CORRECTIONS

Jeroen van Gestel*: Amplification of Chirality in Helical Supramolecular Polymers: The Majority-Rules Principle. Volume 37, Number 10, May 18, 2004, pp 3894−3898.

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 × 2 matrix given in eq 3.

However, the majority-rules effect can in fact be described by a 2 × 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

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

and gives for the transfer matrix

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

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

(1) van Gestel, J.; Palmans, A. R. A.; Titulaer, B.; Vekemans, J. A. J. M.; Meijer, E. W. *J. Am. Chem. Soc.* **2005**, *127*, 5490.

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MA0526138

10.1021/ma0526138
Published on Web 01/31/2006

Gaurav Arya* and Athanassios Z. Panagiotopoulos: Impact of Branching on the Phase Behavior of Polymers. Volume 38, Number 25, December 13, 2005, pp 10596−10604.

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 Θ 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[a]

	$r = 65$	$r = 82$	$r = 101$	$r = 149$	$r = 197$	$r = 293$	$r = 389$
L	4.978	5.610	6.245	7.629	8.793	10.764	12.441
B1	4.488	5.049	5.616	6.848	7.888	9.655	11.151
B2	4.091	4.599	5.110	6.227	7.170	8.767	10.122
B4	3.896	4.388	4.874	5.889	6.753	8.289	9.534
D	3.735	4.221	4.638	5.623	6.464	7.883	9.087

[a] Statistical uncertainties are smaller than ±0.01.

MA052732N

10.1021/ma052732n
Published on Web 01/21/2006

10.1021/ma0526138 CCC: $33.50