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COMPLEXITY AND ULTRADIFFUSION*

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ABSTRACT

We present the exact solution to the problem of diffusion in an arbitrary hierarchical space. We derive rigorous upper and lower bounds for the dynamic exponent describing the decay of the autocorrelation function. We show that the upper bound is saturated by both uniformly and randomly multifurcating hierarchical trees, and identify a class of highly unbalanced trees that saturate the lower bound. We conclude that the speed of relaxation is a measure of the complexity, or lack of self-similarity of the underlyng tree. We point out that complexity may be revealed by the temperature dependence of the dynamic exponent, and in particular by the nature of the transition from exponential to power-lay decay.

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1. INTRODUCTION

A large variety of natural and artificial systems have an exact or approximate hierarchial structure [Simon (1962), Rammal et al. (1986)]. Examples range from the reporting schemes in social organizations, to the way macromolecules are built out of atomic constituents or organisms out of cells, to the way individual spins can be collected into larger blocks at the critical point of ferromagnets. More recently it has been realized that a hierarchical organization of states appears spontaneously in the low-temperature phase of the mean-field theory spin-glass [Sherrington and Kirkpatrick (1975), Mézard et al. (1984)], and it has been conjectured that the same holds true for glasses, hard combinatorial optimization problems [Kirkpatrick and Toulouse (1985), Bachas (1985), Bouchaud and Le Doussal (1986), Sorkin et al. (1986), Fu and Anderson (1986)], the conformational substates of proteins [Ansari et al. (1985), Stein (1985)], and other complex frustrated systems.

A common feature of all these systems is that because of the existence of many different time scales, they appear to relax slower than exponentially when perturbed [Kohlrausch (1847), Williams and Watts (1970), Palmer et al. (1984)]. To model this behavior several authors have considered diffusive processes on hierarchical structures. The earliest variant proposed by Huberman and Kerszberg (1985) and further analyzed by [Teitel and Domany (1985), and Maritan and Stella (1986)], consisted of a particle diffusing over a hierarchical array of energy barriers in one dimension. Allowing for long-rang hoppings leads to the problem of diffusion in a truly ultrametric space, which has been analyzed by a number of authors [Schreckenberg (1985), Ogielski and Stein (1985), Paladin et al. (1985), Qiang (1986)]. Finally, a third related process is the random walk on the backbone of a tree, which has been used to model the observed stickiness in the chaotic transport of particles [Meiss and Ott (1985), Grossman et al. (1985)].

A major limitation of all these treatments is that they only apply to the simple case of uniform hierarchical structures, described by trees whose branches at any given hierarchy-level are totally indistinguishable. The intrinsic self-similarity of such trees allows for the application of renormalization group techniques, so that ultradiffusion is in this case only a variant of the

extensively studied diffusion on fractals [deGennes (1976), Alexander and Orbach (1982), Rammal and Toulouse (1983)]. Hierarchical structures need not, however, be self-similar. For instance, it is hard to imagine how the metastable states of a spin-glass could be represented by the indistinguishable leaves of a uniform tree, when different free energy valleys are known to carry different weights [Mézard et al. (1985)]. And in a more general context, it is precisely the lack of self-similarity, or the appearance of different interactions at every new level of the hierarchy, that accounts for the complexity of hierarchical systems such as biological organisms and social organizations. It is therefore interesting to determine how hierarchical dynamics may depend on the underlying tree structure. This is the subject of this paper, a summary of which has already been published elsewhere [Bachas and Huberman (1986)].

We will restrict ourselves here to the problem of diffusion in a truly ultrametric space. In section 2 we will solve this problem exactly, without making any assumptions concerning the structure of the underlying tree. We will obtain, in particular, a closed expression for the average autocorrelation function, whose asymptotic decay describes the rate of relaxation of the system.

A central thesis of this paper, is that the dynamic exponent v that characterizes this asymptotic decay has the qualitative features of a measure of physical complexity introduced by Huberman and Hogg (1986): namely it is sensitive to the absence of self-similarity, rather than the randomness, or detailed information content of the underlying tree. To be precise, we derive a rigorous upper bound for v, and show in sections 3 and 4, that it is saturated by both uniformly and randomly multifurcating trees. Such trees are therefore optimal in that they lead to fastest relaxation. In section 5 we also derive a lower bound for v, and identify a class of non-self-similar unbalanced trees that saturate it. All these results have recently been shown to hold also for the critical percolation threshold by [Bachas and Wolff (1987)], which can be related to the complexity of games.

A corollary of our results is that in thermally activated processes the temperature dependence of the dynamic exponent is not universal, but varies with the underlying tree structure: in particular the transition to instability is

continuous for self-similar trees, and discontinuous for unbalanced ones. This is explained in section 6 which also contains some concluding remarks.

2. THE GENERAL SOLUTION

Ultradiffusion is described by the dynamical equation

$$\frac{dP_i}{dt} = \sum_{j=1}^{N} \varepsilon_{ij} P_j \tag{2.1}$$

where $i = 1, \ldots, N$ labels the states of the system, $P_i(t)$ is the probability of finding the system at state i at time t, and the symmetric transition matrix ε satisfies the ultrametric property

$$\varepsilon_{ij} \geq min(\varepsilon_{ik}, \varepsilon_{jk}) \tag{2.2}$$

for any three distinct states i, j and k. If ε represents hopping rates between sites i and j, Eq. (2.2) implies that the two smallest hopping rates out of a triplet are equal. The diagonal transition elements are fixed by the requirement that probability be conserved, i.e.;

$$\varepsilon_{ii} = -\sum_{j \neq i} \varepsilon_{ij} \tag{2.3}$$

The ultrametric property (2.2) is equivalent to saying that the states of the system can be represented as the leaves of a generic tree, where the hopping rate between any two of them, say i and j, is only a function of the nearest common ancestor A of i and j on the tree

$$\varepsilon_{ij} = \varepsilon_{ji} = \varepsilon_{A(i,j)}$$

with ε_A decreasing monotonically as one climbs along any path towards the root. By appropriately stretching the tree, we may always assume without loss of generality that $\varepsilon_A = \exp[-h_A]$, where h_A is the height of the branching point A from the bottom of the tree, as shown in Figure 1. We shall refer to such a tree

as a "metric tree", to stress the fact that both its topology and the heights of its branches matter. There is one hierarchical transition matrix and one ultradiffusion problem for every metric tree.

An important remark is in order here: although the assumption of symmetric transition probabilities may seem overly restrictive this is not the case, since we can effectively increase the weight of any state by letting it multifurcate appropriately at low altitude as shown in figure 1.

Before proceeding to an exact solution of equation (2.1), let us first introduce some useful notation and terminology: we shall denote by B_n the unique n^{th} ancestor of any branch-point or tree-leaf B ($B_0 = B$ by convention, B_1 is the father, B_2 the grandfather, and so on, up the the patriarch or root). N_B will stand for the total number of final descendants or tree-leaves generated by B ($N_B = 1$ if B is itself a leaf), and S_B for the number of sons, or immediate offsprings. We also introduce the characteristic function

$$X_i(B) = \begin{cases} 1 & \text{if } i \text{ is a descendant of } B \\ 0 & \text{otherwise} \end{cases}$$

where $i = 1, \ldots, N$ runs over the leaves of the tree. For convenience we will assume that branchings may only occur at integral multiples of some minimum adjustable height interval Δh, and will occasionally refer to all branches at height $h = m \cdot \Delta h$ as the m^{th} generation. If n(h) is their total number, we define the silhouette slopes, which measure the rate of population growth at height h by:

$$s(h) = -\frac{\Delta \log n(h)}{\Delta h} = \frac{1}{\Delta h} \log\left[\frac{n(h)}{n(h+\Delta h)}\right] \qquad (2.4a)$$

We shall refer to its average asymptotic value

$$s \equiv \lim_{h' \gg h \to \infty} \frac{\int_h^{h'} S}{(h'-h)} \tag{2.4b}$$

as simply the tree's silhouette. Large and small values of silhouettes correspond to asymptotically fat and thin trees, respectively.

We are now ready to obtain the complete set of eigenvectors and eigenvalues of any hierarchical transition matrix ε. To this end consider first the action of ε on the characteristic function of some branch-point or tree-leaf B:

$$\sum_{j=1}^{N} \varepsilon_{ij} X_j(B) = -\sum_{j=1}^{N} \varepsilon_{ij} \left[1 - X_j(B)\right] =$$

$$= \begin{cases} N_B \cdot e^{-h_{(A(i,B)}} & \text{if } X_i(B)=0 \\ -\sum_{n=1}^{root} \left(N_{B_n} - N_{B_{n-1}}\right) \cdot e^{-h_{B_n}} & \text{if } X_i(B)=1 \end{cases} \tag{2.5}$$

where A(i,B) is the nearest common ancestor of i and B, and by slight abuse of notation

$\sum_{n=1}^{root}$ stands for a summation over all of B's ancestors, up to and including the root.

We next define the vector

$$V_i(B,\tilde{B}) = \frac{1}{N_B} X_i(B) - \frac{1}{N_{\tilde{B}}} X_i(\tilde{B}) \tag{2.6}$$

for any two brothers B and $\tilde{B}$. Since $B_n = \tilde{B}_n$ for all $n > 0$, and $A(i,B) = A(i,\tilde{B})$ for any i that is neither a descendant of B nor of $\tilde{B}$, we easily deduce from Eq. (2.5)

that V(B,$\tilde{B}$) is an eigenvector of ε, with eigenvalue λ that only depends on the common father of B and $\tilde{B}$, i.e.:

$$\lambda(B_1) \equiv -\frac{1}{\tau_{B_1}} = -N_{B_1} e^{-h_{B_1}} - \sum_{n=2}^{root} \left(N_{B_n} - N_{B_{n-1}} \right) e^{-h_{B_n}} \tag{2.7}$$

Consequently, there are $\frac{1}{2}S_{B_1}(S_{B_1}-1)$ degenerate eigenvectors of type (2.6), corresponding to all pairs of sons of B_1. A convenient basis for the subspace they span consists of the following vectors, one for each son of B_1:

$$V_i(B) \equiv \sum_{brothers\ \tilde{B}\ of\ B} \frac{N_B}{N_{B_1}} V_i(B,\tilde{B}) = \frac{1}{N_B} X_i(B) - \frac{1}{N_{B_1}} X_i(B_1) \tag{2.8}$$

These satisfy the linear relationship

$$\sum_{brothers\ B} N_B V(B) = 0$$

so that only $(S_{B_1}-1)$ of them are linearly independent. Since

$$\sum_{branch\ points\ B} (S_B - 1) = N - 1$$

there is a single missing eigenvector of the NxN transition matrix ε. This corresponds to the steady-state of equal probability for all sites, which we denote by

$$V_i(root) = \frac{1}{N}; \qquad \sum_{j=1}^{N} \varepsilon_{ij} V_j(root) = 0 \tag{2.9}$$

Going back to equation (2.1), consider a particle that starts out at time zero at a given tree leaf L. Writing the initial condition as

$$P_i(t=0)=\delta_{L,i}=\sum_{n=0}^{root} V_i(L_n)$$

we immediately deduce that at later times

$$P_i(t)=\sum_{n=1}^{root} V_i(L_{n-1})\ e^{-t/\tau_{L_n}}+\frac{1}{N} \tag{2.10}$$

From this we can exactly calculate any quantity of interest. We will concentrate on the autocorrelation function, i.e., the probability that the particle returns to its point of departure; this reads

$$P_L(t)=\frac{1}{N}+\sum_{n=1}^{root}\left(\frac{1}{N_{L_{n-1}}}-\frac{1}{N_{L_n}}\right)e^{-t/\tau_{L_n}} \tag{2.11}$$

We will be mainly interested in this quantity averaged over all initial conditions L, which can be written:

$$\mathrm{P}(t)=\frac{1}{N}+\sum_{branch\ points\ B}\frac{1}{N}\left(S_B-1\right)e^{\frac{-t}{\tau_B}} \tag{2.12}$$

where, for later ease of reference, we recall that

$$\frac{1}{\tau_B}=N_B\ e^{-h_B}+\sum_{n=1}^{root}\left(N_{B_n}-N_{B_{n-1}}\right)e^{-h_{B_n}} \tag{2.13}$$

From Eqs. (2.12) and (2.13) it easily follows that for finite trees the decay of the autocorrelation function to its equilibrium value is always exponential, and

dominated by the largest characteristic time,

$$\tau_{root} = \frac{1}{N} \cdot e^{+h_{root}}$$

For infinite trees, on the other hand, either one or both of the following scenarios may take place: a) Some characteristic times may vanish, indicating that relaxation is unstable in part or all of the tree, which can thus be collapsed to a single state, and b) some characteristic times may accumulate to infinity, leading to slower than exponential relaxation at long times. The leading asymptotic behavior of the autocorrelation function is in this case determined by the asymptotic behavior of the spectral density

$$\rho(t) = \sum_{branch\ points\ B} \frac{S_B - 1}{N} \delta(\tau - \tau_B) \tag{2.14}$$

as $\tau \to \infty$. In the following sections we will analyze this behavior for trees on which relaxation is everywhere stable.

3. UNIFORM TREES

We begin with the simplest example of an infinite, regular, uniformly multifurcating tree, for which each member of every generation produces b offsprings. This is shown in Figure 2. Some of the results of this section have already been derived in [Schreckenberg (1985), Ogielski and Stein (1985), Paladin et al. (1985), Qiang (1986)]. If Δh is the height interval between successive generations, the silhouette, (eqs. (2.4 a,b)) is given by

$$s = \frac{1}{\Delta h} \log b \tag{3.1}$$

Using the fact that $N_{B_n} = b^n \cdot N_B$, we can easily calculate from Eq. (2.13) the inverse characteristic time corresponding to any branch point B of the mth generation, with the result

$$\tau_B^{-1} = \left(b e^{-\Delta h} \right)^m \cdot \left[\frac{e^{\Delta h} - 1}{e^{\Delta h} - b} \right]$$

provided $e^{\Delta h} > b$, that is $s < 1$. For $s \geq 1$ all characteristic times vanish and relaxation is unstable. Assuming $s < 1$, we finally obtain the autocorrelation function, Eq. (2.12), in the form

$$\bar{P}(t) = \sum_{m=1}^{\infty} \left(b - 1 \right) b^{-m} \exp\left[-t \left(b e^{-\Delta h} \right)^m \frac{e^{\Delta h} - 1}{e^{\Delta h} - b} \right] \simeq D \; t^{-\nu_{uniform}} \tag{3.2a}$$

where

$$\nu_{uniform} = \frac{s}{1 - s} \tag{3.2b}$$

and

$$D = \Gamma\left(\frac{s}{1-s}\right)\left(\frac{e^{\Delta h}-1}{e^{\Delta h}-b}\right)^{-\frac{s}{1-s}} \frac{b-1}{\log b} \cdot \frac{s}{1-s} \qquad (3.2c)$$

with the corrections to the asymptotic behavior (3.2a) falling off exponentially at large t [Erdélyi (1956)].

Note that, in contrast to the prefactor D, the dynamical critical exponent $\nu_{uniform}$ is only a function of the silhouette and is therefore invariant under $b \to b^{\alpha}$, $\Delta h \to \alpha \cdot \Delta h$. For instance, a tree that tetrafurcates at every unit height interval has the same power law decay as one that bifurcates every half unit interval (see Figure 2). One may also relax the condition that the branching ratio and height intervals be generation-independent (but still insist that all members of a given generation be indistinguishable). By appropriately bounding $\tilde{P}(t)$ from above and below, it is straightforward to show that if the silhouettes can be defined and lies between 0 and 1, the dynamic exponent is still given by expression (3.2b). The prefactor D however, can in this case acquire oscillatory and/or logarithmic time-dependence.

By allowing non-constant height intervals among successive generations, one can also study the limiting cases of vanishing or unit silhouette. Indeed: (a) if the height h_m of the mth generation grows faster than linearly with m (so that $s=0$) the autocorrelation function decays slower than any power of time, implying a 1/f-frequency spectrum (up to logarithmic corrections). We shall refer to such trees with vanishing silhouette as "brooms"; we will later show that ultradiffusion may lead to a 1/f-like spectrum only when the underlying tree is a broom. (b) At the other extreme, the slowest rate of growth of h_m leading to finite characteristic times is given by

$$h_m = m \log b + \alpha \log m, \text{ with } \alpha > 1$$

It is clear that in this case $s=1$, and the autocorrelation function reads:

$$\bar{P}(t)=\left(b-1\right)\sum_{m=1}^{\infty} b^{-m}\, exp\left[-t\left(m^{-a}+\left(1-\frac{1}{b}\right)\zeta\left(a, m+1\right)\right)\right]\simeq D(t)\; e^{-c\cdot t^{\frac{1}{a}}} \qquad (3.3)$$

where $\zeta(a, m+1)$ is the Riemann zeta function, c is a non-universal constant and D(t) decays slower than the leading stretched exponential. The asymptotic behavior (3.3) is the well known Kohlrausch law.

As opposed to the power-law decay, both the Kohlrausch and the logarithmic relaxation processes seem less generic since they occur at special values of the tree's silhouette.

The expression (3.2b) for the dynamic critical exponent shows that fatter trees relax faster. In order to study the effect of the tree's structure on dynamics, it is therefore reasonable to only compare trees with a fixed silhouette (thus avoiding a heavyweight-featherweight bout). We will in fact, restrict ourselves to trees with a fixed silhouette slope $0<s(h)=s<1$. The following result then shows that stable relaxation is fastest on uniform trees:

Theorem 1 (Optimality of infinite uniform trees) - The dynamic critical exponent of any tree with fixed silhouette slope: $0<s(h)=s<1$ is bounded from above by $\nu_{uniform}=s/1\text{-}s$, provided there exist some $x<1$, such that no branch point B has descendants growing faster than $e^{x(h_B-h)}$ with height.

Remark: This assumption ensures stable relaxation everywhere on the tree. Indeed, if some branch-point B has descendants growing like $e^{(h_B-h)}$ or faster, then relaxation among these descendants is unstable. The associated diffusion problem should therefore be reformulated on a new tree, obtained by collapsing the subtree generated by B to a single state.

Proof of Theorem 1: We first break the expression (2.12) into a sum over generations

$$\bar{P}(t)=\sum_{m=1}^{\infty}\ \sum_{B:\,h_B=m\cdot\Delta h}\frac{1}{N}\left(S_B-1\right)e^{\frac{-1}{\tau_B}}$$

We then use the fact that the average of exponentials is larger than the exponential of the average to obtain

$$\bar{P}(t)\geq\sum_{m=1}^{\infty}\frac{1}{N}\cdot A_m\cdot e^{\frac{-t}{\tau_m}} \tag{3.4a}$$

where A_m is the net population increase at the mth generation:

$$A_m=\sum_{B:\,h_B=m\,\Delta h}\left(S_B-1\right)=N\,e^{-s\,m\,\Delta h}\left(e^{s\,\Delta h}-1\right) \tag{3.4b}$$

while τ_m^{-1} is the average inverse characteristic time of the mth generation:

$$\tau_m^{-1}=\frac{1}{A_m}\sum_{B:h_B=m\cdot\ \Delta h}\left(S_B-1\right)\cdot\ \tau_B^{-1} \tag{3.4c}$$

Now, for any B belonging to a generation older than m, let $d_m(B)$ stand for the number of descendants of B at the mth generation. The assumption of stable relaxation ensures that $d_m(B)\leq e^{x(h_B-m\cdot\Delta h)}$. Using this, and Eq. (2.13) in (3.4c) one can obtain an upper bound for τ_m^{-1} as follows:

$$\sum_{B:h_B=m\ \Delta h}\left(S_B-1\right)\tau_B^{-1}=\sum_{B\ h_B\geq m\ \Delta h}N_B\ e^{-h_B}\left(1-e^{-\Delta h}\right)\left(d_{m-1}(B)-d_m(B)\right)$$

$$\leq N\left(1-e^{\Delta h}\right)\sum_{n=0}^{\infty}e^{-(m+n)\,\Delta h}\ e^{x(n+1)\Delta h}$$

$$\rightarrow \qquad \tau_m^{-1} \leq c\ e^{m(s-1)\Delta h} \tag{3.5}$$

with

$$c = \frac{\left(1-e^{-\Delta h}\right) e^{x\,\Delta h}}{\left(e^{s\,\Delta h}-1\right)\left(1-e^{(x-1)\Delta h}\right)} < \infty$$

Using inequality (3.5) back into (3.4a) we finally obtain

$$\bar{P}(t) \geq \left(e^{s\,\Delta h}-1\right) \sum_{m=1}^{\infty} e^{-s\,m\,\Delta h}\ exp\left[-t\cdot\ c\cdot\ e^{m(s-1)\Delta h}\right] = \breve{D}\ t^{-\frac{s}{1-s}}$$

With $\breve{D}$ a constant, which completes the proof of our theorem Q.E.D.

A possible application of this result is in hierarchical organizations, or computer networks, in which information signals are transmitted through diffusion. What we have shown is that uniform structures are in this case optimal. Note however that our result concerns only the asymptotic behavior of the average autocorrelation function, and hence does not in general apply if one is interested, in either a particular initial condition or in small finite trees. For the latter we can, nevertheless, prove a similar but weaker optimality result, as follows:

Let T(M,B) be the class of all finite trees with M generations, and an average overall branching ratio b per generation. For a given tree $T \in T$(M,b) order its characteristic times τ_B in decending order. We say that T_1 relaxes faster than T_2 if for their first non-matching characteristic times $\tau_B^{(1)} < \tau_B^{(2)}$. Then

Lemma 1 (Optimality of finite uniform trees). Among all trees in T(M,b) for which each member of every generation has at least two sons, the uniform tree relaxes fastest.

Proof The smallest inverse characteristic time $\tau^{-1}_{root} = b^M e^{-M\cdot\Delta h}$ is the same for all trees in $T(M,b)$. Consider next the inverse characteristic times corresponding to the b members $B^{(1)}, \ldots B^{(b)}$ of the (M-1)th generation:

$$\tau^{-1}_{B^{(i)}} = N_{B^{(i)}}\, e^{-(M-1)\Delta h} + \left(b^M - N_{B^{(i)}}\right) e^{-M\,\Delta h}$$

These have in general different but non-vanishing multiplicities, since by assumption $S_{B^{(i)}} > 1$. Their sum

$$\sum_{i=1}^{b} \tau^{-1}_{B^{(i)}} = b^M\, e^{-(M-1)\Delta h} + b^M (b-1)\, e^{-M\,\Delta h}$$

is a constant in $T(M,b)$. Hence, to maximize their minimum, they must all be equal, i.e., $N_{B(1)} = \ldots = N_{B(b)} = b^{M-1}$; the proof of the optimality of uniform trees can now be easily completed by induction.

4. STRUCTURAL NOISE

We now turn our attention to uniformly random trees, constructed by allowing the multifurcation number of every branch at every generation to be an independent random variable with probability distribution P(X). These can be considered as uniform trees, with branching ratio

$$<X> = \sum_{x=1}^{\infty} p(X)X$$

per generation* and with some structural noise. Our main result is that such noise is irrelevant in that it leads to at most logarithmic modifications of the autocorrelation decay, and thus leaves the dynamic exponent unchanged, i.e.,

$$v_{random} = \frac{s}{1-s} \; ; \; s = \frac{1}{\Delta h} log <X> <1 \qquad (4.1)$$

The reader not interested in the technical details of the demonstration can skip the remainder of this section.

* If <x> is not an integer, it can be made into one by raising it to a power and appropriately rescaling the inter-generation gap, as discussed in the previous section.

To start with, we briefly review some basic facts from the theory of branching processes [Harris (1963)]. Let X_n be the number of descendants of a given node after n generations, and let $P_n(x)$ be its probability distribution. This clearly satisfies the iteration equation

$$P_n(X) = \sum_{k=1}^{\infty} P(k) \cdot \left(\sum_{X_1, \ldots X_k = 1}^{\infty} P_{n-1}(X_1) \ldots P_{n-1}(X_k) \cdot \delta_{X, X_1 + \ldots + X_k} \right) \tag{4.2}$$

In terms of the generating functionals

$$G_n(s) = \sum_{X=1}^{\infty} P_n(X)\, s^X$$

and since convolution amounts to multiplication, eq. (4.2) becomes

$$G_n(s) = g\Big(G_{n-1}(s) \Big) = g^{(n)}(s) \tag{4.3}$$

where $g^{(n)}$ is the nth iterate of the generating functional g(s) of p(X).

Since $g(1) = 1$ for normalization, we easily find that the average value of X_n is given by

$$< X_n > = \frac{dG_n}{ds}(1) = \left[\frac{dg}{ds}(1) \right]^n = < X >^n$$

Define the random variable $W_n = X_n / < X >^n$. The basic result we will need is that, provided the second moment of P(X) exists, W_n converges as $n \to \infty$ with probability one and in mean square to a random variable W with finite variance, and with an absolutely continuous distribution ρ which satisfies the stationarity condition that follows from eq. (4.2).

$$\rho(W)=<X>\sum_{k-1}^{\infty}P(k)\,..\int_0^{\infty}\cdots\int_0^{\infty}dz_1,\ldots dz_{k-1}\;\rho\left(z_1\right)\ldots\rho\left(z_{k-1}\right) \tag{4.4}$$

$$\cdot\;\rho\left(W<X>-z_1\ldots-z_{k-1}\right)$$

In words, this means that in a random branching process, the population has the expected exponential growth up to a random prefactor.

To illustrate these facts, consider the simple example of an exponentially decaying distribution given by

$$P(X)=\left(1-\frac{1}{c}\right)c^X \quad for\ X\varepsilon Z^+$$

where c<1 and <X> = 1/1-c. Its generating functional

$$g(s)=\frac{(1-c)s}{1-cs}=\frac{s}{<X>-s(<X>-1)}$$

belongs to the class of fractional linear generating functionals, which are closed under iteration. One therefore finds

$$G_n(s)=\frac{s}{<X>^n-s(<X>^n-1)}\;\rightarrow P_n(Y)=\frac{(1-<X>^{-n})^Y}{<X>^n-1} \tag{4.5}$$

from which we deduce that W_n converges exponentially fast in n to a random variable with distribution $\rho(W)=e^{-w}$.

Going back to the problem of diffusion, we would like to average the autocorrelation function over all trees with the appropriate probability distribution. Since averaging over all trees automatically takes care of

averaging over initial conditions, it will suffice to consider expression (2.11) for the autocorrelation function, which we rewrite for convenience as:

$$P_L(t) \equiv \sum_{n=1}^{\infty} S_n = \sum_{n=1}^{\infty} \left(N_{L_{n-1}}^{-1} - N_{L_n}^{-1} \right) exp\left\{ -t\left[N_{L_n} \cdot e^{-h_{L_n}} \right. \right. \tag{4.6}$$

$$\left. \left. + \sum_{m>n} \left(N_{L_m} - N_{L_{m-1}} \right) e^{-h_{L_m}} \right] \right\}$$

According to our previous conventions, the above summation runs over all branch-point ancestors of the initial leaf L. We may however, also take the summation to run over all generations, in which case L_n denotes the member of the nth generation on the unique path from L to the root, and $h_{L_n} = n \cdot \Delta h$. If L_n is not a branch point (i.e., if it has a unique son) then

$$\Delta N_{L_n} \equiv N_{L_n} - N_{L_{n-1}} = 0$$

and L_n makes a vanishing contribution to the autocorrelation function, as it should.

The asymptotic behavior of the average autocorrelation function $\bar{P}(t)$ is determined by the large n behavior of the average summand $\bar{S}_n$; in order to perform this average, the trick is to note that S_n only depends on the independent random variables:

$$W_n \equiv \frac{N_{L_n}}{<X>^n}$$

and on all

$$\tilde{W}_m \equiv \frac{\Delta N_{L_{m+1}}}{<X>^m} \qquad for\ m \geq n$$

whose probability distributions converge at large n to $\rho(w)$ and $P(1)\cdot\delta(\tilde{w}) + \tilde{\rho}(\tilde{w})$ respectively, where

$$\tilde{\rho}(\tilde{w}) = P(2)\,\rho(\tilde{w}) + P(3)\,\rho^{*}\rho(\tilde{w}) + \ldots\ldots$$

with * denoting convolution of probabilities. This latter distribution follows from the fact that with probability P(1) no new line of descendants other than the one leading to L emanates from L_n, in which case $\tilde{W}_n = 0$, while with probability P(k+1), k new lines do emanate and subsequently grow as (practically infinite) independent random trees. We can thus write for large n:

$$\overline{S_n} \sim <X>^{-n+1} \int_{<X>^{-n+1}}^{\infty} \frac{dw}{w}\,\rho(w) e^{-t\,w<X>^{n-1}\cdot}\, e^{-n\cdot\,\Delta h}$$

$$\prod_{m \geq n-1} \left\{ P(1) + \int_0^{\infty} d\tilde{w}\,\tilde{\rho}(\tilde{w}) e^{-t\,\tilde{w}<X>^m}\, e^{-(m+1)\Delta h} \right\}$$

$$- <X>^{-n} \int_{<X>^{-n}}^{\infty} \frac{dw}{w}\,\rho(w) e^{-tw<X>^n}\, e^{-n\,\Delta h}$$

$$\prod_{m \geq n} \left\{ P(1) + \int_o^{\infty} d\tilde{\omega}\,\tilde{\rho}(\tilde{\omega}) e^{-t\tilde{W}<X>^m\cdot}\, e^{-(m+1)\Delta h} \right\} \qquad (4.7)$$

In the above expression, we kept the vanishingly small cutoff of the ω-integrations that comes from the requirement that $N_{L_n} = \omega_n / <X>^n \geq 1$; this is not necessary for the $\tilde{\omega}$-integrations which, as will become clear in a moment, are convergent as $\tilde{\omega} \to 0$. If this were also true for the ω-integrations, the summand would obey the homogeneity relation

$$\overline{S_{n+1}}(t) = \langle X \rangle^{-1} \overline{S_n}(t\langle X \rangle e^{-\Delta h})$$

from which we could easily deduce by a change of variables ($z = t \cdot \langle X \rangle^n \cdot e^{-n \cdot \Delta h}$) that

$$\bar{P}(t) = \sum_{n=1}^{\infty} \overline{S_n}(t) \sim t^{-\nu_{random}} \tag{4.8}$$

with

$$\nu_{random} = \frac{log\langle x \rangle}{\Delta h - log\langle x \rangle} = \frac{s}{1-s} = \nu_{uniform}$$

We will now show that a more careful treatment of the ω-integration cutoff, leads to at most logarithmic modifications of the above power-law decay.

To this end we first prove the following lemma:

Lemma 2: ρ(w) is either bounded, or else diverges at most logarithmically, as $w \to 0$.

Proof: Assume $\rho(w) \sim c \cdot w^{-\alpha}$ as $w \to 0$, with $1 > \alpha > 0$ (since ρ must be normalizable). Plugging this into the stationarity condition (4.4) one then obtains

$$C \cdot W^{-\alpha} = \langle X \rangle \cdot P(1) C \left(W \cdot \langle X \rangle \right)^{-\alpha} \left[1 + 0(W^{1-\alpha}) \right]$$

and hence

$$P(1) = \langle X \rangle^{\alpha - 1}$$

but

$$<X> = P(1) + 2P(2) + 3P(3) + \ldots \leq P(1) + 2(1 - P(1))$$

so that $<X> + <X>^{a-1} \leq 2$. This cannot be satisfied by any $<X> > 1$ which in turn implies that we have derived a contradiction. Thus $\rho(w)$ cannot diverse faster than logarithmically as $w \to 0$.

Note that one can likewise show that $\bar{P}(\tilde{w})$ diverges at most logarithmically as $\tilde{w} \to 0$, which justifies our throwing away the $\tilde{w}$-integration cutoffs.

Converting the sum over generations to an integral, and changing variables to $z = t \cdot <X>^{n} \cdot e^{-n \cdot \Delta h}$, we can write the average autocorrelation function at large in the form

$$\bar{P}(t) \sim t^{-\nu_{uniform}} \left[\int_0^{\infty} \frac{dz}{z} z^{\nu_{uniform}} \int_{(\frac{z}{t})^{\nu_{uniform}}}^{\infty} \frac{dw}{w} \rho(w) f(z,w) \right]$$

with $f(z,w)$ a bounded function that decays exponentially at large z. Since $\rho(w)$ is integrable as $w \to \infty$, and has at most a logarithmic singularity as $w \to 0$, we easily conclude that the term in square brackets has at most a logarithmic time-dependence at large t.

This completes our demonstration that uniformly random trees have the same dynamic exponent as completely ordered uniform trees. One could also verify this assertion directly by calculating the exact average autocorrelation function in the special case of the exponential distributions given by (4.5). Similar results have been obtained by Kumar and Shenoy (1986).

5. COMPLEX HIERARCHICAL STRUCTURES

Both the uniform and the totally random trees are self-similar hierarchical systems, whose parts (or subtrees) are at least on the average identical to the whole. Huberman and Hogg (1986) have argued that they are therefore equally simple structures, which should minimize any physically relevant measure of a tree's complexity. Complexity is in this sense tantamount to lack of self-similarity, or to diversity at all levels of the hierarchy. This is to be contrasted to the information theoretic measure given by Shannon's entropy defined by the size of the smallest algorithm describing how to construct an exact replica of a given tree, and hence maximized by random trees.

Our results place the above ideas in a precise physical context. Indeed, we have demonstrated that for a given tree-silhouette, self-similarity leads to a maximum value for the dynamic critical exponent v, and hence guarantees fastest relaxation. In this section we will obtain a saturated lower bound for v, and will in particular show that non-self-similar structures do indeed lead to a slower power-law decay. Thus complexity or structural diversity is reflected in the rate of relaxation, and -v is a physically sensible measure of it. Similar results have also been obtained in the context of percolation by Bachas and Wolff (1987); with the word "complexity" given in that context a precise operational meaning.

Consider a particular unbalanced tree, constructed by allowing the left half members of every generation trifurcate, while the right half members give rise to a single son each, as shown in Fig. 3a. This is clearly a non-self-similar tree and cannot be analyzed by renormalization-group techniques. Since the total population doubles at every step, its silhouette is given by

$$s = \frac{1}{\Delta h} \log 2$$

As we will now show, its dynamic critical exponent is $v = s$, meaning that relaxation is slower than for the corresponding self-similar structure for which we previously found

$$\nu_{uniform} = \frac{s}{1-s}.$$

Intuitively, this is because different parts of an unbalanced tree relax at different rates, and it is the slowest processes that dominate at long times.

To calculate the average autocorrelation function $\bar{P}(t)$ for our tree of Fig. 3a, assume first that the total number of generations is M (M will be taken to ∞ in the end). We will label the jth from the left node of the ith from the bottom generation by the coordinates (x = M-i, y = log j); the tree is then represented by an orthogonal triangle, as shown in Fig. 3b, with a hypotenuse slope equal to the silhouette times the intergeneration height interval: log 2 = s·Δh. Consider now the descendants of a given node (x,y) with $y \neq 0$; these will trifurcate either until they reach the bottom of the tree, or until they enter the right-half of their generation, from which point on they will continue as single dead branches until the end; these two cases correspond to regions 1 and 2 respectively, in Fig. 3b. The number of fertile (i.e., trifurcating) generations following (x,y) is

$$T(x,y) = \begin{cases} M - x \text{ in region 1} \\ \frac{(x-1)\log 2 - y}{\log 3/2} \pm 1 \text{ in region 2} \end{cases} \qquad (5.1)$$

where the ± 1 ambiguity is due to the fact that (at most) one generation of descendants of (x,y) may be partly fertile and partly infertile. We will in the sequel neglect this ambiguity, since it does not affect the result for the dynamic exponent. Clearly, the number of final descendants or tree-leaves generated by node (x,y) is

$$N(x,y) = 3^{T(x,y)} \qquad (5.2a)$$

For y = 0 and in region 2, the number of final descendants is actually modified, but we may still express its rate of change with x as:

$$\frac{\Delta N}{\Delta x}(x,0) = 2 \cdot \quad 3^{T(x,0)} \tag{5.2b}$$

We are finally in a position to calculate the inverse characteristic time corresponding to the node (x,y), as given by eq. (2.13). Converting the sum over ancestors to a line integral, as shown in Fig. 3b, and using eqs. (5.1, 5.2) we find:

$$\tau^{-1}(x,y)=\left(3\,e^{-\Delta h}\right)^{M-x}+\int_{M-M\frac{\log 2}{\log 3}}^{x} dz\left(3e^{-\Delta h}\right)^{M-z}+ \tag{5.3}$$

$$\int_0^{M-M\frac{\log 2}{\log 3}} dz\; e^{-\Delta h(M-z)}\, 2^{3^{\frac{z\log 2}{\log 3/2}}\frac{z\log 2}{\log 3/2}} \qquad \textit{in region 1}$$

and

$$\tau^{-1}(x,y)=3^{\frac{x\log 2-y}{\log 3/2}}\,e^{-\Delta h(M-x)}+\int_{x-\frac{y}{\log 3}}^{x} dz\; e^{-\Delta h(M-z)}\,3^{\left(\frac{z\log 2-y+(x-z)\log 3}{\log 3/2}\right)} \tag{5.4}$$

$$+\int_0^{x-\frac{y}{\log 3}} dz\; e^{-\Delta h(M-z)}\,3^{\frac{z\log 2}{\log 3/2}} \qquad \textit{in region 2}$$

where once again we have dropped various finite multiplicative constants, which cannot modify the leading power-law in the asymptotic behavior of the spectral density, eq. (2.14). Note also that the first term on the left-hand-side of eq. (5.4) should be changed to

$$-2^M\,e^{-\Delta h(M-x)}$$

if y=0.

These expressions simplify considerably if one takes the limit $M \to \infty$, and notes that for almost all nodes (but a set of measure zero) both x and $y >> \perp$. If

$$s < \frac{log\ 2}{log\ 3}$$

one then finds easily that all inverse characteristic times diverge, implying that relaxation is unstable everywhere on the tree. Let us therefore consider

Up to finite multiplicative constants and exponentially suppressed additive terms, we then find:

$$\tau^{-1}(x,y) = \begin{cases} 3e^{-\Delta h} M - x & \text{in region 1} \\ 3^{\frac{x log\ 2 - y}{log\ 3/2}} \cdot e^{-\Delta h (M-x)} & \text{in region 2} \end{cases}$$

It is not straightforward to analyze the asymptotic behaviour of the average autocorrelation function, eq. (2.12), which can be written as:

$$P(t) \simeq \int\int_{Regions\ 1\ and\ 2} dx\ dy\ e^{y} \cdot\ e^{-t/\tau(x,y)} \qquad (5.5)$$

$$= D_1 t^{-\nu_1} + D_2 t^{-\nu_2}$$

where the two terms in the last expression correspond to the integration over regions 1 and 2 respectively. One finds:

$$\nu_1 = \frac{s}{\frac{log\ 2}{log\ 3} - s} \quad ; \quad \nu_2 = s \qquad (5.6)$$

The second of these two exponents, being smaller, dominates at long times and thus describes the asymptotic decay of the average autocorrelation function. We have underlined the word "average", because for any given initial condition

decay can be much faster; if for example our particle starts out on a tree-leaf in the left-half of its generation, it can be shown that the autocorrelation function dies out with exponent v_1, which incidentally is the exponent obtained for a tree that trifurcates uniformly every height interval Δh. Figure 3b may actually mislead the reader to think that such "fastly-decaying" initial conditions should dominate the average, but this is not the case*: the prefactor D_2 does not vanish.

The dynamic exponent for the unbalanced tree of this section obviously satisfies

$$v = s \leq v_{uniform} = \frac{s}{1-s}$$

Thus rearranging the branches of a uniform tree (without changing its silhouette, i.e. adding new branches) can indeed slow down relaxation. Is there a limit to this slowing-down effect or can we go all the way to a logarithmic time decay (1/f noise) by appropriately complexifying the tree's structure? The following result answers this question:

Theorem 2: The dynamic critical exponent of any tree is bounded from below by its silhouette: $v \leq s$.

Proof: From equation (2.13) it follows easily, since $N_B \geq 1$, $N_{B_n} \geq N_{B_{n-1}}$, that:

$$\tau_B^{-1} \geq e^{-h_B}$$

for all tree-nodes B. Thus we can bound the average autocorrelation function as follows:

* Note that in Fig. 3b, y is a logarithmic scale, so that practically the entire population of tree-leaves is concentrated in the lower left corner of the triangle.

$$\overline{P(t)} \leq \sum_{\text{tree nodes } B} \frac{1}{N}(S_B - 1)\, e^{-t \cdot e^{-h_B}} =$$

$$= \sum_{n=1}^{\infty} (e^{s \cdot \Delta h} - 1)\, e^{-n \cdot s \cdot \Delta h} \cdot e^{-te^{-n \cdot \Delta h}}$$

$$\simeq t^{-s} \qquad Q.E.D.$$

This simple theorem thus demonstrates that the unbalanced tree of this section saturates the lower bound for the dynamic exponent, and leads to the slowest allowed relaxation. We should point out that this slowest-relaxing tree is not unique: for instance any tree for which the bth-fraction of each generation b-furcates (with b some integer), while the remaining members continue as dead branches to the end, would give the same dynamic exponent. The prefactor D, as well as the critical silhouette above which relaxation is unstable, do however depend on b.

6. DISCUSSION

Figure 4 summarizes our results. The dynamic exponent v is maximized by both uniform and random trees, and minimized by the unbalanced trees of section 5. The same qualitative behavior is obtained if instead of v one plots a measure of the tree's complexity defined by counting the number of non-isomorphic pieces at every generation of the tree as shown by Huberman and Hogg (1986) . More recently it has been shown that the critical threshold for percolation on a tree, which can be interpretated as the complexity of winning strategies in a game, is also minimized by uniform and random trees and maximized by the trees of section 5 [Bachas and Wolff (1987)]. We may therefore say that the rate of relaxation is sensitive to the physical complexity or lack of self-similarity, rather than to the structural noise or Shannon entropy of the underlying tree. It would be interesting to see whether quantitative relations among these various complexity measures can be obtained.

Besides slowing down relaxation, the complexity or absence of self-similarity has another, more spectacular effect, when one considers thermally activated processes. Assuming in this case that the hopping rates are given as

$$\varepsilon_{ij} = e^{\frac{-\Delta V_{ij}}{T}} \tag{6.1}$$

with ΔV_{ij} an energy barrier, we easily conclude from the definition (2.4) that the silhouette is proportional to the temperature. Therefore the temperature dependence of the dynamic exponent is given by:

$$\nu_{least\ complex}(T) = \begin{cases} \dfrac{T}{T_c - T}\ ; & T<T_c \\ \infty & T>T_c \end{cases} \tag{6.2a}$$

for self-similar (uniform or random) trees, and

$$v_{most\ complex}(T) = \begin{cases} c \cdot T \; ; & T < T_c' \\ \infty & T > T_c' \end{cases} \qquad (6.2b)$$

for the most complex trees of section 5. This is illustrated in Fig. 5a,b. Note in particular that the transition to instability is continuous in the former case and discontinuous in the latter.

Before proceeding we should point out that ultradiffusion is not just a naive model of the relaxational dynamics of systems with many time scales. It can be actually considered as a universal description of such dynamics, in two different ways:

a) In real space one may describe the spreading of an excitation by lumping together in larger and larger blocks the degrees of freedom that relax at characteristic times $\tau_1 < \tau_2 < \ldots$, as has been suggested by Palmer et al. (1984). Note that for systems with disorder the ensuing hierarchical tree is in general non-uniform.

b) In configuration space one may describe relaxation as a stochastic motion of an ensemble of particles in a valley landscape of metastable states [Dotsenko (1985)]. At sufficiently low temperature, the hopping rate between two such states is:

$$\varepsilon_{ij} \simeq e^{\frac{-minmax(i,j)}{T}}$$

where minmax (i,j) is the minimum over all paths from i to j, of the maximum energy barrier encountered along the path. This satisfies the ultrametric property

$$minmax(i,j) \leq max\left\{minmax(i,k);\ minmax(j,k)\right\}$$

since one can always go from i to j via k, and hence defines a hierarchical structure in the space of metastable states. We owe this argument to Marc Mézard (private communication).

It is this second description of relaxation as ultradiffusion in the space of metastable states that is relevant for studying the temperature dependence of the dynamic exponent. The simple assumption (6.1), however, is a priori justified only in the limit of vanishing temperature. As T is raised, it is in general invalidated for several reasons: to begin with, entropy comes into play and hopping rates are not simply determined by a maximum energy barrier, so that ultrametricity of the transition matrix may be destroyed. One may simply hope that the ultrametricity of equilibrium states, demonstrated in the mean-field spin-glass [Sherrington and Kirkpatrick (1975), Mézard et al. (1984)], and conjectured in a variety of other systems [Palmer (preprint 1986)], implies also an exact or approximate hierarchy of hopping rates among long-lived metastable states.

Even if this is so, free-energy barriers would in general be T-dependent, so that the silhouette is not simply proportional to T. Eqs. (6.2a,b) should therefore be replaced by:

$$\nu_{self\,similar}(T) = \begin{cases} \frac{s(T)}{1-s(T)} & ; \quad T<T_c \\ \infty & ; \quad T>T_c \end{cases} \tag{6.3a}$$

and

$$\nu_{most\,complex}(T) = \begin{cases} s(T) & ; \quad T<T_c' \\ \infty & ; \quad T>T_c' \end{cases} \tag{6.3b}$$

where $s(T_c)=1$ in the first case, and $s(T_c')=\log 2/\log 3$ for the trees of section 5. The precise form of $\nu(T)$ now depends on the unknown function $S(T)$. If, however, the silhouette changes continuously with temperature, the nature of the transition is robust: it is continuous for self-similar trees and discontinuous for complex trees. Note incidentally that the transition

described in eq. (6.2) is unphysical, since relaxation became unstable above the critical temperature. This is, however, only due to the long-range nature of hoppings, and can be easily rectified: by introducing an expontial T-independent cutoff that respects the ultrametric structure of the space, we can ensure that the silhouette is bounded from above at all temperatures, and the transition is to a region of exponential relaxation.

It is tempting to compare these predictions of ultradiffusion with what is known for the mean-field spin glass: as shown by Sompolinsky and Zippelius [Sompolinsky and Zippelius (1981) and (1982)] relaxation in the latter is exponential above the glassy transition, and changes over to a power law with exponent:

$$\nu(T) = \frac{1}{2} - \frac{T_c - T}{\pi T_c} + 0\left(T_c - T\right)^2$$

below. Does this imply that the hierarchical tree in the Sherrington-Kirkpatrick model [Sherrington and Kirkpatrick (1975), Mézard et al. (1984)] is complex?

More work is necessary to answer such questions, and to unravel the rich properties of systems that defy the simplicity of scaling laws.

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FIGURES

Fig. 1: A generic tree illustrating our notation. The node A has three sons ($S_A = 3$) and six final descendants ($N_A = 6$). A_1 is his father and A_2 the grandfather, that also happens to be the root of the tree. The height of a node as measured from the bottom leaves, is minus the logarithm of the corresponding transition rate. The node B illustrates how the weight of a state can be effectively increased (by a factor 8 in the figure) by letting it multifurcate at low altitude.

Fig. 2: Regular uniformly (a) bifurcating and (b) tetrafurcating trees; since the (asymptotic) rate of population growth with height is the same, these two trees have the same silhouette, and hence, as discussed in the text, yield the same dynamic critical exponent.

Fig. 3: (a) An example of a maximally unbalanced tree that saturates the lower-bound for the dynamic critical exponent. The left-half members of every generation trifurcate, while the right-half give rise to a single son each. (b) The orthogonal triangle containing the nodes of this tree, when parametrized as explained in the text. The root lies at the origin. Region 1 is a regularly trifurcating subtree, while region 2 contains those nodes whose descendants trifurcate for awhile, but eventually enter the right-half of their generation and continue as dead branches thereafter. The broken line is the line of ancestors of a typical node A, along which we integrate to calculate τ_A; its slope is initially $\Delta y/\Delta x = \log 3$, until it hits the left-most branch of the tree, from which point on it continues straight up to the root.

Fig. 4: A schematic plot of the dynamic exponent v versus the Shannon Entropy, or detailed information content of the underlying tree. Here s is the silhouette of the tree, which is held constant, and the broken lines are rigorous bounds.

Fig. 5.: The temperature dependence of the dynamic exponent, assuming hopping rates are given by eq. (6.1), for a) self-similar and b) maximally

complex trees. Note that the transition is continuous in the former case and discontinuous in the latter.

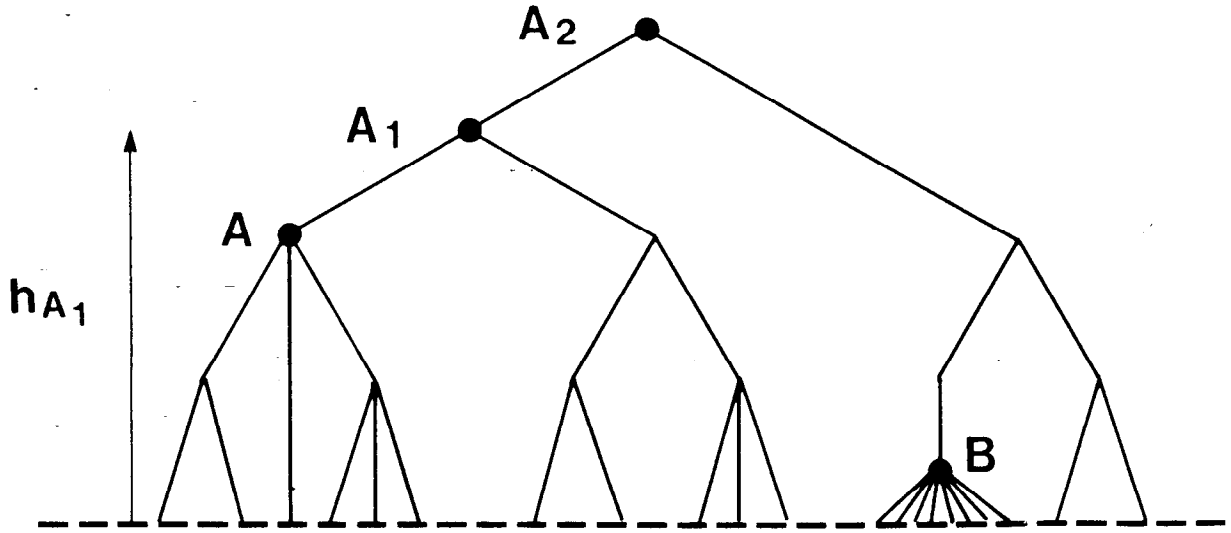


Fig. 1

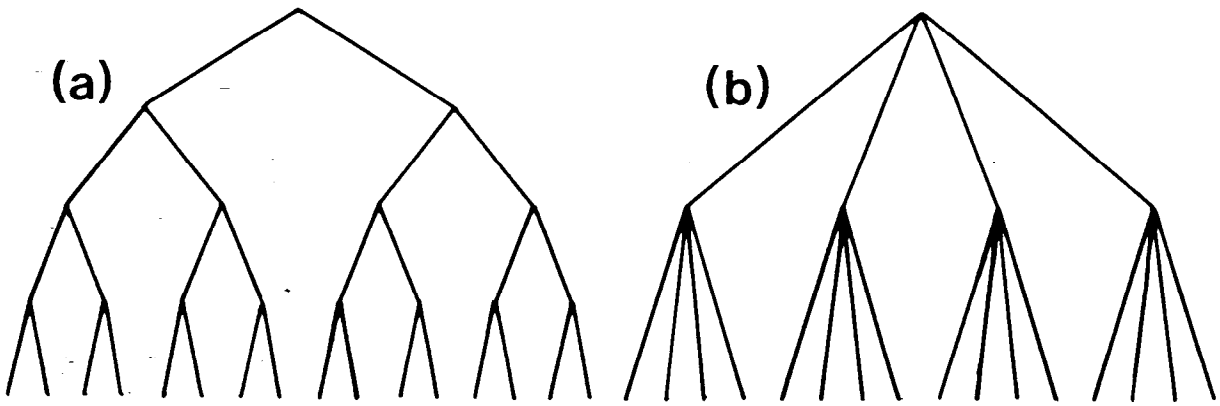
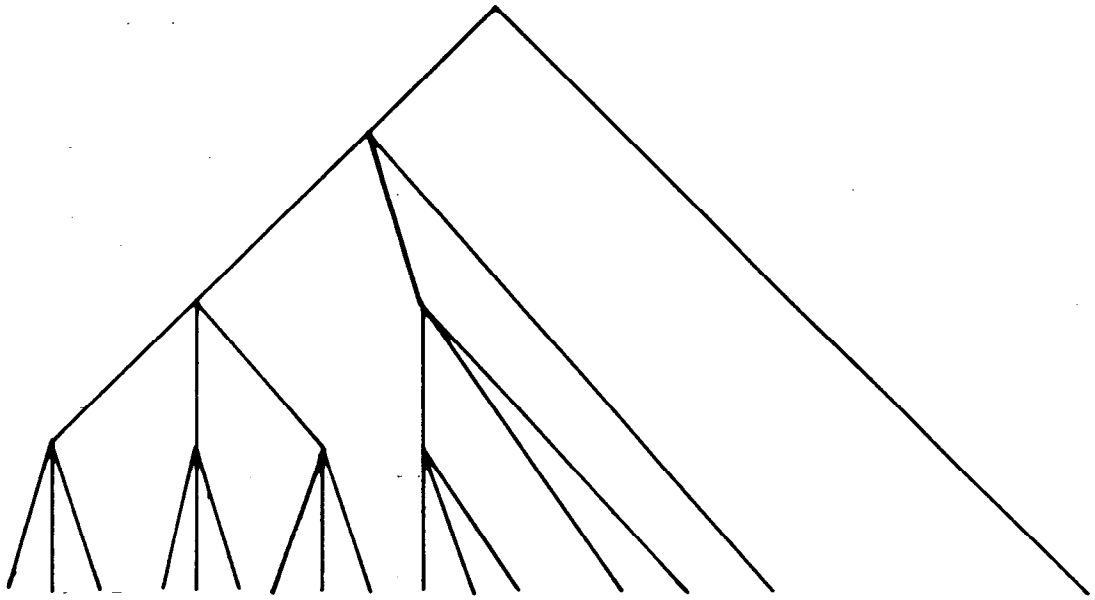


Fig. 2

(a)



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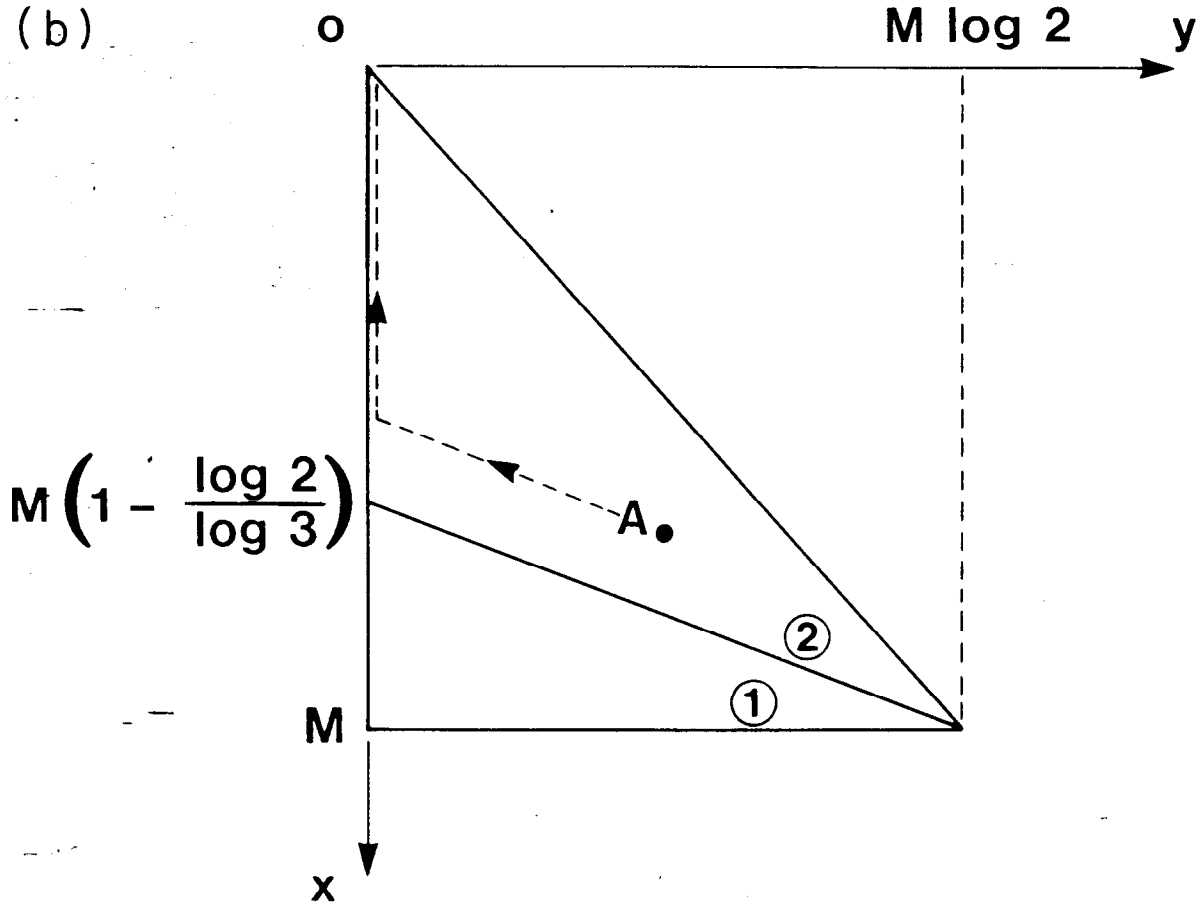


Fig. 3

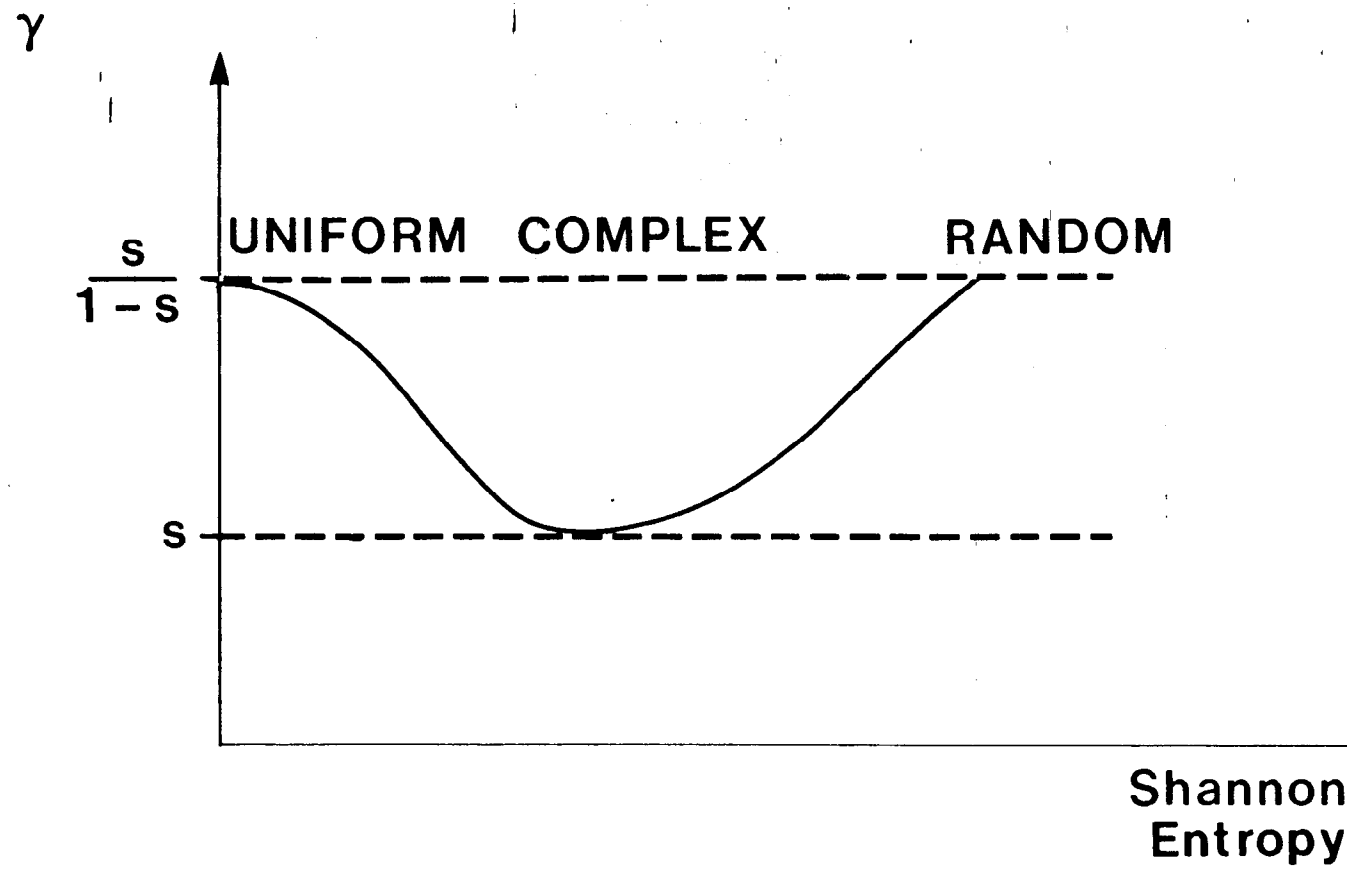
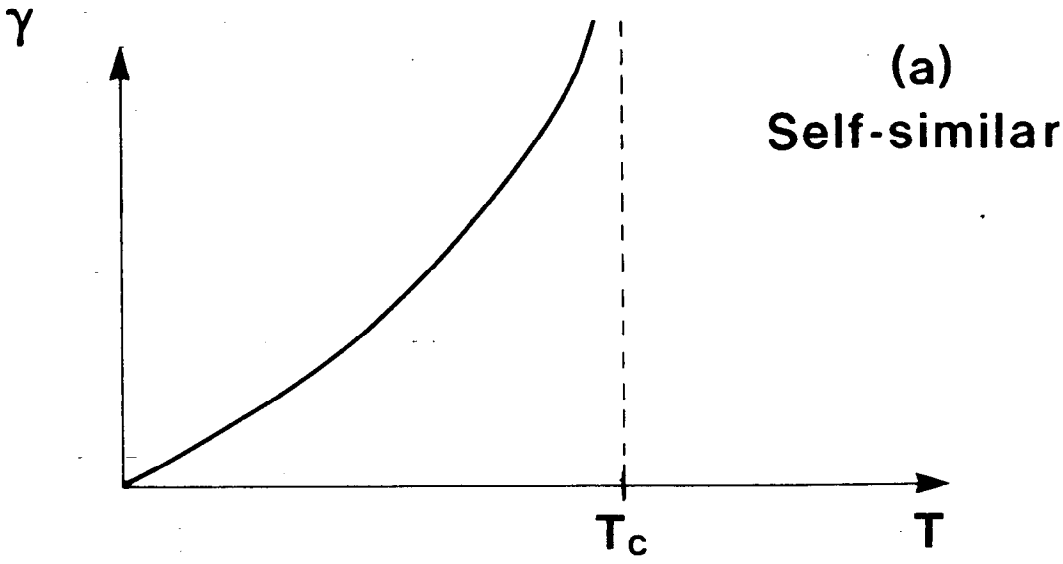


Fig. 4



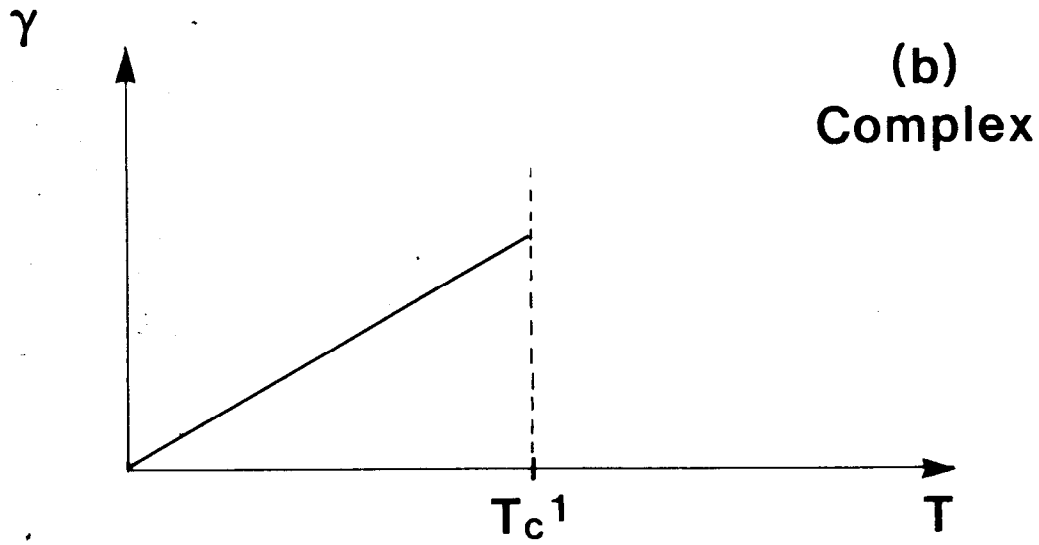


Fig. 5