and their domains of attraction? And how do these properties vary from one rule to another?

Previous studies [1, 4] seem to indicate that for the Kauffman model with \( k \leq 2 \) the typical cycle length is
of order \(N^{1/2}\), whereas for \(k > 2\) it increases exponentially with \(N\). Some interesting numerical results on the sizes of the domains of attraction have recently been obtained by Derrida and Flyvbjerg [5].

In order to study these and other questions one frequently compares the time evolutions of two (or more) configurations. The \((\text{pair})\) overlap between \(s = (s_1, ..., s_N)\) and \(s' = (s'_1, ..., s'_N)\) is defined as

\[
q(s, s') = \frac{1}{N} \sum_{i=1}^{N} s_i s'_i ;
\]

it varies between \(-1\) and \(1\), and the quantity \((1 - q(s, s'))/2\) is also referred to as the \(\text{distance}\) between \(s\) and \(s'\).

One often considers \(\text{averages}\) of quantities with respect to the quenched randomness, i.e. with respect to all possible choices of the random indices \(i_1\) and the random functions \(r_i\). We shall indicate such averages by an overbar. Thus one has, e.g.

\[
\overline{r_i} \left( \sigma_{i_1}, ..., \sigma_k \right) = 0
\]

\[
r_i \left( \sigma_{i_1}, ..., \sigma_k \right) \overline{r_i'} \left( \sigma_{i'_1}, ..., \sigma'_{k'} \right) = \delta_{i i'} \prod_{l=1}^{k} \delta_{\sigma_l, \sigma'_l} .
\]

Similar relations for the higher moments can be found.

The purpose of this work is to describe how the Kauffman model approaches its stationary state in a time regime \(0 \leq t \leq t_N\), with \(t_N \to \infty\) as \(N \to \infty\). It turns out that in this limit the average time-dependent pair overlap function is given exactly by an equation due to Derrida and Pomeau [6]. We shall derive upper bounds for the finite size corrections. Finally we shall find the exact average time-dependent pair overlap function for \(k = 1\) and discuss it in the light of the preceding analysis.

2. \(\text{Large-}\(N\) \(\text{behaviour of time-dependent pair overlaps, and annealed approximation.}\)

Suppose two configurations \(s = s(0)\) and \(s' = s'(0)\) are given at time \(t = 0\). We wish to express the time evolution of their overlap in terms of the initial configurations by using the recursion (1.1). From (1.1) and (1.2) we have

\[
q_w(t) = q(s(t), s'(t)) = \frac{1}{N} \sum_{i=1}^{N} r_i(s_i(t-1), ..., s_k(t-1))
\]

\[
\times r_i'(s'_i(t-1), ..., s'_k(t-1)) .
\]

The spin variables \(s_i(t-1)\) and \(s'_i(t-1)\) that occur in (2.1) can again be expressed in a set of second generation ancestor spins, taken at time \(t = 2\). This involves the set of \(k\) functions \(r_j\) at the ancestor sites \(i_1, i_2, ..., i_k\). If from a given site \(i\) we go back recursively until \(t = 0\) we thus need the functions \(r_j\) at a number \(K_t\) of sites given by

\[
K_t = 1 + k + \cdots + k^t = \frac{k^{t+1} - 1}{k - 1} (k > 1)
\]

(2.2a)

\[
K_t = t (k = 1).
\]

(2.2b)

In principle this can introduce correlations in the \(i\)-th term in (2.1), namely when equals occur among these \(K_t\) sites. However, the probability \(f_{N_t}\) (within the class of all allowed transformations) for this to happen is given by

\[
f_{N_t} = 1 - \prod_{j=1}^{K_t-1} \left(1 - j/N \right) = 1/2 N^{-1} K_t (K_t - 1) + \Theta \left(N^{-2} K_t^2 \right).
\]

(2.3)

This means that it is vanishingly small for \(N \to \infty\) if one keeps \(t\) restricted to the \(N\) dependent domain

\[
1 \leq t \leq t_N
\]

(2.4a)

where

\[
t_N = c_k \log N / (2 \log k)
\]

for arbitrary \(c_k < 1\) (\(k > 1\)).

(2.4b)

\[
t_N = c_1 \log N
\]

for arbitrary \(c_1\) (\(k = 1\)).

(2.4c)

This is readily verified by substitution of (2.4) in (2.2), and of (2.2) in (2.3). (For convenience we take \(t_N\) an integer.) We remark that for \(k = 1\) the choice (2.4c) is not the best possible one (we could have set \(t_N = N^\alpha\) for arbitrary \(\alpha < 1/2\)) however the reason for it will become apparent in the next section.

It follows that in the recursion (2.1) the average on the explicitly displayed product of random functions \(r_i(s_{i_1}, ..., s_k) r_i'(s'_{i_1}, ..., s'_{k'})\) may be carried out, for \(N \to \infty\), independently of the averages on the \(r_j\)'s implicit in \(s_i(t-1)\) and \(s'_i(t-1)\). Upon performing this average with the aid of (1.3) and representing \(\delta_{\sigma \sigma'}\) as \(\frac{1}{2} (1 + \sigma \sigma')\) we obtain

\[
q_w(t) = \frac{1}{N} \sum_{i=1}^{N} \prod_{j=1}^{k} \left[1/2 \left(1 + s_i(t-1) s'_i(t-1) \right) \right]
\]

\[
= \frac{1}{N} \sum_{i=1}^{N} \prod_{j=1}^{k} \left[1/2 \left(1 + s_i(t-1) s'_i(t-1) \right) \right]
\]

\[
= \left(1 + q_w(t-1) \right)^k
\]

(2.5)

(\(s, s'\) arbitrary, \(1 \leq t \leq t_N, N \to \infty\)).

The second equality in (2.5) holds because for \(N \to \infty\) two different branches of a tree of ancestors have no site in common, and the third one uses the equivalence of all sites. Equation (2.4) determines the time evolu-
tion of the average overlap $\bar{q}_{ss'}(t)$ when $q_{ss'}(0)$ is given.

The relation (2.4) was first derived by Derrida and Pomeau [6] in an annealed approximation to the Kauffman model. This approximation consists in neglecting the fact that the transformation (1.1) is quenched, and replacing it at every time step by a new and independently drawn transformation. It has been proved rigorously here that in the limit $N \to \infty$ the annealed approximation is, in fact, exact for the overlaps between configurations (not for the configurations themselves), if one keeps $t$ restricted according to (2.4). This renders more precise the conclusion of Derrida and Weisbuch [7], who, prompted by their simulation data, showed that the time evolution (2.5) is exact in the thermodynamic limit.

One can derive results somewhat stronger than (2.5) by considering how, for given $s(0)$ and $s'(0)$, the quantity $q_{ss'}(t)$ is distributed as the transformation is varied. In reference [5], for example, the second moment of this quantity was considered. Here we shall not pursue such questions any further.

3. Approach of a fixed overlap.

The fixed points $q^*$ of equation (2.5) satisfy

$$q^* = \left(1 + q^*\right)^{k/2}.$$

From now on we shall consider $k$ as a continuous variable in $[1, \infty)$. The stable solution [6] of (3.1) is $q^* = 1$ for $k \leq 2$. For $k > 2$ this solution is unstable and a stable solution $q^* < 1$ appears. Upon putting

$$\bar{q}_{ss'}(t) = q^* + \Delta q_{ss'}(t)$$

and linearizing equation (2.5) around its stable fixed point we find

$$\Delta q_{ss'}(t + 1) = \lambda_k \Delta q_{ss'}(t) + \ldots$$

where

$$\lambda_k = \begin{cases} 1/2 & (k < 2) \\ 1 - 1/2 \delta k + \Theta(\delta k^2) & (k = 2 + \delta k) \end{cases}$$

Here and henceforth it will be understood that $\delta k$ is positive. For large $t$ the fixed point overlap is approached as

$$\left|\Delta q_{ss'}(t)\right| = C_k \lambda_k^t \quad (t \text{ large, } k \neq 2)$$

(3.5a)

where the constant $C_k$ depends on $\Delta q_{ss'}(0)$, whereas in the marginal case $k = 2$ we have

$$\left|\Delta q_{ss'}(t)\right| = 4 \left(t + t_0\right)^{-1} = 4 t^{-1}$$

(3.5b)

with the constant $t_0$ depending on $\Delta q_{ss'}(0)$.

Since equations (3.3) and (3.5) are valid in the time domain $1 \leq t \leq t_N$, with $t_N$ satisfying (2.4b), they cannot be used to approach the fixed point overlap closer than a certain distance $\delta q_{ss'}^\text{min}$. In the regime $k > 1$ and with $t_N$ chosen as in (2.4b) we have, as $N$ becomes large,

$$f_N = 1/2 c^2 N^{-1} \log^2 N \quad (k = 1).$$

(3.7b)

We have no right to expect that one can iterate the recursion (2.5) or (3.3) to a value $\Delta q_{ss'}(t)$ smaller than $f_N$. Therefore we wish to know the value of

$$\delta_N = \inf_{\delta q_{ss'}^\text{min}} \{ \delta q_{ss'}^\text{min} : \delta q_{ss'}^\text{min} = f_N \}.$$

(3.8)

With the aid of (3.6) and (3.7) we can determine this quantity. It appears that the best choices are

$$c_1 = 1/\log 2 - \epsilon$$

(3.9a)

$$c_2 = 1 - \epsilon$$

(3.9b)
where in each formula $\varepsilon$ is an independent arbitrarily small positive constant, and

$$c_k = \left(1 + \left|\log \lambda_k\right|/2 \log k\right)^{-1} \quad (k \neq 1, 2).$$  

(3.9c)

Upon using these values in (3.6) we find

$$\delta_N = C_N N^{-1 + \varepsilon} \quad (\varepsilon > 0 \text{ arbitrary}) \quad (k = 1)$$  

(3.10a)

$$\delta_N = C_N N^{-\left|\log \frac{1}{2}\right|/\log 2} k \quad (1 < k < 2)$$  

(3.10b)

$$\delta_N = \frac{(8 \log 2 - \varepsilon)}{\log N} \quad (\varepsilon > 0 \text{ arbitrary}) \quad (k = 2)$$  

(3.10c)

$$\delta_N = C_N N^{-\frac{1}{2k} \log 2 + o(\log 2)} \quad (k = 2 + \delta k)$$  

(3.10d)

The conclusion of this section is, therefore, that the average overlap $q_{ss}(t)$ of any pair of initial configurations $s$ and $s'$ approaches with increasing $t$ the limiting overlap $q^*$ to within a distance of order $\delta_N$, given by (3.10), which vanishes as $N \to \infty$. The time needed for this approach is $t_N$ as given by (2.4b), (2.4c) and (3.9). The same conclusion can be reached similarly for the average overlap $q_{ss}(t; t')$ of two iterates of the same initial configuration $t$ steps apart.

We emphasize that in all cases the quantities $\delta_N$ are upper bounds to the distance of approach of the fixed point overlap $q^*$, and the $t_N$ are lower bounds to the domain of validity in time of equation (2.5). Since $t_N \to \infty$ and $\delta_N \to 0$ for $N \to \infty$, we may also consider these quantities as bounds for the finite size corrections to equation (2.5). We shall say more about the quality of these bounds later.

4. « Weak » approach of a fixed point configuration for $k \leq 2$.

We now restrict ourselves to the case $k = 2$, where the limiting overlap is $q^* = 1$. Here we shall explicitly indicate as $s(t; r)$ the $t$-th iterate of an initial configuration $s(0)$ under the action of a transformation $r$. As $t$ grows larger and larger, $s(t; r)$ eventually enters a limit cycle which in general will be nontrivial. We shall show that nevertheless, loosely speaking, for each transformation $r$ there exists a configuration $s^*(r)$ such that, for each $s(0)$, for most $r$, and for most $t$ in the range $1/2 t_N \leq t \leq t_N$ ($t_N$ assumed even), the configuration $s(t; r)$ is within a vanishing distance of $s^*(r)$ as $N \to \infty$. This statement will be made precise in the proof below.

We start from the triangle inequality

$$|\delta q(s(t; r), s'(t; r))| \leq |\delta q(s(1/2 t_N; r), s(t; r))| +$$

$$+ |\delta q(s(t; r), s'(t, r))| \quad (4.1)$$

valid for arbitrary $s(0)$, $s'(0)$, $t$, and $r$. Here we have returned to the full notation of equation (1.2), and recall that $|\delta q(s, s')|$ has the properties of a distance in configuration space. Upon averaging (4.1) on all $r$, and again in a simpler notation, we get

$$|\delta q(s(1/2 t_N), s'(t))| \approx$$

$$\approx \left|\delta q(s(1/2 t_N), s(t))\right| +$$

$$+ \left|\delta q(s(t), s'(t))\right|. \quad (4.2)$$

For large enough $N$, and because of (3.6a), the second term on the right hand side in (4.2) is bounded above by $C_k^+ \lambda_k^t$, where $C_k^+$ is a fixed constant larger than the maximum value of $C_k$. If we choose $t$ between $1/2 t_N$ and $t_N$, then $\delta q(s(1/2 t_N), s(t))$ is the $1/2 t_N$-th iterate of $\delta q(s(0), s(t-1/2 t_N))$ and therefore less than $C_k^+ \lambda_k^{1/2 t_N}$. With the definition

$$s^*(r) = s(1/2 t_N; r) \quad (4.3)$$

it follows from (4.2) that, for sufficiently large $N$ and for arbitrary $s'(0)$, the trajectory $s'(t)$ in configuration space satisfies

$$|\delta q(s^*, s'(t))| \approx 2 C_k^+ \lambda_k^{1/2 t_N} \quad (1/2 t_N \leq t \leq t_N, k \neq 2). \quad (4.4a)$$

For $k = 2$ estimates similar to the ones above lead to

$$|\delta q(s^*, s'(t))| \approx 2 C_2^+ t_N^{1/2} \quad (1/2 t_N \leq t \leq t_N, k = 2). \quad (4.4b)$$

For the upper bounds in (4.4a) and (4.4b) one can obtain explicit expressions in terms of the system size $N$ with the aid of equations (3.6) and (3.9); the bound for $k \neq 2$ is easily seen to be proportional to $\delta_N^{1/2}$.

Equations (4.4) express the precise meaning of the « weak » approach to a fixed point configuration. This configuration, $s^*$, depends on the transformation $r$. However, even for a given transformation, $s^*(r)$ is determined only up to a fraction of spins of the order of the upper bounds in (4.4). (We might have defined, for example, $s^*(r) = s'(1/2 t_N; r)$ for any $s'(0)$.) Furthermore, equation (4.4) is a statement about the behaviour of a trajectory $s'(t)$ averaged over all
transformations. We have not succeeded to prove that
a similar weak approach of a fixed point holds, with
probability 1 as $N \rightarrow \infty$, for an arbitrary individual
transformation.

5. Exact solution for the case $k = 1$.

For $k = 1$ the solution $\overline{q_{st}}(t)$ can be obtained
analytically. We shall do so below and compare the
result to our estimates of the previous sections.

5.1 Structure of the trees of ancestors. —
For $k = 1$ and a given transformation, each site has one
ancestor site. We select an arbitrary site $i$, and may put
$i = 1$ without loss of generality. Also without loss of
generality, we label the successive sites in its tree of
ancestors as $2, 3, \ldots$; this can be done until the ancestor
site of, say, the $(M + 1)$th generation is equal to one
of the sites $1, 2, \ldots, M$ already in the tree, say to the site
$m_0$. The tree of ancestors of the selected site $1$ is then
complete. If $m_0 = 1$, this tree is a circular system with
$M$ sites, of which site $1$ is a member. If $2 \leq m_0 \leq M$, the
tree contains a circular system of $M + 1 - m_0$ sites,
with at site $m_0$ (which is the ancestor to both $m_0 - 1$ and
$M$) a linear system of the sites $1, 2, \ldots, m_0 - 1$
branching off. (The selected site $1$ may itself be the
ancestor to zero, one, or more other sites, but this does
not concern us.)

The probability $P_M$ that the tree of ancestors of site $1$
has exactly $M$ sites (also counting site $1$ itself) is

$$P_M = \left(1 - \frac{1}{N}\right) \left(1 - \frac{2}{N}\right) \ldots \left(1 - \frac{M - 1}{N}\right) \frac{M}{N}$$

$$(M = 1, \ldots, N). \quad (5.1)$$

If in the useful relation

$$\sum_{M=m}^{N} P_M = \left(1 - \frac{1}{N}\right) \left(1 - \frac{2}{N}\right) \ldots \left(1 - \frac{m - 1}{N}\right) \frac{m}{N}$$

$$(m = 1, \ldots, N) \quad (5.2)$$

we set $m = 1$, it follows that $P_M$ is normalized to 1. Starting from equation (5.1) Coste and Hénon [8] have
derived several other interesting statistical properties of
the trees of ancestors, but we shall not need those here.

5.2 The random functions $r_i$. — With each site $j$
a random Boolean function $r_j(s_i)$ is associated (i the
ancestor site of $j$). There exist four such functions, but
for our purpose it is sufficient to consider only two
classes, which each occur with probability $1/2$, viz. (i)
$r_j$ is a constant function, i.e. $r_j(\pm 1) = -1$ or
$r_j(\pm 1) = 1$; and (ii) $r_j$ is not a constant function,
i.e. $r_j(\pm 1) = \pm 1$ or $r_j(\pm 1) = \mp 1$.

The probability that an ancestor tree having $M$ sites
(and hence described by $M$ random functions) contains
no constant function, is equal to $(1/2)^M$. Therefore
the probability $Q_{\infty}$ that the ancestor tree of an
arbitrarily selected site $1$ contains no constant func-
tions is given by

$$Q_{\infty} = \sum_{M=1}^{N} \left(1/2\right)^M P_M. \quad (5.3a)$$

The probability $Q_m$ that the tree of site $1$ contains at
least $m$ sites and that the functions $r_1, r_2, \ldots, r_{m-1}$ are
not constant while $r_m$ is constant, equals

$$Q_m = \left(1/2\right)^m \sum_{M=m}^{N} P_M \quad (m = 1, 2, \ldots, N). \quad (5.3b)$$

One can verify the normalization

$$\sum_{m=1}^{N} Q_m + Q_{\infty} = 1. \quad (5.4)$$

5.3 The time-dependent overlap $\overline{q_{st}}(t)$. — We
fix two initial configurations, $s(0)$ and $s'(0)$, of
which we specify only that $s_i(0) = s_i'(0)$ at $N_+$
sites, and $s_i(0) = -s_i'(0)$ at the remaining $N_- =
N - N_+$ sites. The initial overlap then is

$$\overline{q_{st}}(0) = N^{-1} \sum_{i=1}^{N} s_i(0) s_i'(0) = N^{-1} (N_+ - N_-). \quad (5.5)$$

In order to find $\overline{q_{st}}(t)$ we now select an arbitrary
site $i$, relabel as before so that it becomes the site $1$, and
study the time dependence of $s_1(t)$ $s_1'(t)$. The
essential point is that (i) a constant function $r_j$ causes
$s_j(t+1) s_j'(t+1)$ to be equal to 1, and (ii) a
nonconstant function $r_j$ causes $s_j(t+1) s_j'(t+1)$ to
be equal to $s_j(t) s_j'(t)$ (if site $i$ is the ancestor of site
$j$). The time dependence of $s_j(t)$ $s_j'(t)$ therefore
depends on the distance of site $1$ along its ancestor tree
to the nearest constant function. If this is $r_m$ (as will be
the case with probability $Q_m$), then

$$s_j(t) s_j'(t) = \begin{cases} s_{j+l}(0) s_{j+l}'(0) & (t = 1, \ldots, m-l, \quad l = 1, \ldots, m-1) \\ 1 & (t = m-l + 1, \ldots, \quad l = 1, \ldots, m). \end{cases} \quad (5.6)$$
We now take this relation for \( I = 1 \), and average it over all random functions for which site 1 is at a distance \( m \) of the nearest constant function, as well as over all ways to select site 1. Indicating this average by \( \overline{q_{st}(t)}(m) \) we get

\[
\overline{q_{st}(t)}(m) = \begin{cases} 
q_{st}(0) & t = 1, \ldots, m - 1 \\
1 & t = m, m + 1, \ldots 
\end{cases} \quad (5.7a)
\]

If the ancestor tree of site 1 contains no constant function, as is the case with probability \( Q_\alpha \), then \( s_1(t) \) will, after a transient time equal to \( m_0 \), enter a limit cycle of length \( M - m_0 \) in which the values +1 and -1 randomly occur with probabilities \( N_+ / N \) and \( N_- / N \), respectively. Hence we have, in self-explanatory notation,

\[
\overline{q_{st}(t)}(\infty) = q_{st}(0) \quad t = 1, 2, \ldots \quad (5.7b)
\]

Upon weighting each of the cases in equation (5.7) with its probability of occurrence we get

\[
\overline{q_{st}(t)} = \sum_{m=1}^{N} Q_m \overline{q_{st}(t)}(m) + Q_\alpha \overline{q_{st}(t)}(\infty). \quad (5.8)
\]

If in this equation we substitute (5.3) and (5.7), and rearrange terms using (5.2), it reduces to

\[
\overline{q_{st}(t)} = \begin{cases} 
1 - \left(1 - q_{st}(0)\right) & A_N(t) + (1/2)^t B_N(t) \\
1 - \left(1 - q_{st}(0)\right) & A_N(N) 
\end{cases}, \quad t = 0, 1, 2, \ldots, N
\]

\[
A_N(t) = \sum_{M=1}^{t} (1/2)^M P_M, \\
B_N(t) = \sum_{M=t+1}^{N} P_M, \quad t = 0, 1, \ldots, N
\]

(5.10a, b)

This is the main result of this section.

**5.4 DISCUSSION.** — In order to discuss this result we analyse the functions \( A_N(t) \) and \( B_N(t) \). Obviously \( A_N(0) = 0 \) and \( B_N(0) = 1 \). For \( B_N(t) \), defined by (5.10b), we use (5.2). Upon expanding the product in powers of \( N^{-1} \) we find

\[
B_N(t) = 1 - \frac{t(t + 1)}{2N} + O\left(\frac{t^4}{N^2}\right) \quad \text{as } t^2/N \to 0. \quad (5.11a)
\]

If in (5.10a) we use (5.1), expand the product as above, and carry out the sum on \( M \), we find

\[
A_N(t) = \frac{2}{N} \left[ 1 - \frac{t + 2}{2} \left(\frac{1}{2}\right)^t + O\left(\frac{1}{N}\right) \right]
\]

as \( N \to \infty \), \( t \) arbitrary \( (5.11b) \)

From (5.9), (5.10), and (5.11) we obtain

\[
\overline{q_{st}(t)} = 1 - \left(1 - q_{st}(0)\right) \left[ \frac{2}{N} + O\left(\frac{1}{N^2}\right) \right] + 2^{-t} \left(1 - \frac{t^2 + 3t + 4}{2N} + O\left(\frac{t^4}{N^2}\right) \right) \quad (5.12)
\]

valid for \( N \to \infty \) and \( t^2/N \to 0 \). This latter condition is identical to the condition \( f_N \to 0 \) (for \( k = 1 \)) required in section 2.

From (5.12) we deduce that to leading order

\[
\overline{q_{st}(t)} = 1 - 2^{-t} \left(1 - q_{st}(0)\right) \left[ 2N^{-1} + 2^{-t} \right]
\]

for \( 1 < t < (1/\log 2 - \varepsilon) \log N \) \( (5.13a) \)

with \( \varepsilon > 0 \) arbitrary. This expression coincides, as it should, with the solution of equation (2.5) for \( k = 1 \). Moreover the domain of validity in time of (5.13a) is identical to the domain guaranteed by our previous analysis (Eqs. (2.4a), (2.4c), and (3.9a)), which means that in section 3 we have given the best possible estimates for \( k = 1 \).

At \( t = \log N/\log 2 \) a crossover to a new time domain occurs. The first three terms in the large-\( N \) expansion are

\[
\overline{q_{st}(t)} = 1 - \left(1 - q_{st}(0)\right) \left[ 2N^{-1} + 2^{-t} \right] \quad (1/\log 2 + \varepsilon) \log N \leq t \leq (2/\log 2 - \varepsilon) \log N \quad (5.13b)
\]

The term with the power \( N^{-1} \), which is the leading correction, is readily traced back to the fact that certain sites, due to the combined effects of the circular structure in their ancestor tree and the absence of constant Boolean functions in it, enter into a limit cycle.

For \( t \gg 2 \log N/\log 2 \) it no longer makes sense to keep the \( 2^{-t} \) terms in (5.12), since they are negligible compared to the \( O\left(N^{-2}\right) \) corrections. Hence we have

\[
\overline{q_{st}(t)} = 1 - 2N^{-1} \left(1 - q_{st}(0)\right) + O\left(N^{-2}\right) \quad \text{for } t \gg (2 \log 2 + \varepsilon) \log N \quad (5.13c)
\]
in which the $O(N^{-2})$ terms still depend on $t$. We see in particular that for $t \to \infty$ the quantity $\delta q_{ss'}(t)$ approaches a nonzero value of order $N^{-1}$.

6. Conclusion.

We have studied the approach to the stationary state in Kauffman’s random Boolean network with $N$ spin sites and $k$ ancestors per site. It is shown that in the limit $N \to \infty$ the time evolution of the average pair overlap, $q_{ss'}(t)$, is given exactly by the equation of Derrida and Pomeau [5], in a time domain $0 \leq t \leq t_N$ with $\lim_{N \to \infty} t_N = \infty$. As a function of $k$, $q_{ss'}(t)$ shows a crossover between two types of behaviour at $k = 2$. A lower bound for $t_N$ is derived, as well as an upper bound for the finite size corrections to $q_{ss'}(t)$. For $k \leq 2$ the system is shown to approach, in a weak sense, a fixed point configuration. For $k = 1$ we derived the analytic expression for $q_{ss'}(t)$ and saw that the bounds obtained before were optimal. However, simulation data [7] for $k = 2$ show a finite size effect proportional to $N^{-\alpha}$ with $\alpha = 0.27 \pm 0.03$. This should be compared to the bound proportional to $1/\log N$ found for that case in equation (3.10c). Hence we do not expect our bounds to be optimal for $k > 1$, and it would be interesting to improve them. Finally, we remark that we have treated the « easy » problem. Whereas our results apply to times up to $t_N$, and $t_N \to \infty$ as $N \to \infty$, a very different type of behaviour will occur for $t \gg t_N$. On that time scale the system enters a stationary state with much more complicated statistical properties [5] which, except when $k = 1$, are not yet fully understood.

References