# Comment on "Flexibility of short DNA helices with finite-length effect: From base pairs to tens of base pairs" 

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While analyzing the persistence length of DNA atomistic simulations Wu et al. [J. Chem. Phys. 142, 125103 (2015)] introduced an empirical formula to account for the observed length-dependence. In particular they found that the persistence length increases with the distance. Here, we derive the formula by Wu et al. using a non-local twistable wormlike chain which introduces couplings between distal sites. Finally, we show that the same formula can account for the length-scale dependence of the torsional persistence length and is, in fact, applicable to any kind of polymer model with non-local couplings.

In Ref. 1 Wu et al. analyzed the bending flexibility of short DNA segments (of up to 50 bps ) by molecular dynamics and Monte Carlo simulations. They found that DNA is softer at short lengths, which they accounted for with the empirical formula

$$
\begin{equation*}
l_{B}(m)=l_{B}^{\infty}-\frac{A}{B+m}, \tag{1}
\end{equation*}
$$

where $l_{B}(m)$ is the persistence length of a sequence of $m$ base pair-steps, $l_{B}^{\infty}$ the asymptotic persistence length and $A, B$ some fitting parameters. In this comment we show that the above formula is consistent with the asymptotic expansion of the non-local Twistable Wormlike chain (nITWLC) ${ }^{2}$ which gives

$$
\begin{equation*}
l_{B}(m)=l_{B}^{\infty}\left(1-\frac{B}{B+m}\right)+\ldots \tag{2}
\end{equation*}
$$

with the dots indicating higher order corrections. Such expansion is valid both for (1) the local persistence length of a long DNA molecule measured from the tangent-tangent correlation of two base pairs separated by $m$ steps and for (2) the persistence length obtained from the correlation of the endpoint tangent vectors for a DNA molecule of finite length $m$. The latter is the quantity analyzed by Wu et al. ${ }^{1}$. Furthermore, we will show, that an expansion of the type (2) is also valid for the torsional persistence length. Note, that expression (2) contains one parameter less than (1) implying that $A=l_{B}^{\infty} B$. This relation holds approximately for the values reported by Wu et al. ${ }^{1}: l_{B}^{\infty}=50 \mathrm{~nm}, A=450 \mathrm{~nm}$ and $B=10$.

Non-local couplings - The nITWLC describes DNA configurations using the three rotational densities tilt, roll (the two bending modes), and twist indicated with $\tau_{n}, \rho_{n}$, and $\Omega_{n}+\omega_{0}$ respectively, with $n=1,2, \ldots N$ enumerating the base pairsteps along the chain. The twist is subdivided into a constant intrinsic twist density $\omega_{0}=1.75 \mathrm{~nm}^{-1}$, corresponding to one turn of the helix every 10.5 base pairs, and a fluctuating excess twist $\Omega_{n}$. While in the ordinary TWLC couplings are strictly local and the energy is quadratic in $\tau_{n}, \rho_{n}$, and $\Omega_{n}$, the nlTWLC introduces couplings between distal sites, such as for instance $\tau_{n} \tau_{n+m}$ with $m>0$. Non-local couplings have been

[^0]observed in several all-atom simulations ${ }^{3,4}$ and they typically extend to three flanking dinucleotide steps ${ }^{2}$.

Persistence lengths - The nlTWLC predicts similar length scale dependence of both the bending and the torsional persistence length, hence we discuss both. In the limit of an infinite long chain $N \rightarrow \infty$ the correlation functions between two sites separated by $m$ base pairs decay with $m$-dependent persistence lengths given by the following expressions ${ }^{2}$ :

$$
\begin{equation*}
\frac{1}{l_{\chi}}=\frac{1}{m \pi} \int_{-\pi / 2}^{+\pi / 2} \frac{\sin ^{2}(m y)}{\sin ^{2} y} f_{\chi}(y) d y \tag{3}
\end{equation*}
$$

with $\chi=\{B, T\}$ labeling either the bending or the torsional persistence length. The variable $y=\pi q / N$ is the rescaled momentum and $f_{\chi}(y)$ are functions of the bending fields (tilt and roll) and the excess twist field for the $l_{B}$ and $l_{T}$ respectively. The full expressions are reported in Ref. 2. We also note, that while the former expression contains certain approximations, the latter is exact. The functions $f_{\chi}(y)$ are symmetric in $y$, so for small $y$ the following expansions hold

$$
\begin{equation*}
f_{\chi}(y) \approx f_{\chi}(0)+\frac{1}{2} f_{\chi}^{\prime \prime}(0) y^{2}+O\left(y^{4}\right) \tag{4}
\end{equation*}
$$

To proceed further it is convenient to split $f_{\chi}(y)$ in Eq. (3) into two terms, a constant $f_{\chi}(0)$ and the increment $f_{\chi}(y)-$ $f_{\chi}(0)$ and integrate these two terms separately. That way, one obtains (to simplify the formula we omitted the integration boundaries)

$$
\begin{align*}
\frac{1}{l_{\chi}} & =\frac{f_{\chi}(0)}{m \pi} \int \frac{\sin ^{2} m y}{\sin ^{2} y} d y+\int \frac{1-\cos (2 m y)}{2 m \pi} \frac{f_{\chi}(y)-f_{\chi}(0)}{\sin ^{2} y} d y \\
& =f_{\chi}(0)\left(1+\frac{B_{\chi}}{m}\right)+O\left(e^{-m / \lambda}\right) \tag{5}
\end{align*}
$$

where we have used

$$
\begin{equation*}
\int_{-\pi / 2}^{\pi / 2} \frac{\sin ^{2} m y}{\sin ^{2} y} d y=m \pi \tag{6}
\end{equation*}
$$

and the definition

$$
\begin{equation*}
B_{\chi} \equiv \frac{1}{2 \pi f_{\chi}(0)} \int_{-\pi / 2}^{+\pi / 2} \frac{f_{\chi}(y)-f_{\chi}(0)}{\sin ^{2} y} d y \tag{7}
\end{equation*}
$$

The oscillatory term $\cos (2 m y)$ in (5) yields an exponentially small factor proportional to $\exp (-m / \lambda)$, where the characteristic decay length $\lambda$ can be obtained from the poles of

Figure 1. Bending and torsional persistence lengths deduced from Monte Carlo simulations of the nITWLC (black dots). The left-hand panels show $m$-dependent bending (a) and torsional (b) persistence lengths for a chain of length $N=200$, while the right-hand panels show end-to-end bending (c) and torsional (d) persistence length ( $m=N$ ) for various chain-lengths. Non-local energetic couplings are included up to third closest neighbors and are chosen to induce significant length-scale dependence, parameters are given in Table I. Fits of (2) to the respective correlation lengths are shown as blue and green lines.
the integrand ${ }^{2}$. We note that the integral in (7) is convergent, in particular (4) implies that the integrand does not diverge as $y \rightarrow 0$. Finally, inverting Eq. (5) one gets (2) with $l_{B}^{\infty}=1 / f_{B}(0)$ and $B=B_{B}$.

While so far we have considered the limit $N \rightarrow \infty$ we can extend the analysis for a sequence of finite length. For brevity we limit the discussion to the bending persistence length. For finite $N$ this is given by ${ }^{2}$

$$
\begin{equation*}
\frac{1}{l_{\mathrm{B}}}=\frac{a}{2 m}\left\langle\left(\sum_{n=0}^{m-1} \tau_{n}^{*}\right)^{2}+\left(\sum_{n=0}^{m-1} \rho_{n}^{*}\right)^{2}\right\rangle \tag{8}
\end{equation*}
$$

where $\tau_{m}^{*}$ and $\rho_{m}^{*}$ are related to the original variables tilt and roll by a linear transformation ${ }^{2}$. In particular, as in Ref. 1, we are interested, in the case $m=N$, where $l_{\mathrm{B}}$ is obtained from the tangent-tangent correlation function between the two ends of the chain. On general grounds the averages in (8) will produce a bulk type term extensive in $m$ and boundary corrections $\langle X\rangle=m \Gamma_{1}+\Gamma_{2}+\ldots$, with $X$ indicating the terms averaged in (8). Such expression produces again the expansion (2).

Monte Carlo simulations- Figure 1 shows an example of both torsional and bending persistence lengths obtained from Monte Carlo simulations of the nITWLC compared to fits with Eq. (2) (solid lines). Left plots are for $N=200$ and finite $m$, while the right plot for sequences of finite length $m=N$. As expected the asymptotic persistence lengths are the same in these two cases, as both converge towards the same $l_{\mathrm{B}, \mathrm{T}}^{\infty}$ for large $m$. However, the $B_{\chi}$ are determined by the boundary contributions of short segments (small $m$ ). These contributions are manifestly different when comparing a partial segments located within a larger chain ( $m \ll N$ ) and segments spanning the entire chain ( $m=N$ ), as the latter case lacks any couplings spanning beyond the considered range.

Static contributions - Thus far we have solely considered models in which the persistence length only depends on the thermal bending fluctuations of the molecule. However, it is well established, that the ground-state of a DNA molecule is not straight, but exhibits significant static bending. These bending components will further expedite the decorrelation
of tangents. It has been shown ${ }^{5}$, that the bending peristence length can be decomposed into the dynamic component $l_{D}$ determined by thermal fluctuations and the static component $l_{S}$ as

$$
\begin{equation*}
\frac{1}{l_{\mathrm{B}}}=\frac{1}{l_{D}}+\frac{1}{l_{S}} . \tag{9}
\end{equation*}
$$

When considering a sufficiently large chain, one can define
Table I. Real-space couplings used in the Monte Carlo simulation shown in Fig. 1. $X_{k}$ indicates the couplings between sites displaced by $k$ base pair-steps. We used an isotropic model with bending stiffness $A$ and torsional stiffness $C$. The asymptotic bending- and twist-stiffness according to Eq. (2) are indicated by $X^{\infty}$. For the intrinsic twist density and discretization length $\omega_{0}=1.75 \mathrm{~nm}^{-1}$ and $a=0.34 \mathrm{~nm}$ were used for respectively. Since the bending modes are expressed as rotational densities the the couplings are expressed as length in units of $n m$.

|  | $X_{0}$ | $X_{1}$ | $X_{2}$ | $X_{3}$ | $X^{\infty}$ |
| :---: | :---: | :---: | :---: | :---: | :---: |
| $A$ | 25 | 14 | 5 | 2 | 51 |
| $C$ | 40 | 25 | 8 | 2 | 110 |

the average $m$-dependent static peristence length by considering a sequence ensemble. We assume that in this ensemble averaging produces uncorrelated static bends. Following this assumption $l_{S}$ is taken $m$-independent, while for the dynamic component (which is of thermal origin) Eq. (5) still holds. Hence we find

$$
\begin{equation*}
\frac{1}{l_{B}}=\frac{1}{l_{D}^{\infty}}\left(1+\frac{B_{D}}{m}\right)+\frac{1}{l_{S}}, \tag{10}
\end{equation*}
$$

which ultimately gives Eq. (2) with

$$
\begin{equation*}
\frac{1}{l_{B}^{\infty}}=\frac{1}{l_{D}^{\infty}}+\frac{1}{l_{S}} \quad \text { and } \quad B=\frac{l_{B}^{\infty}}{l_{D}^{\infty}} B_{D} \tag{11}
\end{equation*}
$$

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