Nonlinear localization in thermalized lattices: application to DNA

Michel Peyrard*, Jean Farago

Laboratoire de Physique, CNRS UMR 5672, Ecole Normale Supérieure de Lyon, 46 allée d’Italie, 69364 Lyon Cedex 07, France

Abstract

In the last few years numerous studies have been devoted to intrinsic localized modes in nonlinear lattices because they provide examples of localization without disorder. The properties of “discrete breathers” as exact solutions of these nonlinear lattices are now well understood, but this is not the case for the properties of nonlinear localization and energy relaxation in thermalized lattices. In biological molecules such as DNA, where large amplitude nonlinear motions are essential for function, temporary deviations from energy equipartition could play an important role. After a brief introduction to intrinsic localized modes, we address the following questions: (a) does nonlinear localization survive in the presence of a thermal bath and how can we characterize it? (b) what is the origin of localization and how do discrete breathers contribute to it? (c) can we observe nonlinear localization in an experiment? The last point discusses recent results of an experiment performed on DNA, which suggest that the effects of nonlinear localization in a thermalized system may have already been observed. © 2000 Elsevier Science B.V. All rights reserved.

1. Introduction

In physics the idea of localization is generally associated to disorder that breaks translational invariance. However it can exist in the absence of any disorder and, in the last few years, numerous studies have been devoted to intrinsic localized modes, also called discrete breathers [1]. In an homogeneous lattice, localization may come from nonlinearity which introduces a dynamical disorder if sites which undergo large amplitude displacements have vibrational properties different from the properties of the lattice near equilibrium. A proof of existence of time-periodic, spatially localized, solutions has been given for a broad range of Hamiltonian coupled-oscillator nonlinear
lattices [2,3] and approximate solutions have been obtained for one-dimensional or multi-dimensional lattices [4]. A spontaneous localization of energy in such lattices has been found [5–7] and it has been shown that discrete breathers, which store energy locally, can be responsible for very slow relaxations [8].

However these studies are conducted in Hamiltonian systems where discrete breathers are exact solutions that would persist forever in the absence of external perturbations. In a system in contact with a thermal bath, the situation might be very different because the fluctuating forces provided by the environment could destroy the breathers. Studies of the role of localized modes in a thermalized lattice show some similarity with the problem of quantum chaos: we are looking for tracks of phase space trajectories which are well defined in the Hamiltonian system but are blurred by the fluctuations, whether they are thermal or quantum. Few studies have been devoted to thermalized nonlinear lattices [9–11] because it is hard to characterize the effects of nonlinear localization in the presence of a thermal bath, beyond a simple observation of the presence of localized modes in the lattice. In the present work, following a brief introduction to intrinsic localization in a nonlinear lattice, we introduce some quantitative measurements of localization in a thermalized lattice and we examine the mechanisms responsible for this localization. Then we discuss a possible experiment that would allow a direct observation of nonlinear localization in a physical system. As a basic example we use a nonlinear model for the dynamics of DNA, introduced to describe the statistical mechanics of DNA thermal denaturation [9,12,13], which has been recently tested against experimental studies [14]. Biomolecules are good candidates for nonlinear localization because they are highly deformable objects that undergo large conformational changes, often essential for biological function, such as the local opening of DNA which is necessary for the reading of the genetic code during transcription. Although slow relaxation of thermal energy has been observed in proteins [15,16], DNA is more suitable than proteins to study nonlinear localization because its structure is more regular, reducing the effect of disorder-induced localization. Large amplitude localized modes have been observed in artificial DNA homopolymers [17] which almost have the regularity of a crystal on a length of a few hundred Angström, i.e., the persistence length of the molecule. Recently micromanipulations of DNA have been used to study its properties [18,19], and we show in Section 4 that these experiments could perhaps be used for a direct observation of nonlinear localization.

2. Nonlinear localized modes

Nonlinear localization exists in a large class of nonlinear lattices [1]. Except where otherwise specified we shall consider here the specific case of a nonlinear model introduced to study the dynamics and statistical mechanics of DNA thermal denaturation [9,12]. The lattice has the following Hamiltonian:

\[ H = \sum_n \frac{1}{2m} p_n^2 + W(y_n, y_{n+1}) + V(y_n), \]
which is based on a simplified description of the DNA double-helix where only one scalar variable \( y_n \) is introduced for the \( n \)th base pair. It measures the stretching of the hydrogen bonds that connect the bases, and \( p_n \) is the associated conjugate momentum. In the present work the stacking interaction of the bases along the molecule, \( W(y_n, y_{n+1}) \), is simply taken as harmonic \( W(y_n, y_{n+1}) = \frac{1}{2} K(y_{n+1} - y_n)^2 \). The on-site potential \( V(y_n) \) describes the interaction between two bases in a pair including several contributions such as the hydrogen bonds linking the two bases and the repulsion of the charged phosphate groups belonging to the backbone. We use for \( V(y_n) \) a Morse potential, \( V(y_n) = D(e^{-ay_n} - 1)^2 \), which has the appropriate shape to describe the strong repulsion when the bases are pushed toward each other \( (y_n < 0) \) and the vanishing interaction when the bases are pulled very far apart \( (y_n \gg 1/a) \). In order to study nonlinear localization without any disorder, the model is taken to be homogeneous, i.e., it represents a homopolymer. The parameters have been determined from the dynamical and denaturation properties of DNA. They are \( m = 300 \) atomic mass units (a.m.u.), \( K = 0.04 \) eV/\( \text{Å}^2 \), \( D = 0.04 \) eV, \( a = 4.45 \) Å\(^{-1} \). Our system of units (a.m.u., Å, eV) defines a time unit (t.u.) equal to \( 1.021 \times 10^{-14} \) s. With these parameters, the period of the harmonic oscillation at the bottom of the Morse potential is \( \theta_0 = 2\pi/\omega_0 = 2\pi/\sqrt{2Da^2/m} = 86.4 \) t.u., i.e., \( 0.8 \times 10^{-12} \) s, a value which is consistent with the low-frequency vibrational mode of DNA which involve the motion of bases as a whole (40 cm\(^{-1} \) in spectroscopic units). For the study of nonlinear localization, it should be noticed that Hamiltonian (1) is a generic Hamiltonian for a lattice of harmonically coupled nonlinear oscillators. The oscillators are “soft”, i.e., their frequency decreases with the amplitude of oscillation. Such a lattice has exact discrete breather solutions that correspond to a periodic vibration, localized in space, with an amplitude that decays exponentially from the center of the breather. Fig. 1 shows an example of such a solution.

The existence of this localized mode can be understood by analogy with disorder-induced modes if one notices that nonlinearity induces a dynamical disorder. The frequency of oscillation of a particle subjected to a nonlinear potential such as \( V(y_n) \) depends on its amplitude. If the nonlinearity is such that the frequency shifts toward lower values for higher amplitudes, the frequency of an excited site will fall below \( \omega_0 \), in the gap of the phonon spectrum. Therefore if one particle of the lattice is highly excited, it will not be able to radiate away its energy and an intrinsic localized mode may be expected. As the amplitude of the excitation increases the frequency drops even more and the mode gets narrower. Such localized modes are self-trapped by the frequency shift associated to their presence at a given site.

3. Localization in a thermalized nonlinear lattice

3.1. Existence and characterization

While discrete breathers are interesting mathematical solutions which demonstrate that localized modes exist in a translationally invariant lattice, nonlinear localization
can only be relevant in microscopic physical systems if it survives in the presence of thermal fluctuations. In order to study this aspect, we have simulated the dynamics of the model described by Hamiltonian (1) in the presence of a thermal bath. We use an extension of the Nose–Hoover method [20] which includes a chain of thermostats (five thermostats in our calculations) to provide a good exploration of the phase space [21]. For the study of equilibrium properties, it can be shown that the Nose method generates an exact canonical ensemble [20]. The proof does not extend to dynamical properties but we have tested the multiple thermostat Nose simulation in a case where analytical results are available to make sure that it gives valid results [22].

Fig. 2 shows examples of the time evolution of the dynamics of the thermalized lattice at two different temperatures $T = 100$ and $340$ K. This figure clearly shows the persistence of nonlinear localization in the presence of a thermal bath. At $100$ K the discrete breathers are particularly visible. They appear as dotted lines corresponding to alternating large base-pair stretching and closing. Both figures display about 1000 periods $\theta_0$ of the lowest phonon mode. *On this time scale, which is already long*

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1 Simulations of the Toda lattice show that the multiple-thermostat Nose method reproduces the known results on the dynamical structure factor. In this integrable system, the initial configuration must however be properly chosen to avoid extremely long-lived out-of-equilibrium solitons that give spurious peaks in the structure factor.
Fig. 2. Molecular dynamics simulation at controlled temperature ($T = 100$ and $340$ K) of the model corresponding to Hamiltonian 1, for a lattice of 256 sites, with periodic boundary conditions. The horizontal axis indicates the position along the 256 cells. The vertical axis indicates time. The stretching $\gamma$ of the base pairs is indicated by a grey scale, the lighter grey corresponding to $\gamma \leq 0.1$ Å and black indicating large base-pair opening ($\gamma \geq 1.5$ Å).
with respect to the microscopic time scale \( \theta_0 \), the figure shows an absence of energy equipartition which is characteristic of nonlinear localization. Some regions have large amplitude displacements (dark stripes on the figures) while others keep a small amplitude (light grey stripes). The existence of these “hot” and “cold” patches, that we henceforth call “localization patches”, does not mean that the basic rules of thermodynamics are broken. Energy equipartition does exist in the nonlinear lattice, but in order to observe equilibrium properties, one must consider extremely long time averages.

The detection of breathers in the presence of thermal fluctuations cannot be done unambiguously because there is no sharp cutoff between breathers and small amplitude wave packets. Therefore we cannot expect to count breathers and determine their lifetime as one can do for topological kink solitons or for nonlinear excitations in an integrable system where they can be identified with the inverse scattering transform. In order to give a quantitative measurement of localization one can use global quantities such as the space- and time-dependent correlation functions of the position or energy [11]. However, since we are particularly interested in phenomena which are local in space, we have chosen to consider local distribution functions which give a direct meaning to the notion of hot and cold patches mentioned above.

Let us consider a particular dynamical variable \( A(n, t) \) which depends on site \( n \) and time \( t \). \( A \) can be the displacement field \( y_n(t) \), the kinetic energy of an oscillator \( p^2_n/2m \) or the energy density \( u. \)

The local distribution function for \( A \), \( \mathcal{P}(A, n_0, t_0; n, t) \), is the normalized distribution of the values of \( A(n, t) \) within the domain \( n_0 - \Delta n/2 \leq n \leq n_0 + \Delta n/2, t_0 - \Delta t/2 \leq t \leq t_0 + \Delta t/2 \). In the limit \( \Delta n \to \infty \), or \( \Delta t \to \infty \), \( \mathcal{P} \) tends to the equilibrium distribution for the variable \( A \) at the temperature \( T \) of the simulation. On the contrary, for small \( \Delta n \) or \( \Delta t \), \( \mathcal{P} \) depends on space. Fig. 3 shows an example of this variation for the DNA model at \( T = 300 \) K for \( \Delta n = 4, \Delta t = 20000 \) t.u. The spatial dependence of \( \mathcal{P} \) can be measured quantitatively by calculating the distance in probability space, between \( \mathcal{P}(A, n_1, t_0; n, t) \) and the distribution function around a site \( n_0 \) chosen as a reference point, \( \mathcal{P}(A, n_0, t_0; n, t) \). Various measurements of the difference between probability distributions have been proposed. We have chosen the Kullback–Leibler divergence, deduced from the Shannon entropy function [23]

\[
K_l(n_1, n_0, t_0, \Delta n, \Delta t) = \int \mathcal{P}(A, n_1, t_0; n_0, t_0, \Delta n, \Delta t) \ln \frac{\mathcal{P}(A, n_1, t_0; n_0, t_0, \Delta n, \Delta t)}{\mathcal{P}(A, n, t_0; n_0, \Delta n, \Delta t)} \, dA. \tag{2}
\]

The variation of \( K_l \) with \( n_1 \) gives a measurement of the degree of localization. In a uniform system where the distribution function does not depend on space, \( K_l(n_1) \) would vanish everywhere. Fig. 4 compares \( K_l(n_1) \) for the nonlinear DNA model and an harmonic lattice obtained by replacing the Morse potential by its small amplitude harmonic limit, all other parameters being the same. The difference is striking and illustrates quantitatively the dynamical localization which occurs in a thermalized nonlinear lattice.
Fig. 3. Local distribution $P(y, n_0, t_0, \Delta n, \Delta t)$ for the DNA model at temperature $T = 300$ K. $\Delta n = 4$, $\Delta t = 20000$ time units. The axis extending from left to right gives the values of the displacements $y$, the axis going from front to back extends along the 128 cells of the lattice used in the simulation, and the vertical axis corresponds to the distribution function $P$.

Fig. 4. Comparison between $K_i(n_1, n_0, t_0, \Delta n, \Delta t)$ for the displacements in the DNA model and in a lattice with an harmonic on-site potential which corresponds to the small amplitude limit of the Morse potential. Temperature $T = 300$ K, $\Delta n = 4$, $\Delta t = 20000$ t.u.
Fig. 5. Variation of $\sigma_{KL}(\Delta n, \Delta t)$ for the distribution function of the position in the nonlinear DNA model at $T = 300$ K as a function of $\Delta n$ (diamonds) and exponential fit (full line) to determine the size of the patches. $\Delta t$ has been maintained constant equal to 20,000 t.u.

However, the function $K_l(n_1)$ is not interesting by itself because, for given $\Delta n$ and $\Delta t$ it depends on the reference point $n_0$ and reference time $t_0$. But the statistical properties of $K_l(n_1)$, and in particular its various moments, can provide intrinsic characteristics of the localization in a given system because they depend only on the size of the investigated domain. We have chosen to work with the standard deviation $\sigma_{KL}(\Delta n, \Delta t)$ obtained by averaging the standard deviations of $K_l(n_1)$ for various reference points $n_0, t_0$. For the cases shown in Fig. 4, we have $\sigma_{KL}(\Delta n, \Delta t) = 0.156$ for the anharmonic lattice and $\sigma_{KL}(\Delta n, \Delta t) = 0.023$ for the harmonic lattice ($\Delta n = 4$, $\Delta t = 20,000$ t.u.). When $\Delta n$ or $\Delta t$ increase, the distribution functions are evaluated on a larger space-time domain, which tends to average the properties of different patches. As a result the variation of $\mathcal{P}(A, n_1, t_0, \Delta n, \Delta t)$ with site $n_1$ becomes smoother so that $\sigma_{KL}(\Delta n, \Delta t)$ decreases. The decay of $\sigma_{KL}$ versus $\Delta n$ or $\Delta t$ can be used to determine the characteristic size of the patches. Fig. 5 shows the variation of $\sigma_{KL}(\Delta n, \Delta t)$ associated to the position of the oscillators for a fixed $\Delta t = 20,000$ t.u. at $T = 300$ K. The fit of this curve by an exponential function

$$
\sigma_{KL}(\Delta n, \Delta t) \approx \sigma_0(\Delta t) \exp(-\Delta n/\lambda)
$$

(3)
Table 1
Characteristic size and lifetime of the localization patches in the nonlinear DNA model thermalized at two different temperatures

<table>
<thead>
<tr>
<th></th>
<th>$T = 100 \text{ K}$</th>
<th>$T = 300 \text{ K}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\lambda$ in cells</td>
<td>3.5</td>
<td>17.5</td>
</tr>
<tr>
<td>$\Delta \lambda$ in cells</td>
<td>1.5</td>
<td>2.5</td>
</tr>
<tr>
<td>$\tau$ in t.u.</td>
<td>15000</td>
<td>25000</td>
</tr>
<tr>
<td>$\Delta \tau$ in t.u.</td>
<td>20000</td>
<td>40000</td>
</tr>
<tr>
<td>$\tau$ in periods $\theta_0$</td>
<td>175</td>
<td>290</td>
</tr>
</tbody>
</table>

has been used to determine the characteristic size $\lambda$ of the patches. A similar calculation can be made to determine their lifetime $\tau$ by varying $\Delta t$ and using the fit

$$
\sigma_{KL}(\Delta n, \Delta t) \approx \sigma_0(\Delta n) \exp(-\Delta t/\tau).
$$

In both cases the exponential fit is only approximate. For the determination of the lifetime, the results suggest the existence of two time scales. The shorter scale determines most of the decay, and is used for the definition of $\tau$. The numerical results do not allow the determination of the longer time scale with a sufficient accuracy, this is why it is not given here. The variation of $\lambda$ (resp. $\tau$) for different $\Delta t$ (resp. $\Delta n$) has been used to determine the uncertainty in the values given in Table 1. The results agree with the qualitative observations that one can make on Fig. 2. At low temperature localization occurs mainly under the form of narrow breathers, while at high temperature one can observe broader hot and cold patches. The lifetime of the localization patches is always large with respect to the frequency of the vibrational modes. At extremely low temperature, in the limit of a micro-canonical system, breathers would have an infinite lifetime. When temperature is raised, their lifetime decreases because they can be destroyed in their interactions with other breathers with phonons [24]. But as temperature is raised further, the lifetime of the localization patches increases again. As discussed below these patches are generally not associated to a single breather. It is important to notice that the characteristic size of the patches, determined in our analysis is different from the correlation length $L$ that one can determine from the calculation of the correlation function $\langle (y_n(t) - \bar{y})(y_{n+\Delta t}(t) - \bar{y}) \rangle \propto \exp(-\Delta n/L)$ (where $\bar{y}$ is the mean value of $y$). While at low temperature $L$ and $\lambda$ are similar, at $T = 300 \text{ K}$, $L = 2.2$ cells is much smaller than $\lambda$. The origin of this difference will be discussed in the next section.

3.2. The origin of localization

As the nonlinear lattice has localized solutions, the discrete breathers, it is tempting to associate the localization observed in the thermalized system to these discrete breathers. A detailed observation shows that, although breathers play some role, at high temperature the phenomenon that maintains the localization is the existence of cold regions rather than the breathers themselves. This can be understood from
Fig. 6, which compares the patterns for the displacements and energy density in a high-temperature case which exhibits large localization patches. The energy density shows narrow lines of high energy density (black lines on the figure) which are only a few cells wide. These lines correspond to the discrete breathers. Many of them are vertical lines on Fig. 6, which means that the breathers are fixed in space. They are trapped by discreteness effects because their width is of the order of lattice spacing. The phenomenon is similar to the trapping of kinks by the Peierls potential, although the situation of breathers is more complicated because they have an internal degree of freedom [25,26]. These trapped breathers contribute therefore to localizing energy in space. However, trapping by discreteness is not sufficient to explain why the energy is not transferred along the lattice. Looking at Fig. 6 one can notice that some of the breathers move (oblique lines on the figure) although they are as narrow as the trapped breathers. This is particularly visible on the left side of the picture inside a large “hot spot”. The mobility of the breathers in this region is due to their thermal activation over the pinning potential. However, the breathers do not move across the whole system. They stay in a given region of space because they are reflected by the neighboring cold regions which play the role of barriers that split the lattice into nearly independent pieces.

The role of the cold regions as barriers for the transfer of energy form the hot parts of the lattice has a dual origin. First, as mentioned above, breathers cannot penetrate deeply into these regions because they would no longer be thermally activated above the pinning potential due to discreteness and they would be trapped. Second the energy of the small amplitude waves (phonon modes) is not transmitted from a hot to a cold region due to a mismatch of the vibrational spectra in these two regions as shown in Fig. 7. This mismatch is due to the strong anharmonicity of the Morse
potential. In a “cold” region, the particles are near the bottom of the Morse potential and the effective dispersion relation is close to the harmonic approximation \( \omega^2 = \omega_0^2 + 4(K/m) \sin^2(q/2) \), although, due to the anharmonicity of the potential it is broadened and shifted downward. In a “hot” region, the particles spent most of the time on the flat part of the Morse potential and the effective dispersion relation is simply \( \omega^2 = 4(K/m) \sin^2(q/2) \), i.e., the dispersion relation of a lattice without the on-site potential. Fig. 7 shows that this simplified picture gives a good account of the observed structure factor.

This analysis shows that neither the energy of the breather nor the energy of the phonons can easily escape from a hot region into a neighboring cold patch. Therefore, although it does not explain why hot and cold patches can appear, it explains that cold patches play the role of barriers that split the lattice into regions which are nearly independent in terms of energy transfer. A consequence of this picture is that, in the nonlinear lattice, thermal conductivity must depend highly on temperature because at high \( T \) the breathers, which carry a large part of the energy, are thermally excited above the barriers of the pinning potential due to discreteness. A preliminary numerical test of this conjecture has been done by observing the time dependence of the temperature profile in the lattice, starting from a step separating two regions at temperature \( T_1 \) and \( T_2 \). With \( T_1 = 260 \, K \) and \( T_2 = 210 \, K \), the spreading of the interface is much slower that with \( T_1 = 340 \, K \) and \( T_2 = 290 \, K \). Further studies are however needed before a quantitative conclusion can be drawn [27].
Fig. 8. Numerical simulation of the two-dimensional 128 × 128 lattice with Hamiltonian (5), thermalized at temperature \( T = 2.2 \) (in energy units), with the parameters \( \sigma_0^2 = 4, K = 0.05 \). The figure shows the fourth power of the energy density \( \epsilon(l,m)^4 \) with a gray scale, white corresponding to low \( \epsilon^4 = 0 \) and black to \( \epsilon^4 = 5 \) or above. Plotting \( \epsilon^4 \) rather than \( \epsilon \) enhances the contrast between the hot and cold patches. The figure superimposes 10 snapshots of \( \epsilon(l,m)^4 \), each one being separated from the previous one by 40 time units, i.e., about 13 periods of the lowest phonon mode. Therefore the figure spans a time interval of about 130 periods of the lowest phonon mode. The possibility to observe the contrast between hot and cold patches in spite of the superposition of the 10 figures shows the high stability of these patches.

3.3. Localization in a multidimensional lattice

Contrary to solitons, the existence of discrete breathers is not restricted to one-dimensional systems [1,2]. However dimensionality larger than one could restrict the importance of breathers in a physical system because it has been shown that, in this case, breathers exist only above a given energy threshold [28]. Numerical simulations of a two-dimensional system show nevertheless that breathers exist and are spontaneously formed in a two-dimensional lattice. Fig. 8 illustrates the case of the lattice with Hamiltonian

\[
H = \sum_{l,m} \frac{1}{2} \left( \frac{d u_{l,m}}{dt} \right)^2 + \frac{1}{2} K \left[ (u_{l,m+1} - u_{l,m})^2 + (u_{l+1,m} - u_{l,m})^2 \right] \\
+ \frac{1}{2} \sigma_0^2 (e^{-u_{l,m}} - 1)^2 .
\]

(5)
The indices \( l \) and \( m \) denote the sites along the \( x \)- and \( y \)-axis. The displacement at each site is characterized by a scalar variable \( u_{l,m} \), and the harmonic coupling along the \( x \)- and \( y \)-axis is isotropic. Contrary to the one-dimensional DNA model, the two-dimensional model system has not been introduced to describe a particular physical system. This why we have used dimensionless variables and temperature is measured in units of energy. Fig. 8 superimposes 10 snapshots of the energy density on the same diagram, spanning a time interval of approximately 130 periods of the lowest phonon mode. Even on this rather long time interval, one can observe regions of high energy density that coexist with others where the energy density stays low. The persistence of the contrast between these regions for a long time shows first that energy localization does exist in a two-dimensional thermalized lattice, and second that the hot and cold localization patches do not move in the lattice on such a time scale.

4. Observing nonlinear localization experimentally

The experimental observation of nonlinear localization requires an observation in real space while most of the experimental techniques for solids or macromolecules, such as spectroscopy or neutron scattering, provide information in Fourier space. Although the detection of breathers in the structure factor is theoretically possible, in practice it is hard to distinguish them from other excitations, such as nonlinear extended modes, even in a numerical experiment [29]. The current progress in experimental methods, which now allow the manipulation of a single molecule, open the possibility to observe local dynamics in a macromolecule. Using numerical simulations and a statistical mechanics analysis, we recently suggested [30] that extending to a homopolymer the experimental study of the micro-mechanical breaking of DNA performed by Essevaz-Roulet et al. [18,19] could provide an observation of nonlinear localization in real space. However, in order to limit the computation time, in our numerical tests the breaking was driven at a much higher speed than in the actual experiment so that the force applied on the molecule was about 10 times higher than the actual force. Since these first investigations, the gap between the theoretical analysis and the experiment has been significantly narrowed from both sides. The experiment has been conducted at higher speed [31] and, in the numerical study, we have reduced the speed of the breaking by more than two orders of magnitude, bringing the pulling force close to the experimental value. The theoretical results suggest that some of the force fluctuations observed in the high-speed experiments could come from localization patches in DNA dynamics. Here we briefly review the experimental results and our previous theoretical study, and we present and discuss the new numerical results.

The experiment [18,19] is schematized in Fig. 9a. One strand of a long DNA molecule is chemically linked to a glass plate while the other strand is attached to a glass bead which is pulled by a micro-needle. The motion of the bead opens the double-helix by breaking the base pairs connecting the two strands and the force required for the opening is recorded by monitoring the flexion of the micro-needle.
Fig. 9 shows a simplified view of the experiment as it appears when we analyze it with our simplified DNA model. As we introduce only one degree of freedom per base pair, it is equivalent to consider that one strand is fixed. The first base pair is connected to an elastic spring which models the micro-needle. Pulling on the spring with a force $F$ adjusted so that the end of the spring connected to DNA moves at constant speed $v$, we monitor $F$ in a numerical simulation where the molecule is thermalized at temperature $T$. With our system of units, the force unit (f.u.) is equal to $1602 \times 10^{-12}$ N (1602 pN). In our most recent numerical simulations we chose a pulling speed $v = 10^{-5}$ Å/t.u. (98 mm/s). With the model parameters presented previously we observe a propagation of the breaking for a force of the order of 0.012 f.u., i.e., 19 pN while the experiment, performed at lower speed, detects forces of 10 to 12 pN. It is important to notice that the pulling force is smaller than the critical force necessary to break the chemical bonds connecting the two DNA strands. Moreover the lifetime of a base pair under traction is several orders of magnitude larger than that of the period of vibration of the base-pair stretching mode. This indicates that, on the molecular scale, the mechanical denaturation of DNA is a slow process which is thermally activated. Therefore one can expect that the existence of hot and cold localization patches will locally make the breaking easier or harder. This is what we observe numerically, even with a homopolymer, i.e., a molecule where all base pairs are identical. This is attested by fluctuations of the force $F$ and an irregular propagation of the breaking along the molecule as shown in Figs. 10 and 11 obtained from a simulation of 1024 base pairs for $4 \times 10^7$ t.u., i.e., 0.4 μs. Such a simulation, very long at the time scale of molecular dynamics, is only possible with a simple model for the DNA molecule and it is presently completely out of reach of conventional molecular dynamics.

For a theoretical analysis, it is convenient to consider separately two aspects, the breaking of the base pair which is at the front (denoted by its index $M$ along the chain) under the force $F_B$ exerted by the denaturated strand on this base pair itself (Fig. 9b), and how this local force is transmitted to the lever by the denaturated strand, giving rise to the force $F$ which is measured. The breaking of the $M$th base pair under the stretching force $F_B$ can be viewed as a chemical dissociation along the
reactive coordinate $y_M$ for a system that comprises the $N-M$ bases that have not been broken. It is described by the Hamiltonian

$$H_1 = \sum_{j=M+1}^{N} \frac{1}{2} m \left(\frac{dy_j}{dt}\right)^2 + W(y_j, y_{j-1}) + V(y_j) + \left[\frac{1}{2} m \left(\frac{dy_M}{dt}\right)^2 + V_{ef}(y_M)\right],$$

where $V_{ef}(y_M) = D[\exp(-x y_M) - 1]^2 - F_B y_M$ is an effective potential which has a metastable minimum for $y_M \approx 0$, corresponding to the closed state of the $M$th base pair. The breaking of the pair is obtained when $y_M$ overcomes the barrier of $V_{ef}$ under the effect of fluctuations coming both from the thermal bath and from the rest of the molecule due to the coupling potential $W(y_M, y_{M-1})$. The fluctuations transmitted by the molecule have a complex spectrum and their amplitude may depend very significantly on the position along the chain, which explains why the denaturation does not proceed at uniform pace.

A quantitative calculation of the lifetime $\tau$ of the base pair $M$ amounts to solving Kramers problem in the presence of a colored noise resulting from the nonlinear dynamics of the molecule, but an estimation of $\tau$ can be obtained by the multidimensional transition state theory [32] which gives [30]

$$k_{TST} = \frac{1}{\tau} = \frac{\langle\delta(y_M - Y_1)\hat{y}_M \theta(\hat{y}_M)\rangle}{\langle 1 - \theta(y_M - Y_1)\rangle},$$

(7)
Fig. 11. Gray scale picture of the stretching of the base pairs observed in the molecular dynamics simulation of Fig. 10. The horizontal axis extends along the 1024 base pairs. The vertical axis is the time axis. The figure shows a time interval of $3.7 \times 10^6$ t.u. i.e., about 4 μs. The gray scale extends from white ($y=0$) corresponding to base pairs which are closed to black ($y>3$ Å) corresponding to base pairs which are highly stretched or broken. The black region at the left of the figure is the denatured part of the molecule.

where $Y_1$ is the base-pair stretching corresponding to the maximum of $V_{\text{eff}}$, $\theta$ is the step function, and the averages $\langle \cdots \rangle$ have to be calculated with Hamiltonian $H_1$. Introducing the transfer integral operator associated to the homogeneous part of $H_1$ ($j=M+1\ldots N$), in the limit of large $N$ where only the lowest eigenvalue contributes, we get

$$k_{\text{TST}} = \frac{1}{\tau} = \frac{1}{\sqrt{2 \pi \mu \beta}} \frac{\exp[-\beta V_{\text{eff}}(Y_1)]\phi_0(Y_1)}{\int_{-\infty}^{Y_1} \exp[-\beta V_{\text{eff}}(y_M)]\phi_0(y_M)\,dy_M},$$

where $\phi_0$ is the eigenfunction of the transfer integral operator associated to its lowest eigenvalue. Although the limit of large $N$ is formally taken in the calculation, actually the results only depend on the base pairs which are within the correlation length of
the dynamics of the fluctuations, i.e., less than 20 base pairs at 320 K. For the model parameters of DNA a continuum limit approximation for the transfer integral operator is not valid and \( \phi_0 \) has to be obtained numerically [13]. The calculation is the same as the one that has been performed to study the statistical mechanics of DNA denaturation. The expression of \( \tau \) explains why the micro-mechanical denaturation of DNA can be very sensitive to energy localization because, in addition to the usual Arrhenius factor which already generates a fast dependence of \( \tau \) upon temperature, the temperature dependence is magnified by the very fast dependence of \( \phi_0(Y_1) \) upon \( T \). The function \( \phi_0 \) is highly peaked, and \( Y_1 \) corresponds to a point in its tail where the function is small. As the width of \( \phi_0 \), which determines the mean stretching \( \langle y \rangle \) of the base pairs, varies significantly with \( T \), the relative value of \( \phi_0(Y_1) \) can exhibit large variations for small variations of \( T \), or, equivalently with small variations of the local average stretching \( \langle y \rangle \).

The high sensitivity of the breaking to local fluctuations explains the patterns observed in Fig. 11 and the large force fluctuations observed in Fig. 10. Although on average the breaking progresses along the molecule, the simulations shows that sequences of fast opening when the fracture tip reaches a hot patch can be followed by partial reclosing because the breaking has released the stretching of the pulling spring and temporarily reduced the force. The actual experiment is performed on natural DNA which is inhomogeneous due to the genetic information encoded in the base sequence. The large fluctuations of the force, which are recorded, can be correlated to the existence of domains which are easier or harder to break because their content in \( A-T \) base pairs (with two hydrogen bonds) or \( G-C \) (with three hydrogen bonds) is different. However, in the fastest experiments, additional fluctuations of the pulling force, superimposed to the these large variations related to base content, are systematically observed [31]. Our results suggest that these fast fluctuations could be due to the localization patches, i.e., to the temporary inhomogeneities of the thermal fluctuations that have been discussed in the previous sections. Consequently, although they have not been performed on a homopolymer, the latest micro-mechanical breaking experiments on DNA could well have observed the effects of nonlinear localization. This conclusion must however be taken with care because the experiment involves many processes which are not included in our simple model, and in particular the fluctuations of the bending and twist of the helix which are associated to the Brownian motion of the DNA segment in the solution. However, as the persistence length of DNA is large (about 500 Å) and the undenatured part of the molecule is free to rotate, we can expect these twist fluctuations to play a minor role in this case.

5. Conclusion

The study of thermalized nonlinear lattices shows that the thermal fluctuations do not prevent the formation and existence of discrete breathers, although their lifetime is limited by their interactions with other breathers and phonon modes. Moreover thermalized
nonlinear lattices show “localization patches”, i.e., regions which have different local distribution functions for the dynamical variables, which persist for a time that is long with respect to the microscopic time scales of the system. Measuring the distances in probability space between the local distribution functions evaluated on domains of various size and duration, we were able to evaluate the evolution of nonlinear localization with temperature. While at low temperature localization is mainly due to individual discrete breathers, at high temperature we find larger “hot” regions in which breathers are trapped and move back and forth. They are excited by the thermal fluctuations above the barriers due to lattice discreteness. The hot patches are separated by cold regions which act as barriers for the energy transfer in the system. Breathers cannot penetrate into these cold regions due to discreteness effects and the spectrum of the nonlinear phonon modes of the hot patches fall in the gap of the cold regions, reducing the penetration of nonlocalized waves as well.

The mechanisms leading to nonlinear localization should have various experimental consequences. First numerical tests show that, for soft on-site potential $V(y_n)$, the thermal conductivity depends highly on temperature. An analysis of this property is in progress [27]. Second, it should be possible to observe the existence of the localization patches in real space with the recent experimental methods which allow the manipulation of a single molecule. Biological molecules such as DNA are good candidates for these studies. However they are not as regular as crystals and nonlinear localization must be considered in conjunction with localization induced by the inhomogeneities of the macromolecule. Our studies of inhomogeneous systems suggest that both sources of localization cooperate. Inhomogeneities select sites where larger vibrational amplitudes will tend to concentrate and nonlinearity assists the focusing of the energy in these regions which become long-lived “hot spots” in the lattice.

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References

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