Page 3895. The transfer matrix, as defined in eq 3, does not match the model that we introduced in section II and made explicit in the Hamiltonian eq 1. To calculate the majority-rules effect with the model described in section II, monomer—monomer interactions would need to be taken into account, on top of monomer—bond and bond—bond interactions. This requires a larger transfer matrix than the $2 \times 2$ matrix given in eq 3.

However, the majority-rules effect can in fact be described by a $2 \times 2$ transfer matrix. To this end, we consider a somewhat simpler description in which the mismatch penalty $W$ is invoked only when a “+” bond follows a “−” monomer or vice versa. This corresponds to the Hamiltonian

$$H = \frac{1}{2} R \sum_{j=1}^{N-2} (1 - s_j s_{j+1}) + \frac{1}{2} P \sum_{j=1}^{N-1} (s_j + 1) + \frac{1}{2} W \sum_{j=1}^{N-1} (1 - s_j s_{j+1}) - E(N-1)$$

and gives for the transfer matrix

$$M = \begin{pmatrix} zW + 1 & (zW + 1) \sqrt{\sigma} \\ (w + z)s\sqrt{\sigma} & s(w + z) \end{pmatrix}$$

with eigenvalues $\lambda_{1,2} = (1 + zs + zw + sw \pm \sqrt{\alpha})/2$.

While the change we suggest in this Correction is primarily one of definition, we do implicitly assume that we need not take into account both surrounding monomers of a bond to give an accurate description of the majority-rules effect. We demonstrate that this assumption is indeed reasonable by obtaining good agreement with experimental results, as described in a separate publication.1

All subsequent equations, results, and figures remain unchanged when one makes these substitutions.

References and Notes


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The reported values of radii of gyration ($R_g$) in Table 2 (i.e., at the critical point) were incorrectly computed due an error in the subroutine which computes $R_g$ from polymer coordinates subjected to periodic boundary conditions. The error, which causes an improper “unfolding” of these polymer coordinates, only occurs when the polymer chains span distances larger than half the simulation box length. The revised values of $R_g$ and the corresponding uncertainties are given in Table 1 below. The $R_g$ values plotted in Figure 7 (i.e., in the $\Theta$ temperature and athermal limits) did not suffer from this error as the simulation box lengths employed for these simulations exceeded the maximum possible dimension of the polymer chains. We thank Dr. Anastassia Rissanou for her help in identifying this error.

| Table 1. Revised Values of $R_g$ |
|-----------------|----------------|----------------|----------------|----------------|----------------|----------------|
| $r$             | 65             | 82             | 101            | 149            | 197            | 293            | 589            |
| L               | 4.978          | 5.610          | 6.245          | 7.629          | 8.793          | 10.764         | 12.441         |

* Statistical uncertainties are smaller than ±0.01.

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