

Emergence of Helicity in Double-stranded Semiflexible Chains with Interstrand Interactions

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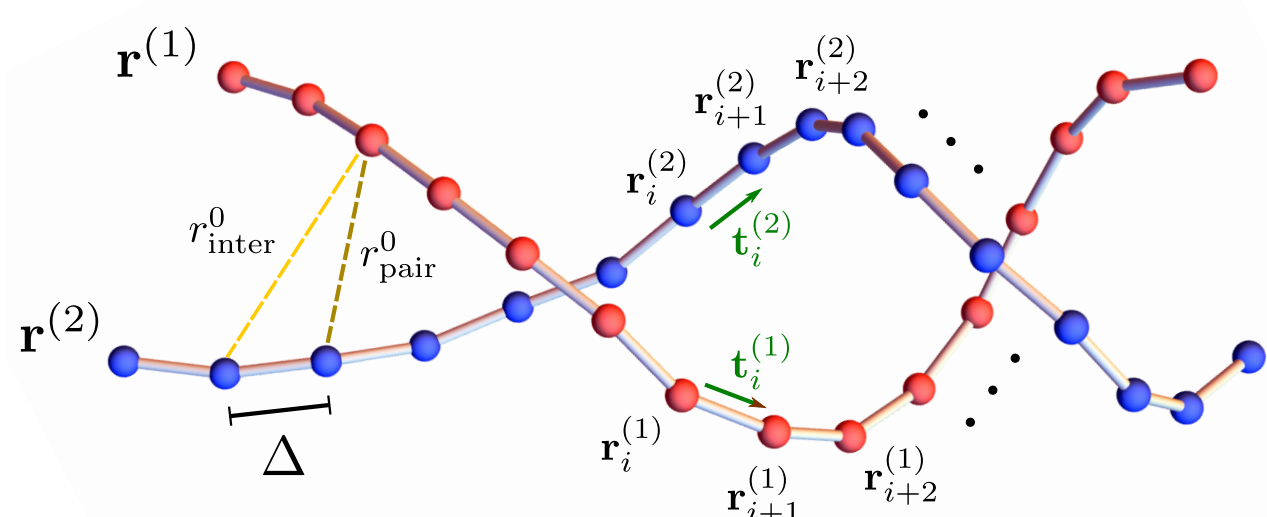
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Abstract

In literatures, there are models with varying levels of complexity and coarse-graining schemes that accurately describe the mechanical and structural properties of dsDNA. However, the interplay between base-stacking interactions in dsDNA and its intrinsic handedness is rarely discussed despite their importance in preserving the double-helix structure of dsDNA. Here we investigate the delicate balance required for the strength of base-stacking interactions D and the twist stiffness P to preserve the double-helix structure in a model made up of two semiflexible chains. We found that our model supports several distinct morphological phases in the parameter space (P, D) : flat, random coil, and the double-helix phase. Transitions between these phases are of different order, and there is also a morphological transition within the double-helix phase signified by the unwinding of the double-helix.

Methods

Model and Parameters



Bending energy:

$$E_{\text{bend}}^{(k)} = \sum_{i=0}^{N-2} \frac{\ell_p^0}{\Delta} \left(1 - \mathbf{t}_i^{(k)} \cdot \mathbf{t}_{i+1}^{(k)} \right)$$

Base-pairing:

$$E_{\text{bond}} = \sum_{i=0}^{N-1} \frac{k}{r_H^2} (r_{\text{bond},i} - r_{\text{bond}}^0)^2$$

where $r_{\text{bond},i} = |\mathbf{r}_i^{(1)} - \mathbf{r}_i^{(2)}|$

Base-stacking:

$$E_{\text{inter}} = D \sum_{i=0}^{N-2} \left[(r_i^{1,2} - r_{\text{inter}}^0)^2 + (r_i^{2,1} - r_{\text{inter}}^0)^2 \right]$$

where $r_i^{m,n} = |\mathbf{r}_i^{(m)} - \mathbf{r}_{i+1}^{(n)}|$

Twist energy:

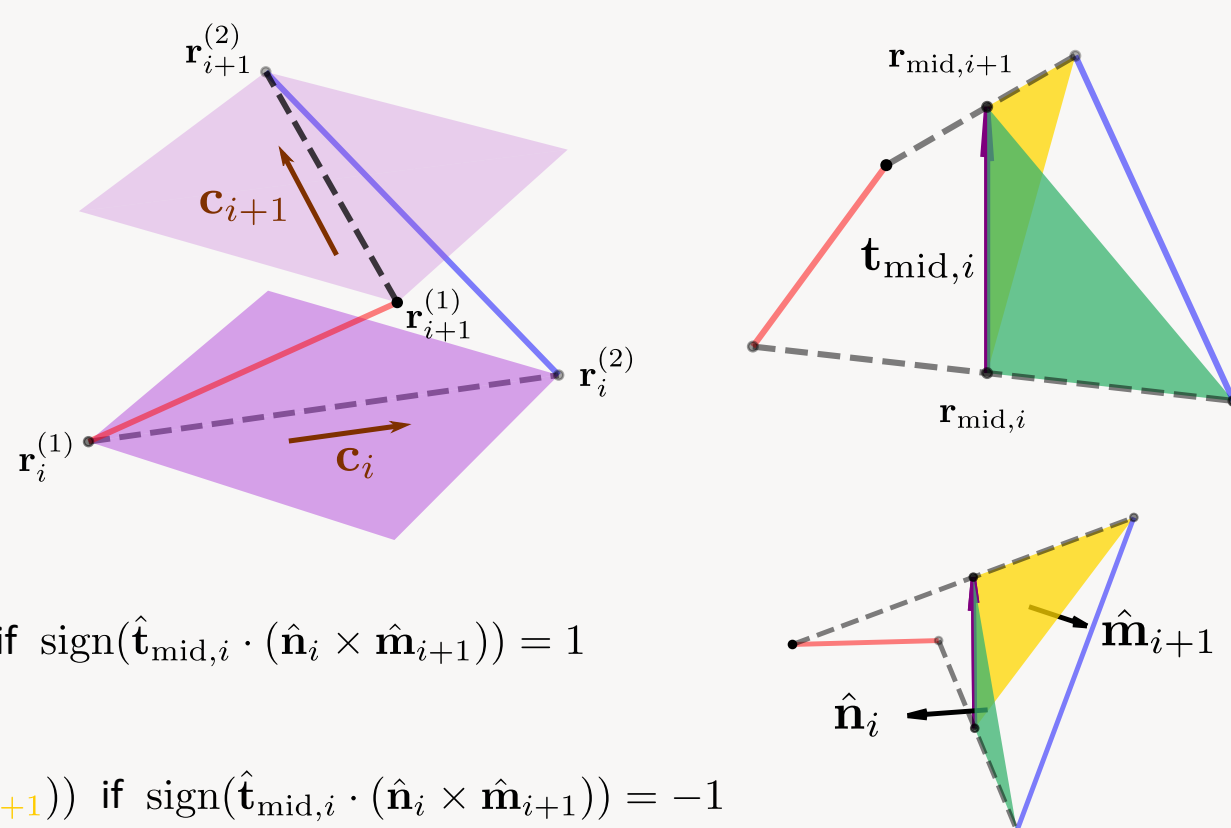
$$E_{\text{twist}} = P \sum_{i=0}^{N-2} (\chi_i - \chi_0)^2$$

where

$$\chi_i = \begin{cases} \arccos(\hat{\mathbf{t}}_{\text{mid},i} \cdot (\hat{\mathbf{n}}_i \times \hat{\mathbf{m}}_{i+1})) & \text{if } \text{sign}(\hat{\mathbf{t}}_{\text{mid},i} \cdot (\hat{\mathbf{n}}_i \times \hat{\mathbf{m}}_{i+1})) = 1 \\ 2\pi - \arccos(\hat{\mathbf{t}}_{\text{mid},i} \cdot (\hat{\mathbf{n}}_i \times \hat{\mathbf{m}}_{i+1})) & \text{if } \text{sign}(\hat{\mathbf{t}}_{\text{mid},i} \cdot (\hat{\mathbf{n}}_i \times \hat{\mathbf{m}}_{i+1})) = -1 \end{cases}$$

Fixed parameters:

$\ell_p^0 = 2$ nm (bare persistence length)
 $\Delta = 0.64$ nm (distance between monomers)
 $r_{\text{bond}}^0 = 2$ nm (pair distance)
 $k = 12 k_B T_0$ (strength of base-pairing)
 $r_H = 0.3$ nm (hydrogen bond length)
 $r_{\text{inter}}^0 = 1.8$ nm (diagonal distance)
 $\chi_0 = 0.2 \pi$ rad (twist angle)



Simulation

Both chains are initially free. The total energy of the system,

$$E = E_{\text{bend}}^{(1)} + E_{\text{bend}}^{(2)} + E_{\text{bond}} + E_{\text{inter}} + E_{\text{twist}}$$

is driven to minimum using Monte Carlo (MC) simulation with 4×10^6 sweeps whereby samplings for each sweep are taken in parallel using 64 CPU-cores. We devote the first half of the MC steps to equilibration, and the configuration of both chains are accepted or rejected via Metropolis algorithm.

ACKNOWLEDGEMENT

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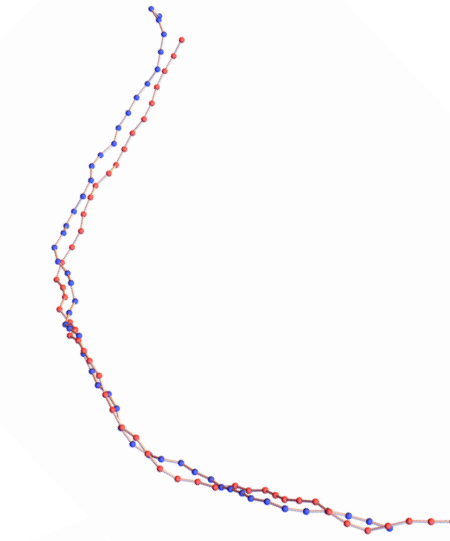
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Results

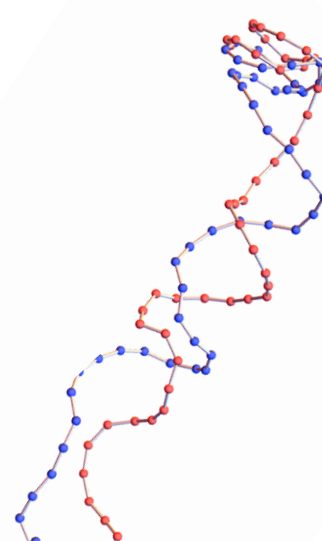
$P = 0$ or $P \neq 0, D = 0$

• Flat



$P = 0, D \neq 0$

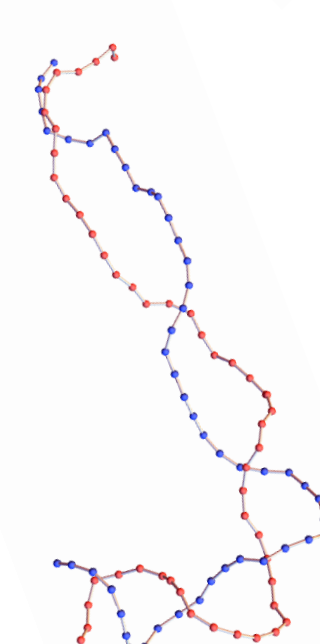
• Random coil



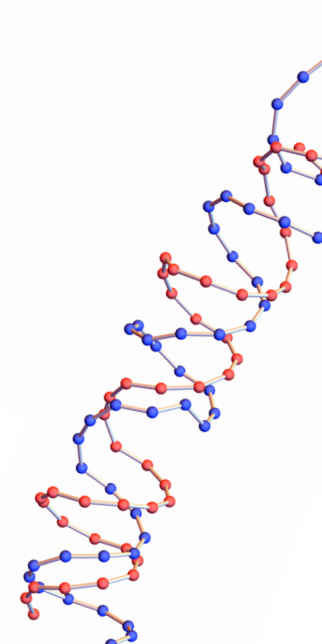
In the case $D = 0$, the chains rarely twist and bend. When D is not zero, the chains start to wind around each other. In the absence of P , the twist direction is not regulated. If P is not zero, only right-handed twist is allowed. For nonzero P and D , the chains gradually form right-handed double-helix as D increases with fixed P . Increasing D further would give rise to the instability in the structure which causes the unwinding of the double helix.

$P \neq 0, D \neq 0$

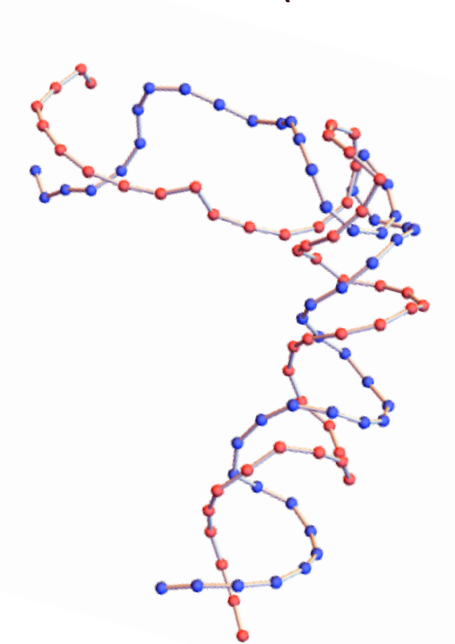
• Flat \rightarrow Double-helix



• Double-helix

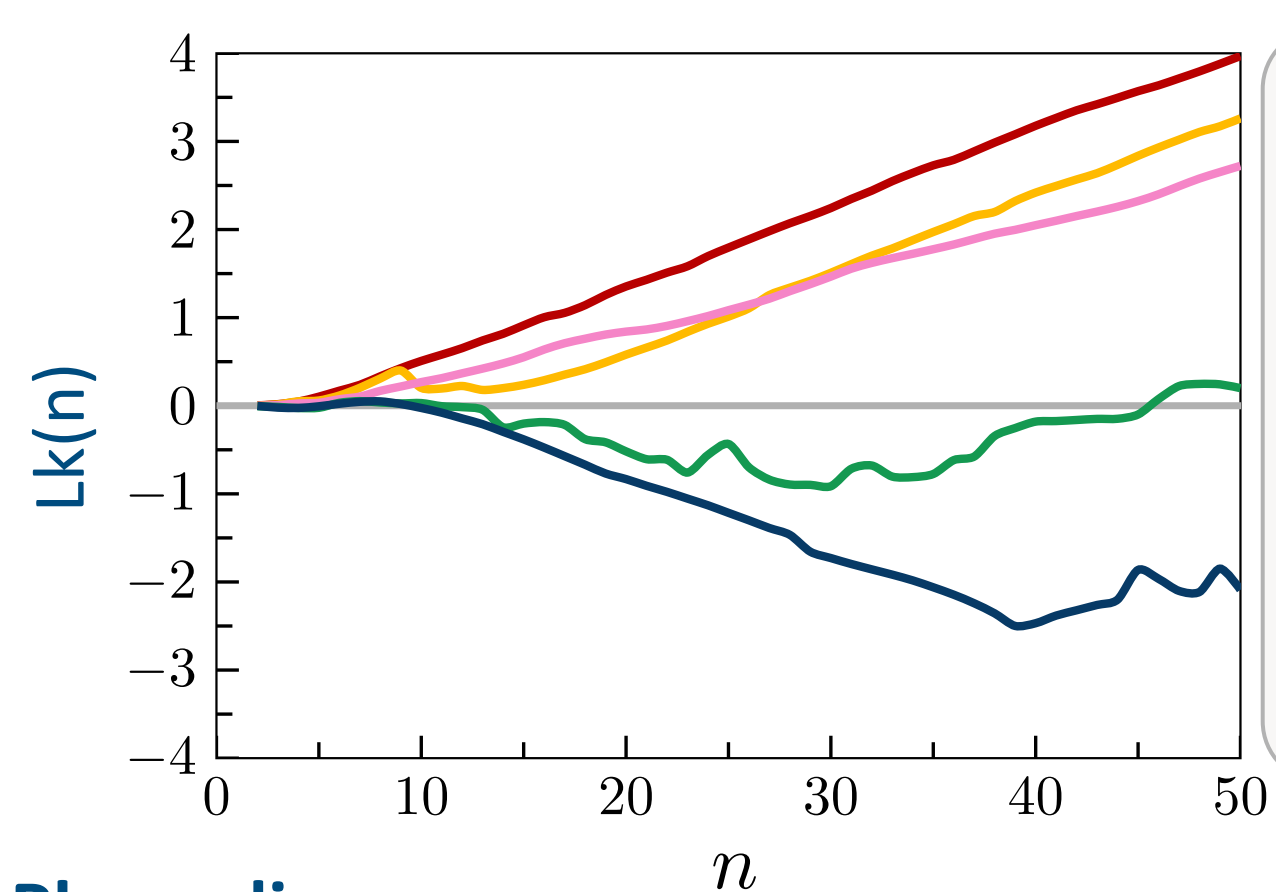


• Double-helix (unwound)



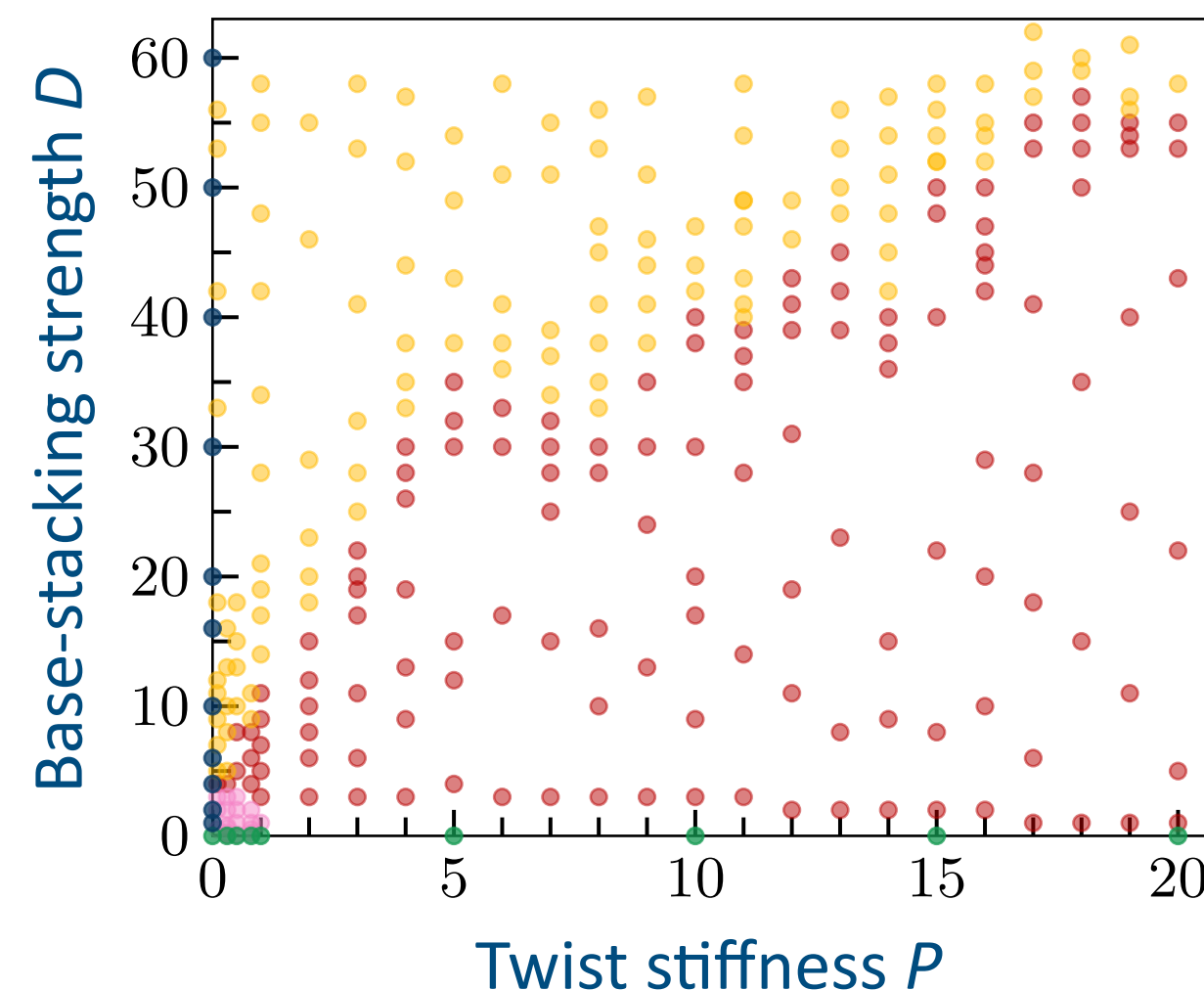
The variation of Gauss linking number

$$\text{Lk}(n) = \frac{1}{4\pi} \sum_{i=1}^{n-1} \sum_{j=1}^{n-1} \frac{\mathbf{r}_i^{(1)} - \mathbf{r}_j^{(2)}}{|\mathbf{r}_i^{(1)} - \mathbf{r}_j^{(2)}|^3} \cdot \left[(\mathbf{r}_i^{(1)} - \mathbf{r}_{i-1}^{(1)}) \times (\mathbf{r}_j^{(2)} - \mathbf{r}_{j-1}^{(2)}) \right]$$



In the **double-helix** phase, the link increases linearly along the chains. Likewise for the **double-helix (unwound)** phase and **flat** \rightarrow **double-helix**, though the total link will be smaller. The link is small in the **flat** phase since bending and twisting are rare. The link can go below zero in the **random coil** phase because there is no preferred twisting direction.

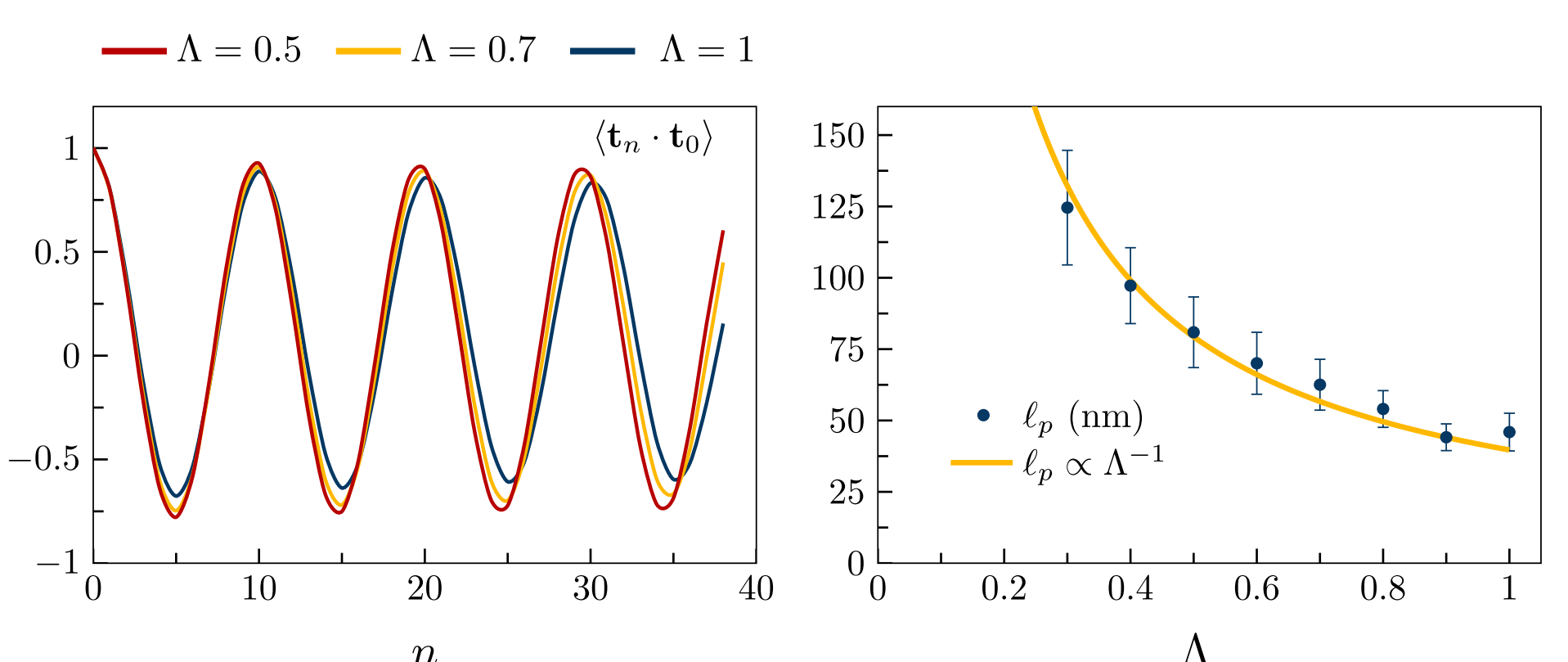
Phase diagram



Morphological phase diagram of our model subject to different base-stacking strength D and twist stiffness P at normalized temperature $\Lambda = 1$.

The phase transitions **flat** \rightarrow **double-helix** and **double-helix** \rightarrow **double-helix (unwound)** are continuous, while the phase transitions from **random coil** phase to the other phases are abrupt due to the handedness-symmetry breaking.

Correlation functions and persistence length



The correlation function $\langle \mathbf{t}_n \cdot \mathbf{t}_0 \rangle$ at temperature $\Lambda = T/T_0$ exhibits oscillatory behavior with amplitudes that decay exponentially: $\langle \mathbf{t}_n \cdot \mathbf{t}_0 \rangle = e^{-s/\ell_p} \cos(\lambda_p s)$, where $s = n\Delta$. The bending persistence length ℓ_p increases as the temperature Λ is lowered.