

**Networks**

**1. Percolation on the Cayley tree:** In simple models of percolation, elements of a lattice (sites or bonds) are independently occupied with a probability  $p$ . A cluster is defined as a connected (by neighboring bonds) set of these occupied elements. At small  $p$ , only small clusters exist, and the probability that two sites, separated by a distance  $r$ , are connected to each other decays as  $\exp(-r/\xi)$ . The correlation length  $\xi(p)$  grows with increasing  $p$ , diverging at the *percolation threshold*  $p_c$  as  $\xi(p) \sim |p_c - p|^{-\nu}$ . A so-called *infinite cluster*, spanning the entire system first appears at the percolation threshold  $p_c$ , covering more and more sites for  $p > p_c$ . We can define a probability  $P(p)$  that a site belongs to this infinite cluster which, on approaching  $p_c$  from above, vanishes as  $P(p) \sim |p_c - p|^\beta$ .

(a) The *Cayley tree* is a hierarchical lattice in which each site at one level is connected to  $z$  sites at the level below. Thus the  $n$ -th level of the tree has  $z^n$  sites. For  $z = 2$ , obtain a recursion relation for the probability  $P_n(p)$  that the top site of a tree of  $n$  levels is connected to some site at the bottom level.

(b) Find the limiting behavior of  $P_\infty \equiv P(p)$  for infinitely many levels. Give the exponent  $\beta$  characterizing the vanishing of  $P(p)$  at  $p_c$ .

(c) Show that for starting values close to  $P(p)$ , the recursion relations admit solutions of the form  $P_n = P_\infty e^{-n/\xi}$ . Find expressions for  $\xi$  for both  $p < p_c$  and  $p > p_c$ , and hence obtain the exponent  $\nu$  for the divergence of  $\xi$  at the percolation threshold (for  $z = 2$ ).

(d) Find the value of  $p_c$  for any branching number  $z$ . Do the exponents  $\beta$  and  $\nu$  depend on  $z$ ?

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**2. Preferential network growth with node removal:** Consider the following extension of network growth by preferential attachment, as explored in *C. Moore, G. Ghoshal, and M.E.J. Newman, Phys. Rev. E 74, 036121 (2006)*: At each time step a new node is created, its  $m$  links attached preferentially proportional to the number of links already present for a pre-existing node. However, before the next node is added, a randomly selected node is removed with probability  $r$ .

(a) Show that after many steps  $t$ , the average number of nodes and links grow as  $N(t) = t(1 - r)$  and  $L(t) = tm(1 - r)/(1 + r)$ , respectively.

(b) Write down the recursion relation governing the probability  $p(k, t)$  of nodes with  $k$  links at time  $t$ .

(c) Show that in steady state  $p^*(k) \propto k^{-\gamma}$ , and find the exponent  $\gamma$ .

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**3. 'Feed-down' network:** Consider a set of non-negative variables  $\{x_n(t)\}$  (e.g. chemical concentrations), evolving in time according to first order differential equations

$$\frac{dx_n}{dt} = f_n(x_{n+1}, x_{n+2}, x_{n+3}, \dots) - g_n(x_n).$$

While the equations are quite general, we make the following assumptions:

(i) Each component decays at a rate  $g_n \geq 0$  which only depends on its value  $x_n$ ;  $g_n(x_n)$  is a monotonically increasing function of  $x_n$ , with  $g_n(0) = 0$ .

(ii) Each component is generated at a rate  $0 \leq f_n \leq \max(g_n)$ , which can depend only on variables numbered higher than  $n$ ; i.e.  $f_n$  does not depend on  $x_1, x_2, \dots, x_n$ .

(a) By considering eigenvalues of the stability matrix show that these equations admit a *stable* fixed point.

(b) If the variables  $\{x_n(t)\}$  are made space dependent and allowed to diffuse, such that a term  $D_n \nabla^2 x_n$  is added to  $\partial x_n / \partial t$ , can these equations admit Turing patterns?

(c) If all  $f_n$  are monotonically increasing functions of their arguments, show that starting from  $\{x_n(t=0) = 0\}$ , the variables proceed monotonically to the fixed point values.

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**4. Hopfield network with correlated states:** In a recent work (arXiv:1211.3133) a type of Hopfield Lyapunov function is used to characterize the epigenetic landscape of cells. The expression profiles of transcription factors (simplified to a binary code of off or on for roughly hundred TFs) are specific to each cell type (e.g. liver, skin, heart,  $\dots$ ), and are modeled as ‘associative memories’ in the parlance of neural networks. An important subtlety is that unlike typical ‘memories’ stored in a neural net, the expression profiles are highly correlated. A corresponding variant of the Hopfield model is examined in this problem.

The desired states are characterized by set of binary vectors  $\{\xi^\mu\}$  for  $\mu = 1, 2, \dots, M$ ; each vector has components  $\xi_i^\mu = \pm 1$  with  $i = 1, 2, \dots, N$ . We would like to encode these states into the couplings  $\{J_{ij}\}$  of a Hopfield network, composed of variables  $\{-1 \leq x_i \leq +1\}$ , evolving as

$$\frac{dx_i}{dt} = -\frac{x_i}{\tau} + \tanh \left( h_i + \sum_j J_{ij} x_j \right).$$

(a) Compute a Lyapunov function that is minimized by the above dynamics.

(b) For one state vector  $\vec{\xi}$ , show that the couplings  $J_{ij} = \xi_i \xi_j / N$  (with  $h_i = 0$ ) enable recovery of the pattern, provided  $\tau > \tau_c$ .

(c) Consider a set of  $M$  uncorrelated states, corresponding to orthogonal binary vectors such that  $\sum_i \xi_i^\mu \xi_i^\nu = N \delta_{\mu\nu}$ . Show that multiple states can be encoded via  $J_{ij} = \sum_\mu \xi_i^\mu \xi_j^\mu / N$  (again with  $h_i = 0$ ).

(d) We now relax the condition of orthogonal memories. Show that in this case states can be encoded through the couplings  $J_{ij} = \sum_{\mu\nu} [\xi_i^\mu (C^{-1})_{\mu\nu} \xi_j^\nu] / N$ , where  $C^{-1}$  is the inverse of the correlation matrix, whose elements are  $C_{\mu\nu} = \sum_i \xi_i^\mu \xi_i^\nu / N$ .

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