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FRACTONS AND THE FRACTAL STRUCTURE OF PROTEINS

by

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Abstract

We propose a model for (low spin) hemoproteins and ferredoxin which takes into account *both* the fractal structure of the protein backbone (polypeptide chain) *and* the cross-connections (H-bridges) between segments of the folded chain. Within this picture the *fracton* dimensionality d_{fr} (recently introduced by Alexander and Orbach), the *fractal* dimensionality d_f and the Stapleton et al. experimental non-integer exponent n (spin-lattice relaxation rate $1/T_1 \propto T^n$) become satisfactorily consistent.

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In low spin hemoproteins and ferredoxin, the spin-lattice relaxation of the Fe^{3+} ions is dominated by a two-phonon process (Raman)[1]. This mechanism leads to a relaxation rate $1/T_1$ whose temperature dependence is given by

$$\frac{1}{T_1} \propto T^{3+2\bar{d}} f(T/\Theta, \bar{d}) \qquad (1)$$

where Θ is the Debye temperature and f is a smooth finite function of T/Θ. The dimensionality $\bar{d}$ enters into the exponent of T through the phonon density of states ρ, which at low frequencies has the form

$$\rho(\omega) \propto \omega^{\bar{d}-1} \qquad (2)$$

For an ordinary d-dimensional object $\bar{d}$ coincides with the euclidian dimensionality d.

Experiment[2,3] shows that in low spin hemoproteins and ferredoxin, the low temperature (4 - 20K) behaviour of $1/T_1$ is best described by a non-integer power law of the form

$$\frac{1}{T_1} \propto T^n \qquad (3)$$

with $n \simeq 6.3$ for hemoproteins[2] and $n \simeq 5.67$ for ferredoxin[3]. Such a temperature dependence cannot be satisfactorily adjusted by expression (1) using $\bar{d} = 3$ and a single value of Θ. Attempts to fit with $\bar{d} = 2$, presuming a dominant role of the planar structure of the heme group where the Fe sits (in hemoproteins) were not satisfactory either[3].

A new and appealing approach was proposed by Stapleton et al.[2] who took at face value the non-integer experimental power law (3). They postulated the validity of Eq. (2) also for non-integer values of $\bar{d}$, which would be a result of the complex space structure of the proteins. They identified $\bar{d}$ with the fractal dimension d_f of the protein backbone, defined through $R^{d_f} \propto N$ where N is the mean value of the number of alpha carbons which lie within a sphere of radius R centered in an arbitrary alpha carbon (Fig. 1a). The concrete value for d_f was calculated on the basis of the detailed structure of the protein as obtained from X-ray data; they obtained $d_f \simeq 5/3$ for the hemoproteins and $d_f \simeq 4/3$ for the ferredoxin (the value obtained for the hemoproteins coincides with the fractal dimension of a random self-avoiding walk, as pointed out by the authors [2]). The agreement between d_f calculated from the X-ray structure and $\bar{d}$ obtained from the temperature dependence of $1/T_1$ turns out to be very satisfactory for all hemoproteins[2] and ferredoxin[3].

Recently, however , the frequency dependence of the phonon density of states in fractal systems was actually calculated by Alexander and Orbach[4], showing that

$$\rho(\omega) \propto \omega^{d_{fr}-1} \qquad (4)$$

where the "fracton dimensionality" d_{fr} *differs* in general from d_f. In fact d_{fr} reflects the topological aspects of the system. For instance, for a *linear* chain (and this includes random walk or self-avoiding walk configurations) it is $d_{fr} = 1$, no

matter what its fractal dimensionality is. Thus, if only the backbone of the protein is considered, it results $d_{fr} = 1$ and the *correct* Eq. (4) leads to $1/T_1 \propto T^5$ which disagrees with experiment.

In this paper we propose a fractal model for the protein which incorporates massless springs cross-connecting the folded backbone (Fig. 1b). They may represent for instance the hydrogen bonds which bridge close monomers in the folded polypeptide chain (Fig. 1c)[5]. Thus, the protein is no longer described by a one-dimensional chain but by a more complex topological object for which $d_{fr} \neq 1$. We argue that for a high enough density of bridges d_{fr} equals d_f, and the agreement with experiment is restaured.

Within the Alexander-Orbach theory[4] it is established that

$$d_{fr} = \frac{2d_f}{d_w} \tag{5}$$

where d_w is the fractal dimensionality of a random walk constrained to the fractal; it is defined by the relation $\langle r^2 \rangle^{d_w} \sim t^2$, where $\langle r^2 \rangle$ is the mean square end to end distance of the walk after t steps. For a linear chain (Fig. 1a) with fractal dimensionality d_f, it is $d_w = 2d_f$[4,6], therefore $d_{fr} = 1$ independently of d_f. The bridges incorporated in our model (Fig.1b) are massless and therefore the fractal dimensionality of the chain is not changed. However, they do change d_w since the random walk is no longer constrained to be along the chain but has the possibility of taking short cuts. We argue that in this

case $d_w = 2$ *independently of* d_f. In order to show this, let us consider a linear chain with $d_f = 2$ embedded in a two-dimensional plane. For a high enough concentration of bridges between monomers of the chain (Fig. 2), the system looks two-dimensional from the point of view of a random walk, hence $d_w = 2$. The same result holds for a linear chain of fractal dimensionality $d_f = d$ embedded in a d-dimensional euclidean space. Now, even if the fractal dimensionality of the linear chain is smaller than d, we can conceive that by adding enough bridges we can reach a point where $d_w = 2$ (Fig.3). Thus, it follows from Eq. (5) that for a sufficiently high concentration of bridges, $d_{fr} = d_f$, in agreement with the experimental results.

In conclusion, we are proposing for proteins a model which consists of a linear chain with cross-connecting bridges. It seems to contain the basic ingredients to account for the low temperature dependence of the spin relaxation time of Fe^{3+} in hemoproteins and ferredoxin. It should be useful also for other proteins, in order to describe properties which depend on the phonon density of states.

The considerations made in this letter are quite general. We would like to caution, however, that these results should apply whenever the number of all possible bridges that one can add is large enough. This can be realized when the euclidean dimensionality d in which the linear chain is embedded is not too high compared to d_f (if $d >> d_f$ the different pieces of the folded chain will seldom become close to each other to allow the incorporation of cross-connecting bridges

of reasonable length, that is, of lengths much smaller than the end to end separation of the chain). We believe that this is still the case for $d = 3$ and $d_f = 5/3$ or $4/3$. It would certainly be interesting to test the validity of these predictions by direct numerical simulations, and to extend this analysis to other fractals. Finally, through the Einstein relation between conductivity and diffusion, considerations completely parallel to those presented herein should apply to conducting fractal structures.

Acknowledgments

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References

[1] R. Orbach, Proc. Roy. Soc. London, 264, 458 (1961).

[2] H.J. Stapleton, J.P. Allen, C.P. Flynn, D.G. Stinson and S.R. Kurtz, Phys. Rev. Letters 45, 1456 (1980).

[3] J.P. Allen, J.T. Colvin, D.G. Stinson, C.P. Flynn and H. J. Stapleton, Biophys. J., 38, 299 (1982).

[4] S. Alexander and R. Orbach, J. de Physique/Lettres, 43, L625 (1982).

[5] R.E. Dickerson and I. Geis, *Hemoglobin* (The Benjamin/Cummings Pub. Co. Inc., Menlo Park, Cal., U.S.A., 1983).

[6] This can be easily seen if one considers that along the chain the mean square displacement $\langle \ell^2 \rangle$ is related to the number of steps t in the usual way $\langle \ell^2 \rangle \sim t$. Since both $\langle \ell^2 \rangle$ and $\langle r^2 \rangle^{d_f}$ are proportional to N^2, it follows that $\langle r^2 \rangle^{d_f} \sim t$, hence $d_w = 2d_f$.

Caption for Figures

Fig. 1 - Schematic draw of a portion of a folded protein. ●: monomer of the polypeptide chain; ——: backbone of the polypeptide chain; ----: cross-connections (e.g., hydrogen bonds). (a) Stapleton et al picture; (b) Picture proposed herein; (c) chemical structure of a protein chain (▽ are side chains attached to alpha carbons; beautiful pictures are found in Ref. [5]).

Fig. 2 - Schematic representation of a massive self-avoiding linear fractal chain of dimension $d_f \leq d$ (dimensionality of the euclidean space into which it is embedded). The massless bridges (----) provide short cuts for a random walker on the fractal.

Fig. 3 - Variation of the random walk dimensionality d_w as a function of d_f for a massive linear fractal, with and without bridges.

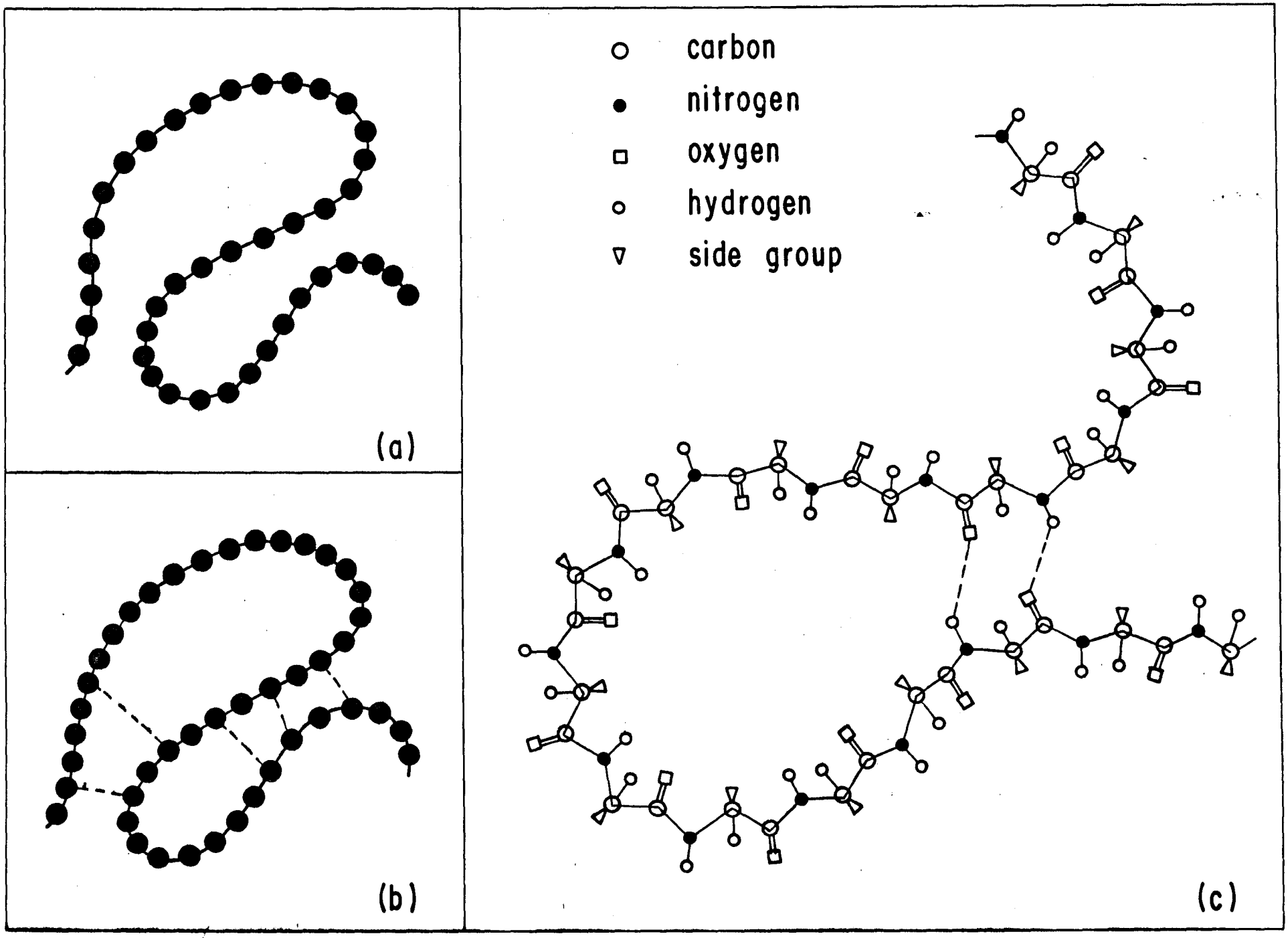

FIG.1

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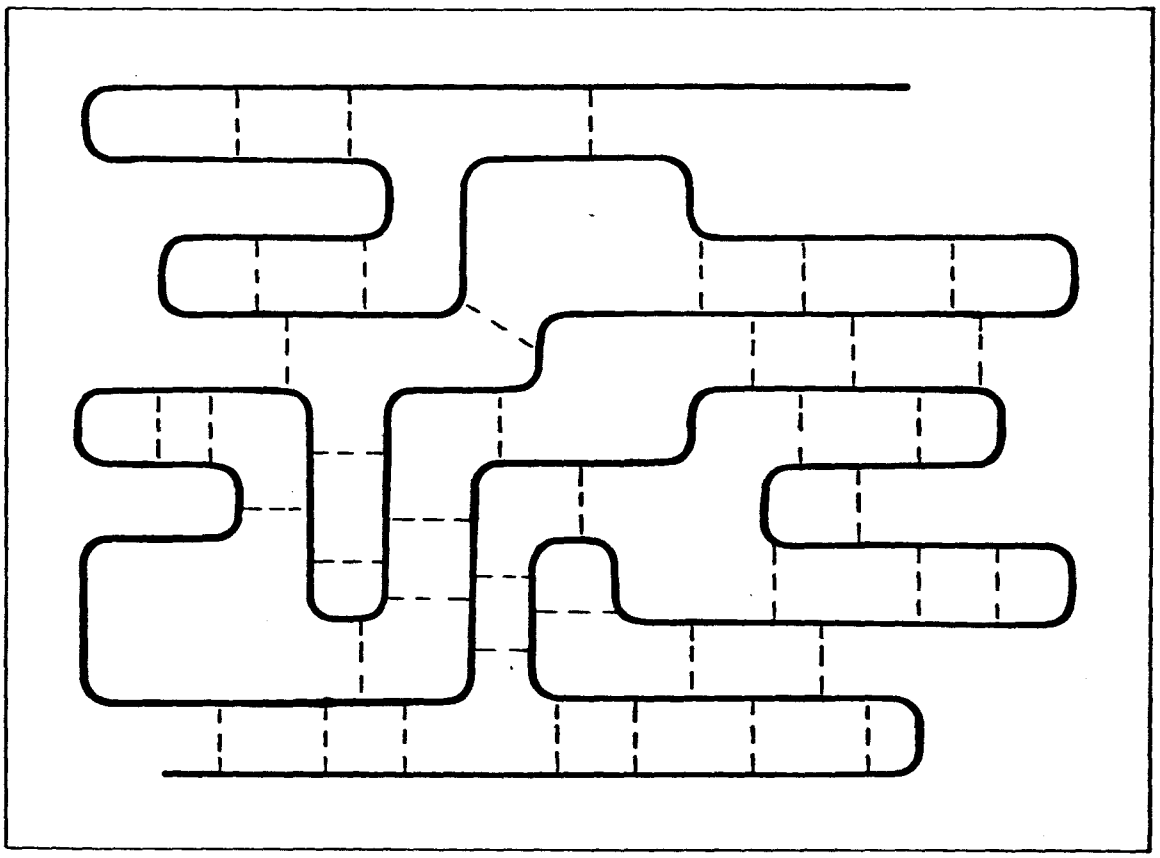

FIG.2

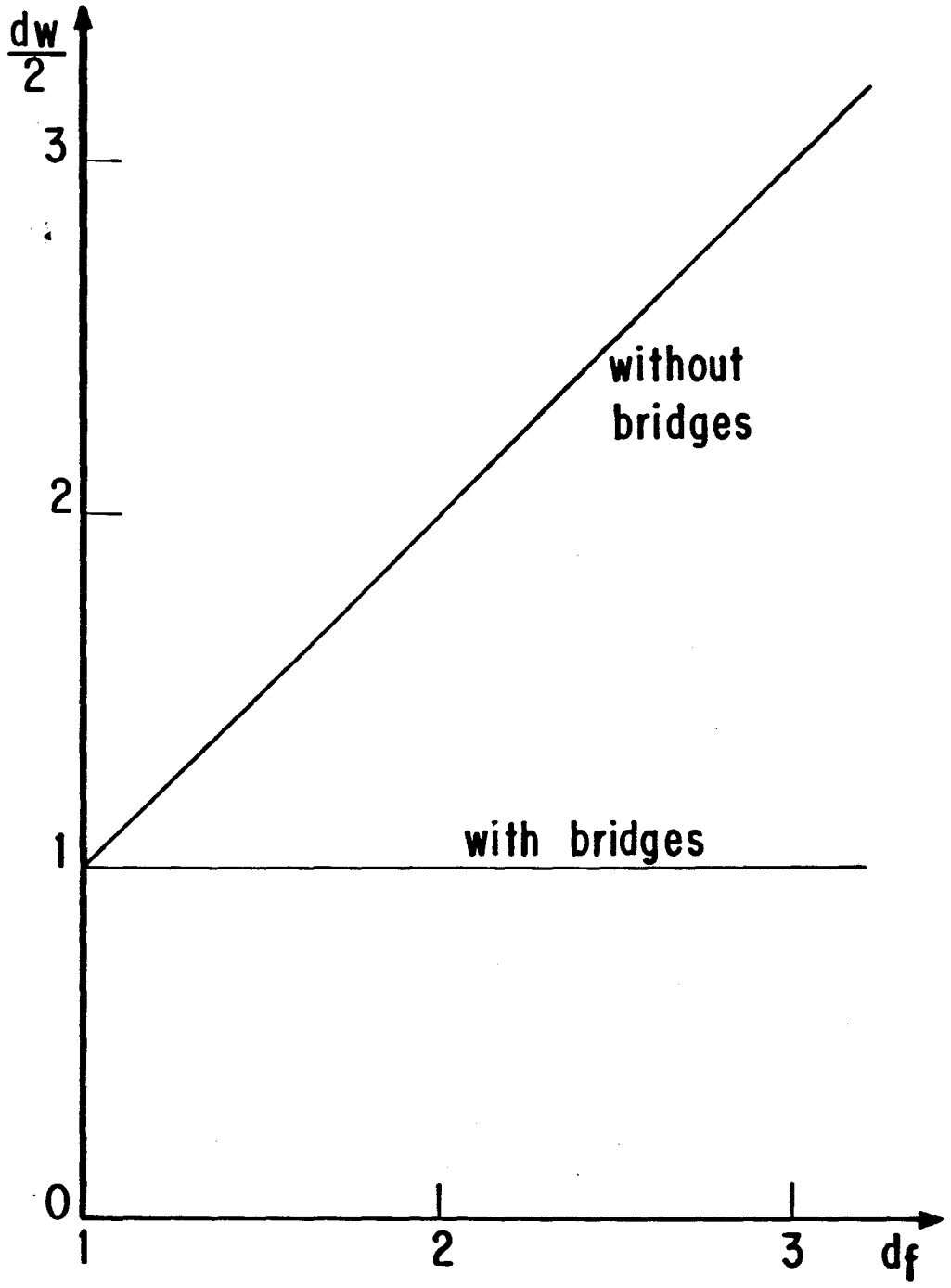

FIG.3