Erratum: Application of a free-energy-landscape approach to study tension-dependent bilayer tubulation mediated by curvature-inducing proteins [Phys. Rev. E **92, 042715 (2015)]**

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We acknowledge a sign error in Eqs. (7), (8), and (9) of our paper. This error is due to the Laplacian of $\sum_q h_q e^{iqx}$ resulting in a prefactor of i^2 for the second and third terms. This prefactor was absent in the initial derivation. The correct equations are

$$\langle \mathcal{H} \rangle = \frac{A_p}{2} \sum_{\vec{q}} \sum_{\vec{q}'} \{ [q^2 q'^2 \langle h_q h_{q'} \rangle + q^2 \langle h_q h_{0,q'} \rangle + q'^2 \langle h_{0,q} h_{q'} \rangle + \langle h_{0,q} h_{0,q'} \rangle] \kappa_{q+q'} + q q' [\langle h_q h_{q'} \rangle] \sigma_{q+q'} \}, \quad (7)$$

$$\langle \mathcal{H} \rangle = \frac{A_p}{2} \sum_{\vec{q}} \{ [q^4 \langle h_q^2 \rangle + q^2 \langle h_q h_{0,q} \rangle + q^2 \langle h_{0,q} h_q \rangle + \langle h_{0,q}^2 \rangle] \kappa + q^2 \langle h_q^2 \rangle \sigma \}, \quad (8)$$

$$k_B T = A_p \{ [q^4 \langle h_q^2 \rangle + q^2 \langle h_q h_{0,q} \rangle + q^2 \langle h_{0,q} h_q \rangle + \langle h_{0,q}^2 \rangle] \kappa + q^2 \langle h_q^2 \rangle \sigma \}. \quad (9)$$

This sign change caused small differences to the results presented in Figs. 9, 10, and 11 in our paper. The difference in the resulting renormalized tension is depicted in Fig. 9. It can be seen in Fig. 9 that the change is within statistical error. Hence the conclusions presented in the original paper are qualitatively and quantitatively valid. Nevertheless, we regret the error in the equations. For the benefit of the reader, we also provide the corrected Figs. 10 and 11.

FIG. 9. Plot of σ^* , the membrane tension at tubulation as a function of A/A_p for a membrane with $C_0 = 0.8a_0^{-1}$ for both the corrected Eq. (9) and the previous (incorrect) equation. Error bars correspond to two times the standard deviation.

FIG. 10. Comparison of experimental (filled symbols) [47] and simulation data (open symbols) for the averaged membrane tension and protein concentration at the point of tubulation. Simulation data are shown for three different values of the length scale a_0 . In simulations, the protein concentration is calculated as $\zeta n_p^{\text{nit}}/A_p$, where the coarse-graining parameter $\zeta \approx 10$. Error bars of simulation data correspond to two times the standard deviation.

FIG. 11. Plot of the values of (a) κ and (b) σ obtained by nonlinear fitting of the complex spectrum (9) with tubules removed. A bin size of 0.02 in q and a maximum q of 1 were used for these fits. Error bars correspond to two times the standard deviation.