

Reply to ‘‘Comment on ‘Writhe formulas and antipodal points in plectonemic DNA configurations’’’

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We persist in considering that, for a wide range of (experimentally available) forces and torques, evaluating the writhe of a DNA molecule in magnetic tweezers experiments should not be done with Fuller’s formula. We propose a tentative plot of the limit of applicability of Fuller’s formula in the (force, torque) plane.

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I. INTRODUCTION

The comment by Samuel *et al.* [1] repeats and discusses what was published in a previous paper of theirs [2]. The disagreement is about the computation of the writhe of a space curve, an important quantity in single molecule studies of DNA, which is given by the Călugăreanu-White double integral Wr_{CW} [3]. Fuller has shown [4] that a single integral formula,

$$Wr_F(\Gamma, \Gamma_0) = Wr(\Gamma_0) + \frac{1}{2\pi} \int_0^{\sigma_L} \frac{\mathbf{t}_0(\sigma) \times \mathbf{t}(\sigma)}{1 + \mathbf{t}_0(\sigma) \cdot \mathbf{t}(\sigma)} \cdot \frac{d}{d\sigma} \times [\mathbf{t}_0(\sigma) + \mathbf{t}(\sigma)] d\sigma \quad (1)$$

could be used under certain assumptions, which are in general not met by space curves (i.e., DNA configurations). For a fluctuating DNA molecule under tension and torsion, the partition function is computed using either the (correct) double integral (and is denoted Z_{SAWLC}), or Fuller’s single integral (and is denoted Z_{WLRC}).

Samuel *et al.* main point in their comment, which is a conjecture, is that even if for lots of DNA configurations Fuller’s formula does not yield the correct value, their Boltzmann weight is negligible and consequently the partition function is dominated by configurations for which Fuller’s formula holds. They claim that this happens for a wide range of forces and torques. In such cases we have

$$Z_{SAWLC} \approx Z_{WLRC}. \quad (2)$$

The point is to elucidate over which range of forces and torques Z_{WLRC} is a good approximation to Z_{SAWLC} . We note that this question was already studied numerically in [5] for the case with no applied torque ($n=0$ turns imposed on the magnetic bead, $n \equiv \Delta Lk$).

II. CASE WITH NO IMPOSED ROTATION ($n=0$)

In [5] the second moment of Wr_{CW} and Wr_F have been computed as functions of the applied tension. The results are summarized in their Fig. 8, where we see that the two curves (for $\langle Wr_{CW}^2 \rangle$ and $\langle Wr_F^2 \rangle$) differ at low forces and join at high force. We introduce the relative difference

$$\delta(F, n) = \frac{\langle Wr_F^2 \rangle - \langle Wr_{CW}^2 \rangle}{\langle Wr_{CW}^2 \rangle}, \quad (3)$$

as a test for the applicability of Fuller’s formula. From Fig. 8 of [5], we have $\delta(0.1 \text{ pN}, 0) = 40\%$ which means that in the case of zero torque, $F \leq 0.1 \text{ pN}$ is definitively outside the range for which Eq. (2) is a good approximation. Still, we note that the difference between the two curves is vanishing as F increases, being 20% at $f \equiv AF/(k_B T) = 2$ and 10% at $f = 3$ ($A = 50 \text{ nm}$ is the bending persistence length of DNA, k_B is the Boltzmann constant, and T is the absolute temperature). Anyhow our paper [6] was about the case where a substantial amount of rotation ($n \gg 1$) is imposed on the magnetic bead, generating supercoiling in the DNA molecule.

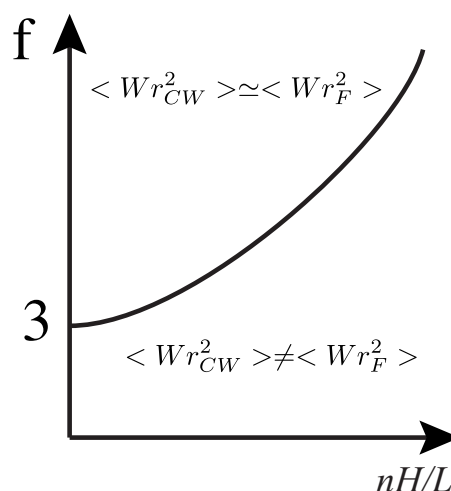


FIG. 1. The curve shows the values of the applied tension $f = FL_p/(k_B T)$, as a function of the supercoiling ratio nH/L , for which the error δ , between the second moments $\langle Wr_{CW}^2 \rangle$ and $\langle Wr_F^2 \rangle$ of the writhe, is 10%. The molecule length is L and $H = 3.6 \text{ nm}$ is the DNA helical repeat length. Under the curve, $\delta > 0.1$ and consequently Fuller’s formula should not be used.

III. CASE WITH IMPOSED ROTATION ($n > 0$)

In [6] we showed, from geometrical and topological arguments, that for a curve with plectonemes the values given by Wr_F and Wr_{CW} differ by up to 100%. This is yet another source of discrepancy (compared to what was discussed in [5]) for Fuller's formula. We consequently tend to think that, at fixed F , δ increases with n .

Consider now a DNA molecule subjected to relatively "high" forces such as $F=1, 2$, or 3 pN. If a large enough torsional constraint is imposed, the molecule exhibits plectonemes. These plectonemic configurations are stable equilibrium configurations, i.e., most probable configurations (ground states) in the sense of statistical mechanics. We tend to think that these configurations dominate the partition function. Consequently, when $F > 1$ pN and n large enough to

have a well-grown plectonemic phase, we conjecture that $\delta(F, n)$ is substantially above 10% and that approximation (2) is incorrect.

IV. CONCLUSION

We have seen that at $n=0$ turns and $f=3$ the error δ is 10% and that when turns are imposed on the bead, δ is increasing. In order to state things in a more quantitative way and to resolve the dispute over the applicability of Fuller's formula, we propose that δ be computed for various values of n and f and that the curve $f_{10\%}(n)$, for which δ is 10%, be plotted in the (f, n) plane. Figure 1 shows a rough attempt to draw such a curve. It starts at $f_{10\%}(0)=3$ and its parabolic shape stems from the threshold for plectonemic configuration $f \propto n^2$ given in [7].

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