Kafri, Mukamel, and Peliti Reply: The Comment of Hanke and Metzler questions the validity of the analysis presented in [1] to DNA chains of finite length as used in experiments. Their argument is that for the analysis to be valid “each of the three segments going out of a vertex must be much longer than the persistence length \( \ell_p \) of this segment”. By using the persistence lengths \( \ell_p(L) \sim 40 \text{Å} \) for a single strand and \( \ell_p(H) \sim 500 \text{Å} \) for a double helix (bound segment) they arrive at the conclusion that in order to observe the asymptotic behavior found in [1] one needs chains which are far longer than those studied experimentally.

This assertion constitutes a misunderstanding of the analysis given in [2]. In this analysis one considers a loop interacting with the rest of the chain and not just with the vicinal double helices. Thus, in [2] each of the two lines attached to the loop is in fact composed of an alternating sequence of bound segments and denaturated loops. It may be viewed as a stick and joint structure, whereby adjacent double helices (which may be considered as rigid rods as they are shorter than \( \ell_p(H) \)) are loosely attached to each other via an open loop (see Fig. 1). Thus, the “rest of the chain” as considered in reference [2] is in fact a random rod structure with a persistence length given by the length of the rod connecting two loops. This length can be easily estimated from the analysis of Poland and Schera and its generalization as given in [2]. It can be shown that the probability distribution of rods of length \( k \) at the transition is \( P(k) \sim (w/s)^k \). Here \( w = \exp(\beta M E_0) \) is the Boltzmann weight of a bound pair with energy \( -E_0 \) at the melting temperature, \( 1/\beta M \), and \( s \) is a non-universal geometrical factor. This is an exponentially decaying distribution with a typical length of order \( \xi \sim 1/|\ln(w/s)| \). This length has nothing to do with the persistence length of the bounded segments and in fact it is far shorter (of the order of a small number of base pairs). An estimate of this length can be obtained using Eq. 4 of [2] at the transition

\[
\frac{s}{w} = \sum_{k=1}^{\infty} \frac{1}{k^c} + 1. \tag{1}
\]

With the estimated value of \( c = 2.115 \) (in three dimensions) this yields \( \xi \approx 1.07 \) in units of \( \ell_p(L) \). Note that this length is non-universal and it depends on the details of the model, such as the statistical weight of small loops, the stacking interactions and other details. However, these features are not expected to change this length considerably. Therefore, the criticism expressed in the Comment is not valid and the analysis in the Letter is applicable to finite chains of the length studied experimentally. In reference [3] the detailed structure of the “rest of the chain” is ignored when the self-avoiding interaction is considered. However, as argued in [2] this assumption is reasonable and should yield a good estimate of the effect of self-avoiding interactions.

A strong support for this picture is provided by numerical simulations of Causo et al. [3] and Carlon et al. [4] of chains of finite length in which the self avoiding interactions are fully taken into account. In both studies the melting transition was found to be first order, compatible with \( c > 2 \) as found in [2]. In [4] the exponent \( c \) is evaluated directly for chains of length 50-200 monomers (each monomer corresponds to \( \ell_p(L) \) namely to about 8 base pairs). Moreover, the inclusion of the different stiffnesses of the bound and unbound segments (in simulations persistence length ratio, \( \ell_p(H)/\ell_p(L) \), was taken to vary between 1 and 10) did not change the estimate significantly. The fact that the observed \( c \) is consistent with that obtained by reference [2] strongly supports the basic assumptions behind this analysis. It also indicates that the scaling behavior predicted in [2] may be observed in finite chains of lengths between hundreds to thousands base pairs, which is the experimentally relevant range.

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FIG. 1: Schematic representation of a microscopic configuration of the DNA molecule. Here the flexibility of the “rest of the chain” emerges from the presence of loops which connect short but more rigid bound segments.