Random-Walk Networks

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Abstract

We study in detail the behavior of random-walk networks: RWN's. These networks are a generalization of the well-known random Boolean networks RBN's, a classical approach to the study of the genome. RWN's are also discrete networks, but their response is defined by small variations in the state of each gene, thus being a more realistic representation of the genome and a natural bridge between discrete and continuous models. RWN's show a clear transition between order and disorder. Here we explicitly deduce the formula of the critical line for the annealed model and compute numerically the transition points for quenched and annealed models. We show that RBN's and the annealed model of RWN's act as an upper and a lower limit for the quenched model of RWN's. Finally we calculate the limit of the annealed model for the continuous case.

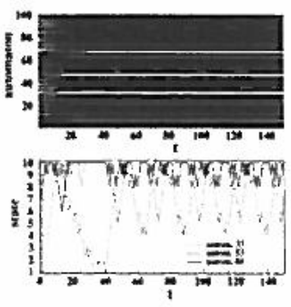

FIG. 1. Example of complex RWN behavior. Top: dynamics of a RWN with $N=100$ automata, $K=2$, $p=0.79$ and $r=10$. The horizontal axis represents time steps and the vertical axis shows the 100 automata. Different gray intensities correspond to different states for each automaton, ranging from 1 (white) to 10 (black). Bottom: evolution of the automata states (automata values) in time for the same RWN. For simplicity, only automaton nos. 33, 51 and 88 are shown (figure from [8]).

boundary between ordered and disordered phases obtained through the annealed model for N tending to infinity coincides with the boundary of the quenched model, hence the power of this method.

Therefore following Derrida and Pomeau we will derive the boundaries separating order and disorder for the RWN annealed model. In order to avoid time correlations, each time step we redefine both the automaton inputs $i_1, i_2, \ldots, i_K$ and functions ϕ_i for each automaton $i=1,2,\ldots,N$. The avoiding of time correlations is strictly true for RBN's, but for annealed RWN's the memory dependence is not totally avoided as C influences x^{-1} [see Eq. (1)]. Nevertheless the RWN annealed model shows also an ordered-disordered transition and we can compute it as a mean field of the RWN quenched model.

If every time step each automaton i has K new inputs and new p-biased functions ϕ_i, then the state x_i of each automaton i behaves as a biased random walk, with probability p of moving upwards and $(1-p)$ downwards. The behavior of the automaton i is constrained by the reflecting states 1 and r. For this arbitrary automaton i, we define P_x as the probability of being in state $x \in \{1,2,\ldots,r\}$. If we assume no correlations between automata, we can write the evolution of the probabilities as

$$\begin{cases} P_1(t+1) = (1-p)[P_1(t) + P_2(t)] \\ \vdots \\ P_x(t+1) = (1-p)P_{x-1}(t) + pP_{x+1}(t) \\ \vdots \\ P_r(t+1) = p[P_{r-1}(t) + P_r(t)] \end{cases} \qquad (4)$$

with $x = 2, 3, \ldots, r-1$.

But in RBN's the behavior of the automata in the ordered zone is far away from such a biased random walk. The stationary quenched distribution of the automaton values will not be an exponential like the one described by the previous equation.

Figure 4 shows the stationary automaton-state distribution $\{P_x\}_{x=1,\ldots,r}$ for a quenched RWN in the case $r=6$. It can be seen that at we enter the disordered zone (i.e., big values of the connectivity K) it tends to an exponential distribution, according to Eq. (10). In that zone, each automaton is being perturbed by a nearly pure biased random walk. But in the ordered zone (small values of the connectivity), the distribution tends to be limited basically to the extreme values, 1 or r, the intermediate states having a probability close to 0. One can see how the ordered state has basically a binary outcome. Notice also that as this zone the probability for an automaton to be 1 or r is clearly determined by the bias p, being p and $(1-p)$, respectively.

If we now use the stationary quenched values of the automata distribution in the ordered zone—that is, if we use

$$P_x = \begin{cases} (1-p) & \text{if } x = 1 \\ p & \text{if } x = r \\ 0 & \text{otherwise} \end{cases} \qquad (12)$$

and we apply them to Eq. (7), we obtain that the boundary condition becomes

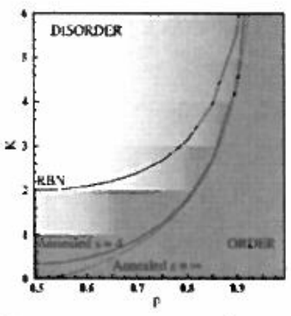

FIG. 5. Gray pixels: stationary overlap a^* between two quenched RWN's as a function of p and K. Gray intensities indicate different values of the stationary overlap. Dark gray corresponds to a perfect overlap—that is, to $a^*=1$ (ordered phase)—and white to uncorrelated a^* (completely disordered phase). For each point we have performed 10 000 simulations with $N=10\,000$ and $r=4$. Superimposed are the order-disorder frontiers for RBN's (upper solid line) and for the annealed model of RWN's (lower solid line) in the case $r=4$. We can see how the transition from order to disorder in the quenched RWN's happens at the zone between both curves. The dashed line corresponds to the critical K-p curve from Eq. (12) in the annealed case when $r \to \infty$.

that is again the boundary condition for RBN's.

Therefore, RBN's and the annealed model of RWN's are the limiting cases for quenched RWN's (corresponding only in the case $r=2$), and the critical transition order-disorder curve for quenched systems lies between both transition frontier curves, as can be seen in Fig. 5.

As Fig. 5 implies, when passing from these discrete networks to the continuous case—that is, when r tends to infinity—the transition from order to disorder is still well defined. It is possible to calculate the limit of Eq. (7) for annealed RWN's when $r \to \infty$. In the continuous case, the critical curve becomes

$$K = \frac{2[p-(1-p)]^2}{p(1-p)[1+(p-(1-p))^2]} \qquad (14)$$

which defines an order-disorder critical curve in the K-p space (Fig. 5, dashed line). Equation (14) can be expressed in a more compact form, but we prefer to write it this way because it explicitly shows its invariance under the exchanges of p and $(1-p)$.

As the annealed model is a lower limit for the K and upper for the p axis of the quenched systems, then for quenched RWN's in the continuous limit ($r \to \infty$) the transition is also well defined and enclosed between the annealed model and the classical transition for RBN's.

VI. CONCLUSIONS

The study of the genome has revealed a complex world of relationships and couplings among genes, which produces what is indeed a genetic network. As a consequence, the study of its behavior by means of classical, linear methods is not possible given that the real behavior is highly nonlinear and shows complex dynamics. Therefore new type of models and methods of analysis are needed to face its study and understanding.

RBN's were one of the first ways proposed to study statistically genome global properties. Unfortunately, this is a model of all-nothing behavior where the state of a given gene is completely determined by the input genes and where smooth variations of state are not allowed, contrary to what happens in the real genomes. On the other hand, differential equation systems, which in principle should give a better understanding of such continuous behavior, are difficult to solve and analytical results are hard to obtain.

This paper deals with random-walk networks, a simple random network model which largely resembles real genetic networks. RWN's are a natural link between discrete all-nothing models (like RBN's) and continuous differential equations systems, as RWN's allow small, continuous-like variations in the behavior of the genome.

RWN's allow for analytical treatment, and in this paper we have deduced the critical frontier for the annealed model. Unfortunately, due to the memory of the system, the annealed solution does not coincide with the quenched critical frontier. Nevertheless, the annealed critical boundary acts as a lower limit for the real case. On the other hand, we have shown how RBN's act as an upper limit for the quenched case and we have delimited an order-disorder transition frontier to be between both transition frontiers. If RWN's pretend to be a bridge model between RBN's and continuous models, we have demonstrated that in the continuous limit (r tending to infinity) RWN's are well-behaved and, as RBN's, have a well-defined order-disorder transition, usually so difficult to prove for continuous systems.

As we have seen, RWN's can be considered a natural generalization of RBN's. In fact, RBN's are a subcase of our model which trivially reduce to them when the number of allowed states r equals 2. RBN's have been studied extensively over the past three decades [13] and are still used as a model to study competitive genes [14], synchronization [15,16], scale free connectivity [17,18], self-organized criticality [19], or time-reversible models [20,21]. RWN's now offer a more general and richer frame to study all these phenomena.

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