Elasticity of strongly stretched ssDNA

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Abstract

We present a simple model which describes elastic response of single-stranded DNA (ssDNA) to stretching, including the regime of very high force (up to 1000 pN). ssDNA is modelled as a discreet persistent chain, whose ground state is a zigzag rather than a straight line configuration. This mimics the underlying molecular architecture and helps to explain the experimentally observed staturation of the stretching curve at very high force.

Key words: DNA, elasticity

1 Introduction

Over the recent years, impressive progress has been made in understanding of the physics of DNA. To a large extent, this development was due to the introduction of novel micromanipulation techniques suitable for study of the mechanical response of a single molecule [1][2]. The mechanical properties of double-stranded DNA (dsDNA) have been studied in pioneering experiments of Smith et al [1]. These experiments agree remarkably well with Worm-Like Chain (WLC) model which describes DNA as an elastic rod, whose bending modulus is proportional to chain persistence length \( l_p \) (\( l_p \approx 50 \text{nm} \) for dsDNA, which is the only adjustable parameter of the model) [3].

In the case of single-stranded DNA (ssDNA) and RNA molecules the choice of an adequate elastic description remains an open problem. On the one hand, ssDNA and RNA were traditionally described by Freely Joint Chain model (FJC). Its extensible version has been originally used for fitting of the early ssDNA stretching data [2]. On the other hand, the chemical structure of ssDNA strongly support the picture with a finite bending modulus, reminiscent of WLC model. However, being a continuous model, the WLC description is unlikely to be valid in the regimes when discrete nature of chemical bonds
becomes relevant (e.g. for a sufficiently high stretching force). To overcome these limitations, Discreet Persistent Chain (DPC) model has been proposed for ssDNA by Storm and Nelson [4]. Interestingly, WLC itself was introduced as a continuous limit of a similar discrete model, originally proposed back in late 40s by Kratky and Porod (KP) [5]. Authors of Ref. [4] succeeded in calculating the response of DPC to an arbitrary stretching force, by combining the Transfer Matrix method with a variational procedure. Nevertheless, the discreet model yields only a marginal improvement of the fit of ssDNA force–extension curve, compared to WLC and FJC cases.

In order to improve the fitting, the extensible versions of the above models are typically used, i.e. the linear deformations of the bonds are introduced. However, the AFM experiments done in the limit of very high force (up to 1000 pN) [6], exhibit surprising saturation of the end-to-end distance at certain value above the chain counter length. Any model which treat deformations of the ssDNA backbone in a linear manner, is unable to capture this phenomenon. The experimental behavior is however consistent with results of detailed \textit{ab-initio} calculations [7]. In this paper, we propose a simple model motivated by actual microscopic architecture of ssDNA. Without introduction of extra fitting parameters, our “zigzag” model adequately describe both low- and high-force regimes of ssDNA stretching.

2 Zigzag model for ssDNA elasticity

Discreet Persistent Chain (DPC), also known as Kratky and Porod (KP) model, has the following Hamiltonian:

\begin{equation}
H = \sum_i \left[ \frac{J}{2} \Theta_{i,i+1}^2 - b f \cdot \hat{t}_i \right]
\end{equation}

Here $\hat{t}_i$, is $i$-th bond orientation, $b$ is (fixed) bond length, $\Theta_{i,i+1}$ is the angle between $i$–th and $i + 1$-th bonds (i.e $\cos \Theta_{i,i+1} = \hat{t}_i \cdot \hat{t}_{i+1}$), and $f$ is external stretching force. Interestingly, two other common models can be obtained from DPC Hamiltonian, by taking limits of zero bond length (WLC), or zero coupling $J$ (FJC).

At the atomistic level, the backbone conformation of ssDNA is often parameterized by several torsional angles per nucleotide, as shown in Figure [1]. From this point of view, WLC and DPC models describe small deviations from the ground state configuration. However, at the microscopical level, all the valent angles have certain preferred values different from 180$^\circ$. The minimal generalization of DPC model which mimics this observation is a chain whose ground
state is zigzag (all-trans) configuration:

\[ H = \sum_i \left[ \frac{J}{2} \left( \Theta_{i,i+1} + (-1)^i \Theta_0 \cos \psi_{i,i+1} \right)^2 - bf \cdot \mathbf{t}_i \right]. \]  

Here \( \psi_i \) is the torsional angle associated with rotation of \( i-th \) bond. For simplicity, we assign the same preferred angle \( \Theta_0 \) to each bond pair. Surprisingly, this minimal model results in a significant improvement over the previous attempts to describe the experimentally observed large force behavior of ssDNA.

3 Mapping on DPC model

In order to calculate the stretching curve of the "zigzag" chain, we note that the model can be mapped back onto DPC model, with renormalized parameters. Let us consider a chain consisting only of odd (or only even) nodes of the zigzag (i.e. \( \ldots -i" - (i + 2" - (i + 4" - \ldots \). The ground state of this chain is a straight line, but the bond length (even without thermal fluctuation) is a function of applied force: \( b^* = 2b \cos \theta^* \), where \( \theta^*(f) \) is the preferred bond orientation angle \( \theta_i \), with respect to the direction of \( f \). In ground state configuration (i.e. zigzag) \( \theta_i = (-1)^i \theta^* \) The value of \( \theta^* \) may be obtained by minimizing the Hamiltonian, at given stretching force:

\[ H (\theta^*) = \sum_i \left[ \frac{J}{2} (2\theta^* - \Theta_0)^2 - fb \cos \theta^* \right] \]  

In the limit of small \( \Theta_0 \), we obtain::

\[ \theta^* (f) = \left( \frac{bf}{2J} + 1 \right)^{-1} \frac{\Theta_0}{2} \]  

(4)
\[ b^*(f) = 2b \cos \Theta^* \approx 2b \left( 1 - \left( \frac{bf}{2J} + 1 \right)^{-2} \frac{\Theta^2}{8} \right) \] (5)

It is also easy to demonstrate that the renormalized coupling in the final DPC Hamiltonian will be \( J^* = J/2 \). The parameters of the renormalized model are related to the experimentally observable persistence length as \( l_p = b^*(0) J^* / kT \approx Jb / kT \). We can now use DPC model to calculate the stretching curve \( z/L = x(f) \), and include the effect of renormalization in the following manner:

\[ \frac{z}{L} = \frac{b^*(f)}{b^*(0)} x(f) \approx \left( 1 + \left[ 1 - \left( 1 + \left( b \frac{l_p}{kT} \right)^2 \frac{fl_p}{2kT} \right)^{-2} \frac{\Theta^2}{8} \right] x(f) \right) \] (6)

Here \( z \) and \( L \) are end-to-end distance and the original chain counter length, respectively. Since the discreetness of DPC is only marginally important, one can relate \( x \) to \( f \) with a simple interpolation formula proposed by Marko and Siggia for continuous WLC model:

\[ \frac{fl_p}{kT} = \frac{1}{4} \left( \frac{1}{(1-x)^2} - 1 \right) + x \] (7)

Fig. 2. Stretching behavior of ssDNA, given by the zigzag model. Experimental points are from Refs \[6\] (circles) and \[2\] (diamonds). Insert: Fitting of the experimental data with extensible FJC, WLC and DPC models \[4\].

The resulting stretching curve is shown in Figure 2. It is remarkable that the very good fit can be achieved with the same number of free parameters, as in
the earlier models: \( b \) (which is fixed at its physical value of a typical chemical bond length, \( 0.1 \text{nm} \)), ssDNA persistence length \( l_p \approx 0.85 \text{nm} \) (extracted from the moderate force stretching behavior). The only fitting in our model is angle \( \Theta_0/2 \approx 25^0 \) which essentially replaces the bond rigidity commonly used in the extensible versions of classical models.

4 Conclusions

In conclusion, we proposed a new model for ssDNA elasticity. It differs from the earlier ones by an explicit account for certain features of microscopic architecture of the chain backbone. Qualitatively, our model attribute the ultra-high-force stretching behavior to the perturbations to the valent angles rather than deformations of the bonds themselves. This implication can be directly checked by the first principle calculations.

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