AN EXACT METHOD FOR THE COMPUTATION OF THE CONNECTIVITY OF RANDOM NETS

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The problem of finding the "weak connectivity" of a random net is reduced to one involving a Markov process. This provides a mathematically exact treatment of the problem which had previously been treated by an approximation, whose justification was not rigorous. The exact method allows in principle not only the calculation of the "weak connectivity," but also of the "strong connectivity," and, in general, the probability that from a randomly selected neuron in the net there exist paths to a specified number of neurons. The computations become exceedingly involved for large nets.

A previous paper (Solomonoff and Rapoport, 1951) dealt with an approximate method for determining the "weak connectivity" of random nets. The reader is referred to that paper for the definitions of terms and the statement of the problem.

In this paper we will indicate a mathematically exact method for calculating the probability that from an arbitrarily selected neuron in a random net paths exist to any specified number of neurons. The expected number of such neurons is then the "weak connectivity." On the other hand, if the specified number is the largest possible, the associated probability is the "strong connectivity."

We follow the "tracing procedure" described in the previous paper. Let x(t) represent the actual number of neurons contacted in all by the tth tracing inclusive, and let y(t) be the number of neurons newly contacted by the tth tracing. Then

$$x(t) = \sum_{i=0}^{t} y(i). \tag{1}$$

Let p(x, t) be the probability that there were x neurons in all contacted by the tth tracing. Then p(x, t) depends not only upon the possible values of x on the (t-1)th tracing, but also upon those values on the (t-2)th

tracing, since only the newly contacted neurons of the (t-1)th tracing are traced on the tth. If x(t-1) = i and x(t-2) = j, then

$$p(x, t) = r_{x-i}[a(i-j), i].$$
 (2)

Here $r_k(s, m)$ is the probability that k neurons will be newly contacted, when there are s axones being traced and there have been m neurons already contacted. The equation

$$r_k(s, m) = {N-m \choose k} N^{-s} \sum_{j=0}^k {k \choose j} (m+k-j)^s$$
 (3)

was derived by A. Rapoport (1951). This can be more compactly written in the notation of finite differences as

$$r_k(s, m) = {N-m \choose k} \frac{\Delta^k(m^s)}{N^s}, \tag{4}$$

where $\Delta^{k}(m^{s})$ is given by the following iteration formula:

$$\Delta(m^s) = (m+1)^s - m^s,$$

$$\Delta^k(m^s) = \Delta^{k-1} [(m+1)^s] - \Delta^{k-1} [m^s].$$
(5)

Consider now an abstract system with N^2+1 possible states. We can designate each state by an ordered pair (i,j), where i and j range independently from 1 to N, and an additional (initial) pair (0,1). Furthermore, suppose that if the system is in state (i,j) at time t, then the probability that it will be in state (k,l) at time t+1 is independent of t and equals p[(i,j),(k,l)]. Hence if we designate by D[(i,j),t] the probability density distribution over all the possible states at time t, this distribution at time t+1 will be given by

$$D[(k, l), t+1] = \sum_{(i, j)} p[(i, j), (k, l)] D[(i, j), t].$$
 (6)

This equation is obtained by summing over all possible ways in which the system can make transitions from states (i,j) to a state (k,l). The p's are, of course, the transition probabilities. The D's are probability density distributions of the N^2+1 possible states. We shall refer to the D's simply as the distribution vectors.

It is now clear that we are dealing with a process which can be described in terms of a vector-matrix equation, in fact, a Markov process. The vectors have $N^2 + 1$ components and the matrices $N^4 + 2N^2 + 1$ com-

ponents. If we designate our transition matrix by P, equation (6) can be immediately generalized to

$$D[t+n] = P^n D(t). (7)$$

This follows by a simple induction on n.

In terms of our problem we then have the following interpretation. Let i(t) be the total number of neurons contacted by the (t-1)th tracing and j(t) the total number contacted by the tth tracing. Then p[(i, j), (k, l)] is the probability of the following combination of events:

- 1. At t-1, there were i neurons contacted in all.
- 2. At t, there were j neurons contacted in all.
- 3. At t, there were k neurons contacted in all.
- 4. At t + 1, there will be l neurons contacted in all.

Evidently 2. and 3. are either identical or incompatible. They were stated separately only to give meaning to the quadruple index (i, j, k, l) in terms of which the vector-matrix formulation was obtained. In view of the meaning of our indices, we see that p[(i, j), (k, l)] = 0 unless $i \le j = k \le l$, so that our transition matrix P has non-zero elements at most at those loci [(i, j), (j, l)], where $i \le j \le l$.

Now let an initial condition be known, e.g., at t = 1 exactly one neuron is contacted. Then the initial distribution vector is (1, 0, 0...) with the unity representing the certainty of the initial state (0, 1) at t = 1. The elements of the transition matrix are given by

$$p[(i, j), (j, l)] = {N - j \choose l - j} \frac{\Delta^{(l-j)}[j^{a(i-i)}]}{N^{a(i-i)}}.$$
 (8)

This is essentially the expression (4) with

k=l-j, the number of newly-contacted neurons at t+1; m=j, the number of neurons in all contacted at t; $s=a\ (j-i)$, the number of axones to be traced at t.

To find the final distribution vector at t = n + 1, we multiply the initial distribution vector (1, 0...) by the *n*th power of the transition matrix. Note that if on any tracing no new neurons are contacted, there will be no axones to trace on any subsequent tracing, and, therefore, the total number of neurons contacted will remain stationary. But there are exactly N - 1 uncontacted neurons at t = 1. Hence there can be at most

N-1 tracings, and we can set n=N-1. The distribution vectors will remain unchanged for t>N.

Another way of looking at it is by noting that for t = N, the distribution vector is the sum of eigenvectors, each of eigenvalue unity. All the components of these eigenvectors vanish, except one of the (i, i) components. There are exactly N such eigenvectors, one for each i.

It appears, therefore, that the final distribution vector D [(i, j), N] will have non-zero components only where i = j. Each of these components with index (i, i) will represent the probability that there exist paths from an arbitrary neuron to exactly i other neurons. In particular, the component (N, N) is the "strong connectivity" of the net, which, as will be recalled, was defined in the previous paper as the probability that paths exist from an arbitrary neuron to all the other neurons of the net.

To find the weak connectivity γ , we take the expected value of x/N at t = N, so that

$$\gamma = \frac{1}{N} \sum_{i} i D[(i, i), N].$$
 (9)

In the following numerical example N=4, a=2. Our transition matrix, computed from (4), is shown in Table I.

TABLE I

The initial distribution vector of 17 components is (1, 0, 0...). At t = 4 the (final) distribution vector is

$$D(4) = (0, .0625, 0,1407,316,481).$$
 (10)

The non-zero components of this vector give the probabilities that there exist paths from an arbitrary neuron to 1, 2, 3, and 4 neurons respectively. In particular, the last value, .481, is the strong connectivity of the random net with total population 4 and axone density 2.

The weak connectivity is

$$\frac{1}{4}(1 \times .0625 + 2 \times .1407 + 3 \times .316 + 4 \times .481) = .804$$
. (11)

The value of γ given by the approximate equation (cf. Solomonoff and Rapoport, *loc. cit.*),

$$\gamma = 1 - e^{-a\gamma} \,, \tag{12}$$

turns out to be 0.8, a good approximation for this case.

LITERATURE

Rapoport, Anatol. 1951. "The Probability Distribution of Distinct Hits on Closely Packed Targets." Bull. Math. Biophysics, 13, 133-38.

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