

Erratum to: Modulating DNA configuration by interfacial traction: an elastic rod model to characterize DNA folding and unfolding

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The author regrets that the sign in (8) and some terms in (11) of the paper cited above were missing. Corrections to these errors are given as follows:

As a coarse-grained continuum model, DNA can be regarded an elastic thin rod. The central axis of rod is a spatial curve $R(s, t): \mathbf{R}^2 \rightarrow \mathbf{R}^3$ parameterized by arc length s and time t . At a point P on the curve $R(s, t)$, the Frenet frame $P-NBT$ and a local orthonormal basis $P-xyz$ are simultaneously set. In $P-NBT$, the positive direction of the principal normal PN points toward the concave side of the curve $R(s, t)$; whereas in $P-xyz$, the x -axis and y -axis are the two principal inertia axes of the cross section through the point P . The angle between the principal normal PN and x -axis (or the binormal PB and y -axis) is called the twisting angle, denoted by χ . On the interfacial surface between the rod and solution, the Young-Laplace equation reads

$$p' - p_0 = \sigma \left(\frac{1}{r} - \frac{1}{R} \right), \quad (\text{R1})$$

where R and r are two principal curvature radii in which r is the radius of the rod cross-section, p_0 is a constant pressure applied on the interfacial surface by the solution and p' is the pressure on the interfacial surface by the rod. In (R1), we have reckoned a principal curvature radius as positive if it is drawn into the interior of the rod.

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In terms of the action and reaction law, the pressure p applied on the rod by the interfacial surface is equal to p' in magnitude, but they are opposite in direction. So in coordinates P - xyz , p can be decomposed into

$$p_1 = \left[\sigma \left(\frac{1}{R} - \frac{1}{r} \right) - p_0 \right] \cos(\theta - \chi), \quad p_2 = \left[\sigma \left(\frac{1}{R} - \frac{1}{r} \right) - p_0 \right] \sin(\theta - \chi) \quad p_3 = 0, \quad (\text{R2})$$

where θ is the angle between PQ and PN . It has been proven [1] that R can be written as

$$R = \frac{1 - r\kappa \cos \theta}{\kappa \cos \theta}, \quad (\text{R3})$$

where κ is the curvature of the rod axis. Substituting (R3) into (R2) and integrating along the perimeter of the rod cross-section leads to

$$f_1 = \frac{2\pi\sigma}{r\kappa} \left(\frac{1}{\sqrt{1 - r^2\kappa^2}} - 1 \right) \cos \chi, \quad f_2 = -\frac{2\pi\sigma}{r\kappa} \left(\frac{1}{\sqrt{1 - r^2\kappa^2}} - 1 \right) \sin \chi, \quad f_3 = 0, \quad (\text{R4})$$

which are the correct formulas characterizing the interfacial traction. Clearly, physics requires that $-1 < r\kappa < 1$. Compared with (11) in [1], $1/\sqrt{1 - r^2\kappa^2} - 1$ in (R4) can be regarded as a positive scaling factor. Therefore, using (R2), we can repeat the results in [1] and the conclusions in [1] are still available. A detailed investigation can refer to [2].

It should be stressed that, in a salt solution, geometrical configuration of a DNA chain is controlled by van der Waals force or electrostatic force between the DNA chain and the solution molecules. The interfacial traction is only a coarse-grained model characterizing these microscopic interactions. Since the interfacial traction is curvature-dependent, it is adequate to describe the shape of DNA in solution.

It is noted that the basic idea and main results presented in the paper are not affected by these missing terms [2].

References

1. Zaixing, H.: Modulating DNA configuration by interfacial traction: an elastic rod model to characterize DNA folding and unfolding. *J. Biol. Phys.* **37**, 79–90 (2011)
2. Ye, X., Zaixing, H., Shengnan, W.: An elastic rod model to evaluate effects of ionic concentration on equilibrium configuration of DNA in the salt solution. *J. Biol. Phys.* **40**, 179–192 (2014)