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Collapse Transitions in Thermosensitive Multi-block Copolymers: A Monte Carlo Study

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Abstract

Monte Carlo simulations are performed on a simple cubic lattice to investigate the behavior of a single linear multiblock copolymer chain of various lengths $N$. The chain of type $(A_nB_n)_m$ consists of alternating $A$ and $B$ blocks, where $A$ are solvophilic and $B$ are solvophobic and $N = 2nm$. The conformations are classified in five cases of globule formation by the solvophobic blocks of the chain. The dependence of globule characteristics on the molecular weight and on the number of blocks, which participate in their formation, is examined. The focus is on relative high molecular weight blocks (i.e., $N$ in the range of 500 – 5000 units) and very differing energetic conditions for the two blocks (very good – almost athermal solvent for $A$ and bad solvent for $B$). A rich phase behavior is observed as a result of the alternating architecture of the multiblock copolymer chain. The comparison among equivalent globules consisting of different number of $B$-blocks shows that the more the solvophobic blocks constituting the globule the bigger its radius of gyration and the looser its structure. Comparison between globules formed by the solvophobic blocks of the multiblock copolymer chain and their homopolymer analogs highlight the important role of the solvophilic $A$-blocks.
I. Introduction

Linear multiblock $A, B$ copolymers, which are the focus of the present study, exhibit a rich phase behavior. In the melt, they can undergo microphase separation, akin to that of diblock copolymers (i.e., order-disorder transitions, ODT) when the incompatibility between the blocks is sufficiently strong, with a phase diagram that depends on the number and relative length of the blocks.\(^1,2,3\) In solution, they can demonstrate either a first-order macrophase separation, akin to normal solution behavior of polymers (i.e., a binodal separating the one-phase and two-phase regions, characterized by an upper or a lower critical solution temperature), or a microphase separation (i.e., intramolecular or intermolecular aggregation or micellization). Which scenario will be favored depends on copolymer architecture, composition and concentration, as well as on solvent quality and selectivity for the two blocks.\(^4,5\) The intermolecular aggregation is similar to the manner that surfactant molecules behave in water, i.e., by clustering in multi-chain aggregates—micelles—formed with cores of collapsed hydrophobic blocks surrounded by a corona of hydrated hydrophilic blocks. An example of intrachain aggregation is that of proteins dissolved in water: in the simplest description, they undergo a very specific intrachain aggregation—protein folding—with hydrophobic segments clustering in the inner part of the collapsed coil leaving most of the hydrophilic parts on their exterior and exposed to water.

Amphiphilic linear multiblock copolymers with well-controlled phase behavior are particularly useful in many industrial applications\(^6,7,8,9,10,11,12,13,14\) as thermoplastic elastomers, lubrication and processing additives and blend compatibilizers, as well as in the life sciences\(^15,16,17\) in protein folding\(^18\), in drug and protein encapsulation and delivery, etc. The study and understanding of the solution properties of such multiblock copolymers can yield molecular-based insight into design strategies and, ultimately, lead to the development of generally applicable models for polymers with desired characteristics.

Towards this end, computer simulations have recently made substantial strides\(^4,19,20,21,22,23,24,25,26,27,28,29,30,31\) focusing on solutions of linear multiblock copolymers of the $(A_nB_m)_m$ type, where $n$ is the degree of polymerization of each block and $m$ is the number of blocks. Systematic explorations within the large parameter space established
quantitative relations on how copolymer architecture and intermolecular interactions determine the macroscopic phase behavior and the related chain conformations changes. The various studies reveal that the number of blocks, the number of block types, the degree of polymerization of each block and the interaction parameters are primary molecular variables that influence the self-assembly of linear multiblock copolymers. Additional variables such as block flexibility, molar mass distribution and composition heterogeneity are considered as secondary factors.\(^3\)

In particular, Gindy, et al.\(^4\) presented interesting simulation results on solutions of multiblock copolymers of type \((A_nB_m)_m\) in a solvent selective for the \(A\) blocks. They found that fewer or longer blocks along the linear copolymer chain favor microphase separation (i.e., formation of aggregates) while multiple or short blocks result in a first-order macrophase separation. Microphase separation was shown to occur below a “critical” value of the ratio \(m/n\); otherwise macrophase separation takes place. Regarding the polymer concentration, in the dilute regime all systems were found to form well defined, almost spherical, multichain, core-shell type aggregates. By increasing polymer concentration, a bridging across the insoluble segments of multichain clusters was observed. An analogous macrophase separation has been observed experimentally by Rackaitis, et al.\(^32\)

Lewandowski, et al. in a series of papers\(^{19,20,21}\) performed off-lattice Monte Carlo simulations on a single multiblock copolymer chain using different architectures in non-selective solvents. His main findings for small \(m\)-values reported a two-stage transition upon solvent quality decrease, with swollen/solvated coils collapsing first towards a pearl-necklace microstructure and, upon worsening of the solvent quality, towards a single-globule microstructure. A rich phase diagram with a variety of intraglobular structures has been presented for larger \(m\)-values. Above a certain value of chain length, the self-assembled globule was observed to develop a non-spherical globular structure with multiple cores. Furthermore, the competition between the interfacial area between \(A\) and \(B\) blocks and the solvent quality was reported as critical in the self-assembly procedure.

An extensive study on the phase behavior and the static properties of linear multiblock copolymers has been presented in a series of papers by Theodorakis, et
Molecular Dynamics simulations of single linear multiblock copolymer chains were performed under various solvent conditions. In all cases, the $A$ and $B$ blocks were of equal length and with the same self-energetic interactions (i.e., common solvent conditions), whereas the unmixing tendency was introduced via $A$-$B$ interactions. The block length, the number of blocks and the temperature were the varying parameters and their combination is found to be crucial for all possible modes of microphase separation. Moreover, the presence of well-defined $A$-$B$ interfaces between the blocks was found to play a major role on the static properties of multiblock chains, such as the shape and the bond orientation correlation function.

Furthermore, in a very recent publication of Zhang, et al.\textsuperscript{30} the influence of the solvent conditions and the chain backbone stiffness of an amphiphilic multiblock copolymer was studied utilizing Brownian Dynamics simulations. They found that the cooperative influence of both factors leads to many interesting structures. Moreover, a higher ratio of the hydrophobic to the hydrophilic blocks favors the formation of micelles with various structural patterns.

Many of the simulation studies described above explored the effect of the block length on the phase behavior of multiblock copolymers;\textsuperscript{4,19,21,24,30} however, they were limited to short lengths of the corresponding blocks and, in most cases, of the total chain length although a wide range of $m$-values has been explored. The results of our earlier study on the coil-to-globule transition of single homopolymer chains\textsuperscript{33} had illustrated very clearly that there is a very strong dependence of the features of the transition and of the globule characteristics on the polymer molecular weight (MW). The compactness and, consequently, the stability of the aggregate, which is abusively called “globule” for short chains, are strongly dependent on the MW; for short chains, the term “globule” is used for a simply shrunk conformation. More specifically, at poor solvent conditions low molecular weights undergo a gradual broad transition with a fairly uniform densification of all chain portions. A somewhat narrower coil-to-globule transition is observed at intermediate molecular weights, characterized by the development of a “shoulder” in the inner portion of the density distribution. A fairly sharp transition exists only for molecular weights of several hundred thousands, signified by the formation of a core with constant polymer density.
In this work, we performed Monte Carlo simulations on systems of a single linear multiblock copolymer chain with total number of beads, \( N \), in the range of 500 to 5000 units. These values would correspond to molecular weights in the range of a few hundreds of thousands to a few millions for most real flexible polymers. We selected model systems of type \((A_nB_n)_m\) with degrees of polymerization for each block from 50 to 500 units. This approach is complementary to that of other studies, but with much longer block lengths, so as to better mimic experimental systems.\(^{34}\) Besides, the two blocks are subject to very differing energetic conditions which are kept constant for all systems.

In the current study, we have opted to monitor the tendency for globule(s) formation by sequential segments of a single multiblock copolymer chain with constant number of blocks in the “limiting” conditions of relatively high MWs and totally opposite selectivity of the two blocks. The stability and the features of globules formed by the solvo-phobic portions of the copolymer chain are examined as well. Moreover, the present study is carried out in an identical simulation “environment” (i.e., simulation model, energetic interactions) as that of our earlier works.\(^{33,35}\) Therefore, direct comparisons on the globule formation and the features of the globules in the case of multiblock copolymers and in the “reference” case of a homopolymer “chemically” identical with the solvophobic portions of the multiblock copolymer can be performed. Interesting information for the size and the compactness of globules formed by the solvophobic blocks of the multiblock copolymer chain compared to their homopolymer analogs is revealed.

The rest of the paper is organized as follows: Section II provides detailed information about the simulation methodology as well as the model systems studied in this work. Our results are presented in Section III, where a division in two subsections according to the properties of multiblock copolymer chains and their comparison with the corresponding homopolymer systems has been made. Finally, Section IV contains a discussion and the conclusions of the current study.

II. Model and Simulation Method
Conventional lattice Monte Carlo (MC) simulation on a simple cubic lattice is applied to a single multiblock copolymer chain of type \((A_nB_m)_m\). Each lattice site is occupied by a bead \(A\) or a bead \(B\) and solvent implicitly fills any empty sites. We simulated systems with the same block sequence \((m = 5)\) and of the same length \((n)\) for blocks \(A\) and \(B\), in the canonical \((NVT)\) statistical ensemble. In all cases, each polymer chain is divided in 10 alternating blocks, 5 of which are solvo-philic and the other 5 are solvo-phobic. Block length and consequently the total length \((N = 2nm)\) of the multiblock copolymer chain were used as varying parameters. Five systems were simulated with \(n = 50, 100, 200, 300, 500\) and \(N = 500, 1000, 2000, 3000, 5000\), correspondingly. Local MC moves are used in combination with the original configuration bias Monte Carlo (CBMC), applied only to the one end of the chain, in order to maintain the chain identity (order of blocks). A modification of CBMC\(^{36}\) applied to internal portions of the chain (“bridging” moves\(^{37}\)) is also utilized and proved very efficient for the relaxation of our systems.

Interactions are quantified through the energetic parameters \(E_{AA}\) and \(E_{BB}\), where \(E_{ii}\) represents the non-bonded interactions between species of the same kind of the macromolecule. \(E_{ii}\) are expressed in \(k_B T\) units and, consequently, they account for temperature and enable selective solvent quality. The solvent conditions were kept constant for all systems, representing a very poor solvent for the solvo-phobic blocks and a very good (almost athermal) solvent for the solvo-philic ones. Thus, interactions between beads of \(A\) blocks, \(E_{AA}\), are set equal to 0.1, rendering block \(A\) as solvo-philic.\(^{33}\) Interactions between beads of \(B\) blocks, \(E_{BB}\), are set equal to 0.45, rendering block \(B\) as solvo-phobic,\(^{33}\) while the interactions between beads of different blocks, \(E_{AB}\), are given by a common combinational rule, i.e., the geometric mean: \(E_{AB} = (E_{AA} \cdot E_{BB})^{0.5}\). All the other interactions, between polymer-solvent molecules and solvent-solvent molecules, are set to zero. The excluded volume is enforced through the requirement of self-avoidance.

The unit length is the monomer length \((a)\). The chain is contained in a cubic simulation box with sides at least five times larger than the swollen chain radius of gyration (i.e., the homopolymer analog chain in athermal solvent conditions). Periodic boundary conditions are applied in all three directions. A polymer chain of the corresponding length, in an extended conformation for both \(A\) and \(B\) blocks, was used as
the initial configuration for the simulation of each system, whereas in some cases, which will be discussed in more details in the following section, we performed additional simulation runs starting from different initial configurations. Simulations were carried out for $10^9-10^{10}$ MC cycles depending on the molecular weight of the simulated chains. Note here that these values are almost two orders of magnitude larger than those used in the simulation of homopolymer chains of the same molecular weight for the study of the coil-to-globule transition under identical energetic conditions. $^{33}$

III. Results

The parameter space, which has to be examined for the investigation of a single polymer chain consisting of two types of blocks, which are under very differing solvent conditions, is quite large. For this reason, the knowledge of the behavior of a single homopolymer chain under different solvent conditions is not only helpful but necessary as well. The study of the coil-to-globule transition for isolated flexible polymer chains$^{33}$ gives us a good estimation for the energy values under which the chain behaves as it should in good, theta ($\Theta$) or poor solvent conditions. In this model, $\Theta$ conditions correspond to an energy value equal to 0.28. Although the energy values are molecular weight dependent and can not serve as strict definitions of the corresponding solvents for the blocks of all multiblock copolymer chains, we use the “limiting” cases of $E_{AA} = 0.1$ (i.e, very close to athermal conditions) and $E_{BB} = 0.45$ (i.e., deep in the poor solvent regime), in order to ensure the desired selectivity of the blocks for all the molecular weights studied here. The current study has been performed in a simulation “environment” identical with the one of our previous work on a single homo-polymer chain,$^{33}$ which allows direct comparisons between the various conformational transitions and the characteristics of different conformations.

In the following, we present simulation results for all systems studied here, while in the next subsection comparisons among the conformations of the multiblock copolymer chains and their homopolymer analogs are depicted.

III.1. Conformational Transitions:
In order to study the preferable conformations of the multiblock copolymer chains under the specific solvent conditions, we selected a large number of configurations of all systems that we simulated. A general observation is that the $B$-blocks of the multiblock copolymer chain (i.e., the ones which are under poor solvent conditions) shrink forming “globule-like” structures while the $A$-blocks (i.e., the ones which are under good solvent conditions) are extended among or around the $B$-blocks. Figure 1 presents snapshots of the most preferable types of conformations of the chain, where the appearance of five, four, three, two and one “globules” formed by the $B$-blocks is evident. In the Figure, the solvo-phobic $B$-blocks are represented with red beads while the solvo-philic $A$-blocks with blue beads.

The classification of configurations in five cases of globules (i.e., 1-5 globules), which are formed by the solvo-phobic blocks of the multiblock copolymer chain is based on a simple algorithm, which has been used in the past for the determination of micelles in micellar solutions. A brief description of the algorithm is as follows: first the center of mass of each $B$-block is defined and, subsequently, all distances between the centers of mass of the five $B$-blocks are calculated. A globule is defined as a group of $B$-blocks such that each $B$-block in the group is at a distance less than the diameter of a collapsed $B$-block (i.e., $2R_g$) from at least one $B$-block of the same globule and at a distance more than $2R_g$ from all other $B$-blocks, which consequently are not considered as parts of this globule. $R_g$ is the radius of gyration of a homopolymer chain of the same length as the particular $B$-block under the same energetic conditions (i.e., $E_{BB} = 0.45$). This definition is schematically portrayed for all possible configurations of five collapsed $B$-blocks in the insets of Figure 1 as $a$-$g$ pictures. Note here that for the cases of the two and the three globules there are two possible arrangements of $B$-blocks, which result in the same class of globules, according to the present definition.

An important observation at this point is that the sequence of snapshots depicted in Figure 1 (i.e., from five to one globules) is not followed by the time evolution of the simulation, i.e., the appearance of this sequence is not due to the kinetics of the globule formation. On the contrary, all cases appear at any time during the simulation, through a continuous switching from one to another. This is depicted in Figure 2, where the time evolution of conformations during the simulation is presented as a function of the number.
of globules for all five systems. Increasing configuration number, normalized with the total number of configurations, represents the time progress. The above observation is clearly apparent for the shorter chains up to $N=1000$ ($n=100$) (Figure 2a and 2b). For longer $N$’s, the terminal cases (i.e., five and/or one globule) are very limited and appear scarcely or do not appear at all, in the sample of the configurations that we have encountered.

A quantification of the above information is given by the calculation of the probabilities of occurrence for each of the five classes of conformations for all systems. These are presented in Figure 3, where different features appear as a function of globule size. For the shortest chain ($n=50, N=500$), the formation of only a single globule from all five $B$-blocks of the multiblock copolymer chain seem very unfavorable; this behavior is a result of the low $n$-value for $B$-blocks, which form a very loose aggregate under the poor solvent conditions, which is easily dissolved. Increasing the chain length and for $n=100, (N=1000)$, there is an almost equal probability for all five cases of globule formation. These observations are in agreement with previous studies of even shorter block lengths. For the $N=2000$ multiblock copolymer chain ($n=200$), the probabilities from one to five globules follow a decreasing order, with the limiting case of five globules very rare (Figure 3c). The error bars of these calculations, which are presented on the Figure, increase with the molecular weight as expected. These are very small for the two smaller systems and an abrupt increase is observed at $N=2000$, especially for the cases of one and two globule formation, whereas error bars are expected even larger for the rest two systems. For the higher molecular weights (i.e., $n \sim 300\text{-}500$), the probability of the formation of one globule becomes extremely small (not detected in our simulation time), while intermediate cases are favored. More specifically, for $N=3000$, two to four globules appear while the terminal case of five globules is very rarely detectable and, for $N=5000$, only the three, four and five globules are detected after $10^{10}$ MC cycles.

A well-known issue for these high molecular weights is the very slow kinetics of the system, which hinders its escape from possible local energetic minima where it is trapped. For this reason and in order to explore the phase space of $N=5000$ chain more thoroughly, we performed an independent simulation, starting from a different initial configuration which is already in the case where the solvo-phobic $B$-blocks have formed
three globules and the $A$-blocks are swollen in solution, connecting them. The time progress of the conformations and the probability histogram of this run are presented in Figures 4a and 4b respectively. In Figure 4b the same preferable states are observed as those of Figure 3e, albeit with different probabilities. This difference underlines the large statistical uncertainty of these calculations; however, it also shows the preference of the specific system to form more than one separate globules. Furthermore, the large gaps in the plots of the time evolution of conformations during the simulation beyond $N=2000$ (e.g., Figures 2d, 2e and 4a) confirm the slower kinetics compared to the shorter lengths, but they also indicate a bigger stability of the larger globules. This is a consequence of the dependence of the globule density on the molecular weight, as will be presented later (Figure 8) and has been discussed extensively in our previous study of homopolymers.33

The transitions among the various configurations of the phase space can be better understood with the findings of Figure 5. According to the classification of configurations we have calculated the mean energy of $B$-blocks (solvo-phobic), averaging over all detected conformations of each case. Here the error bars introduced illustrate the minimum and the maximum energy values, which have been calculated for each case. It is very interesting to observe the considerable overlap in energy values among the different cases of globules for all systems. This is due to the very large energy fluctuations of the specific conformations. In the first three systems ($N = 500, 1000$ and 2000), where all five cases of globule formation are detected, we can clearly notice that the energy (in absolute values) is a decreasing function of the number of globules, although the error bars establish a common energy region for all five classes of globules. The five-globule and the one-globule cases have the lower and the higher energy correspondingly, as expected.

The extensive energy fluctuations are responsible for the continuous interchange among the different conformations during the simulation. The extent of the overlap is better visualized in Figure 6 for the $N=1000$ multiblock copolymer chain, whereas a similar picture holds for all systems for the states detected in each of them. In Figure 6, the distribution of energies of the $B$-blocks around their mean value for all five cases of $N=1000$ chain are presented. The overlap is clear even between the two limiting cases of
one and five globules although to a smaller extent. This picture supports the reversibility in globule formation from five to one and vise-versa, during the simulation.

The calculation of a mean value for the relative error of the mean energy of $B$-blocks, $\langle \Delta E / \langle E \rangle \rangle_{i=5}$, over the five states of conformational interchanges, provides a rough comparison for the extent of energy fluctuations among the different systems. Equivalent comparisons can be made only among the three shorter multiblock copolymer chains because for the other two systems one or two classes of globules have not been detected during the simulation. The values for the corresponding systems are listed in Table 1 and show a systematic decrease in energy fluctuations with the molecular weight. This result is in accordance with the greater stability, which is observed for globules formed by longer $B$-blocks.

In the following the compactness of the formed globules is examined for all cases and all systems. We calculated the distances between the centers of mass of all pairs of $B$-blocks of the chain and we constructed the histogram shown in Figure 7. Each curve corresponds to each class of globule formation (one to five globules per chain) and the dashed vertical line signifies the length of one diameter (i.e., $2R_{gn}$) of a globule of size $n$ for each system, respectively. This value has been calculated averaging over all $B$-blocks, which are presented in the simulation of each system, and is equal to the $2R_{gn}$ value, within error bars, of the homopolymer chain study. $^3$ $R_g$ calculations will be discussed extensively in the next subsection. The part of histograms at distances smaller than $2R_{gn}$ provides substantial information for the compactness of the formed globule. Its meaning is that there is a fraction of pairs of $B$-blocks, which participate in the globule formation, with a high degree of fusion. This fraction is high for the one globule case and it gradually decreases with the number of globules although it does not vanish in any case. Therefore, despite the almost complete merging of at least one pair of $B$-blocks, the globules can still be dissolved and interchange their conformations among the five states. This is a result of the alternating architecture of the multiblock copolymer chain with the specific values of parameters of the presently examined phase space ($N$, $n$, $E_{AA}$, $E_{BB}$), as it has also been discussed in previous works. $^3$ $^4$ $^{21}$ $^{30}$ It is noted here that the part of all curves to the right of the $2R_{gn}$ line is not presented in the Figure, as it does not contain
important piece of information, because distances between pairs of $B$-blocks which do not belong to the same globule have been counted as well. As a consequence the five globule curve is not shown in Figure 7 because it lies totally to the right of the $2R_{cp}$ line, since this is implied by the criterion for globule definition. More information about the compactness of the formed globules is extracted from the density profiles, which are presented in the following subsection.

A comparison of the degree of fusion among the different systems is not straightforward because it is a combinatory result. The molecular weight of the formed globules determines the compactness and, consequently, the degree of fusion. The compactness influences the ability of dissolving and, thus, the interchange among the various globule cases. On one hand, when the formed “globule” is of low molecular weight, fusion is very probable whereas the rate of interchange (formation and dissolving) is very fast as well. On the other hand, in globules of high molecular weight the chance of high fusion between a pair of solvo-phobic blocks is small but its existence favors more stable structures.

Finally, an interesting observation is that the average number of globules (data not shown here) which are formed in all simulated systems, as extracted from the probabilities shown in Figure 3, is not a monotonic function of the molecular weight. This does not agree with the observation of a previous study for systems with aggregates of very small length (i.e., number of units equal to 5). In that study, the molecular weight dependence was examined by increasing the number of blocks of the copolymer (i.e., block sequence 10-60) and the average number of aggregates was found to be an increasing function of the molecular weight. This emphasizes once more that it is the length of the individual blocks in a multiblock copolymer chain that diversifies the system phase behavior.

III.2. Comparison between the Multiblock and the Homopolymer Analogs

Very instructive information is revealed from the comparison of the density profiles of the classes of globules formed by $B$-blocks among the different systems. The limiting case of the formation of one globule from all five $B$-blocks is presented in Figure 8a for chains with $N = 500, 1000, 2000$. It is observed that for $N = 500$ and 1000 (i.e.,
globules of $5\times50 = 250$ and $5\times100 = 500$ units, respectively) the increase of the molecular weight leads to a gradual densification at any distance from the center of mass of the formed globule, whereas, for the longer $N = 2000$ chain (i.e., a globule of $5\times200 = 1000$ units), a “shoulder” appears in the density curve at distances close to the center of mass. This “shoulder” is a precursor of a “core”, which will be completely formed and obtain a constant density only for very high molecular weights, signifying the coil-to-globule transition. In addition, qualitative and quantitative differences in the density profiles exist between the single globule that contains $1000 B$-units that is formed by the $B$-blocks of the $N = 2000$ multiblock copolymer chain and a globule formed by a homopolymer with $1000$ units, also shown in Figure 8a. Two observations are evident. First, there is quantitative difference between the copolymer and the homopolymer curves: the homopolymer globule is much denser at short distances whereas the density profile in the case of the copolymer is extended at longer distances from the center of mass of the globule. Second, the “shoulder” at short distances is more pronounced for the homopolymer. This behavior denotes the looser structure of the globule, which is formed by the solvophobich blocks of a multiblock copolymer chain compared to its homopolymer analog.

A complementary comparison is that of Figure 8b, where the density profiles of equivalent globules, formed by one or more $B$-blocks of the different copolymer systems together with the density profile of the globule formed by the homopolymer analog are depicted. In this figure we compare densities of a globule formed by the five solvophobic blocks of a $N = 1000$ multiblock copolymer chain (i.e., one globule case – $n = 100$) with a globule formed by one solvophobich block of a $N = 5000$ multiblock copolymer chain (i.e., five globule case – $n = 500$) and with a globule for a homopolymer with $N = 500$ at identical solvent conditions ($E_{BB} = 0.45$). Again, the density of the globule formed by the homopolymer is higher than for the other two copolymer systems whereas the copolymer curves extend over longer range. In addition, in the homopolymer curve a very initial sign for the core development appears at short distances, which is missing from the curves of both copolymer chains. Nevertheless, this is a different case from that of Figure 8a because the globule of the $N = 5000$ chain consists of one $B$-block
(n = 500) and its comparison with the corresponding homopolymer is direct. The result underlines the role of A-blocks (solvophilic) connecting the B-blocks influencing their conformations (i.e., reduce their density) via A-B interactions. The effect of the interface interactions between A and B blocks on the conformations of multiblock copolymer chains has been reported previously as well. A comparison between the two copolymer globules shows that the one, which belongs to the one globule case (i.e., formed by five B-blocks), is less compact than that which belongs to the five globule case (i.e., formed by one B-block). This feature shows that the more the blocks that compose a globule the less compact it is. An unambiguous verification of this behavior is given in the next paragraph by the calculation of the radius of gyration \( R_g \). Finally, in Figure 8c the density profiles of globules, which belong to the five globule case (i.e., globules consisting of one B-block of \( n \)-units), are presented for the copolymer systems. This figure shows the molecular weight dependence of the density of the globule and is in qualitative agreement with the homopolymer behavior. For this range of lengths (50-500), the increase of \( n \) leads to an increase in the density values throughout the profile. However, large quantitative differences from the corresponding homopolymers exist, as it was mentioned in previous Figures 8a and 8b as well.

Figure 9 is a combinatory figure of the mean radius of gyration which provides a comparison among equivalent globules, formed by one or more B-blocks of the different copolymer systems together with the values of the globules formed by the homopolymer analogs. In order to obtain a complete picture of the radii of gyration for the different cases of globule formation as a function of the molecular weight we proceeded as follows: we combined the five classes of globules in such a way that we extracted information for globules comprised by one, two, three, four and five B-blocks respectively from all our cases. This combination can be extracted from the cartoon images shown in the insets of Figure 1. The values for the homopolymer globules are obtained from our earlier study and do not correspond to every single point of the \( x \)-axis of the copolymer data, but they are sufficient even for a detailed comparison. Dashed lines are to guide the eye to the set of values being compared. The error bars of the data fall within \( \pm [5\%-15\%] \) of the actual value of \( R_g \); these errors are generally larger for the multi-species globules. Comparison between the \( R_g \) values of equivalent globules (formed
by the same number of B-units) allows one to reach the following conclusions: (a) The fewer the B-blocks, which constitute the globule, the smaller the radius of gyration. (b) The difference in $R_g$ values of equivalent globules is larger for larger $n$ values; these observations are in agreement with the density results and the previous discussion for the compactness of the globules. (c) A copolymer globule formed by one B-block has almost equal $R_g$ with the corresponding homopolymer within the range of the statistical uncertainty; this does not agree with the density profiles of Figure 8b, which shows that the copolymer density is smaller than the corresponding homopolymer one. Consequently for aglobule formed by one B-block of an alternating multiblock copolymer chain the solvo-phobic A-blocks do not affect the size but the density distribution of the globule. However, for multi-species globules both density and size are influenced by the alternating A-B architecture.

IV. Conclusions

Monte Carlo simulations in mesoscopic level have been employed to model the self-assembly behavior of multiblock copolymers. We examined the case of a single polymer chain in a selective environment utilizing a series of relatively long lengths both of the whole chain and of the individual blocks. We simulated chains with equal size of the alternating blocks $n_A=n_B=n$ with $n=50, 100, 200, 300, 500$ and $N = 500, 1000, 2000, 3000, 5000$, respectively. In all cases the number of individual A and B blocks was equal to 10 ($m = 5$). The blocks were under very differing energetic conditions with the A-blocks being very soluble $E_{AA} = 0.10$ (good solvent, almost athermal) and the B-blocks very insoluble $E_{BB} = 0.45$ (poor solvent).

For all systems a rich phase behavior is detected with continuous conformational transitions among various cases of globule formation. We classified conformations in five cases where the solvo-phobic (B-blocks) of the multiblock copolymer chain are combined is such a way that they form from one to five globules, while the solvo-phlic (A-blocks) are extended between or around them. Crucial role in the configuration space, which is explored by our systems, play the block length ($n$) and consequently the total length of the polymer chain ($N$), the total number of $A$ and $B$ blocks ($m$), that was kept constant.
herein, together with the very differing solvent conditions. A common observation for all systems is the very large energy fluctuations which lead to an extended overlap between the energy distributions of different states. This overlap allows the continuous interchange among conformations which is observed throughout the simulation. Nevertheless a rough estimation for the extent of energy fluctuations shows that they are larger in the smaller systems, something which renders the conformations of the larger systems more stable. On top of that, kinetics is considerably slower for the larger systems and, as a result of both these reasons, some of the five cases of globule formation are very rarely detected or are not detected at all in the time window of the simulation for the $N = 3000$ and $N = 5000$ systems. Therefore, for the smallest system with $N = 500$ the multiglobule cases are almost equally probable, while the single globule has the smallest probability. Increasing $N$ to 1000, there is an almost equal probability of all five classes of globules. For $N = 2000$, the combination of values in the parameter space (i.e., $N, n, E_{AA}, E_{BB}$) seem to be the appropriate in order to lead the system to the minimum energy state, where all $B$-blocks can form a large globule while the $A$-blocks are dispersed around them. For even higher $N$ there is non-preference of conformations which belong to the limiting cases, whereas conformations of intermediate cases are favorable. For $N = 3000$ this applies to both terminal cases of one and five globules, while for $N = 5000$ to one and two globules. Error bars of these calculations increase with the molecular weight; these are sufficiently small only for the two smaller systems and become very large for the longest chain.

Furthermore, the compactness of the formed globules has been examined through a distribution of the distances between the centers of mass for all pairs of $B$-blocks of the chain. In all cases there is a fraction of pairs of $B$-blocks with a high degree of fusion, which is larger for the one globule case and it gradually decreases with the number of globules but does not reach zero in any case. Nevertheless, although this considerable degree of fusion, globules are formed and dissolved interchanging their conformations among the five states. This is a result of the alternating architecture of the multiblock copolymer chain with the specific values of parameters within the phase space probed.

The simulation data for all systems of mutiblock copolymer chains are, then, compared to those of their homopolymer analogs. The simulation model and the
energetic conditions, which have been used in both cases of homopolymers and copolymers are identical, so a direct comparison between them is possible. The coil-to-globule transition of a single homopolymer chain and the globule characteristics have been studied previously and results for the density distribution and the radius of gyration of various globules are used here for comparison. This comparison reveals quantitative difference in the influence of the chain molecular weight on the characteristics of the globules formed by the multiblock copolymers and the respective homopolymers. Moreover the effect of the number of solvo-phobic blocks, which participate in a globule, on the globule characteristics is underlined.

Starting with the density profiles of the globules which are formed by one or more \(B\)-blocks we observe a gradual densification with the molecular weight at all distances from the center of mass of globule. Moreover beyond a certain length (1000 \(B\)-units), a precursor of a growing core in the central region of the globule exists, just as in homopolymer globules, although at higher lengths (for homopolymers this behavior is apparent beyond a length of 500). Quantitative and qualitative difference are detected in the density profiles of a homopolymer globule and an equivalent copolymer globule, where, for the latter, the curve is of much lower values close to the center of the globule but with a long range tail. It is interesting that this difference is observed even in the case of a globule formed by one \(B\)-block and it is attributed to the existence of the solvo-philic \(A\)-blocks between \(B\)-blocks, which affect the density of the latter, via the \(A\)-\(B\) interface interactions. The comparison among equivalent globules consisting of different number of \(B\)-blocks shows that the higher the number of solvo-phobic blocks in a globule the less compact it is.

A second observation was relative to the size of the globules in terms of \(R_g\) values and a comparison among equal size globules and the corresponding homopolymer globules is summarized in Figure 9. The effect of the multi-species contribution in the globule size is in accordance with the density observations. Between globules of the same number of units, the more the solvo-phobic blocks in a globule the larger the globule is and, consequently, the looser. Finally, interesting is the observation for a globule formed by one \(B\)-block where although its density is much lower at distances close to the center of mass and more long ranged than the homopolymer one, its size is equal to that of its
homopolymer analog within error bars. On the contrary, for globules formed by more $B$-blocks both density and size diversify from those of the corresponding homopolymers.

Overall, the current study explores the phase behavior and the conformational transitions of systems consisting of a single multiblock copolymer chain of different numbers of $N$ units, distributed in alternating ($A$- and $B$-) blocks, which are subject to very different energetic conditions. The combination of all parameters of the phase space plays a key role in the preferred conformations. Although the high energetic contrast between the two blocks and their relatively long lengths, multi configurational transitions occur among various classes of globule formation by the solvo-phobic blocks. This result predisposes us for even richer phase behavior at moderate energetic difference between the two blocks. This also happens in the case of shorter blocks as has been observed in previous studies. On top of that, the difference in the characteristics among the globules formed from one or multi-species of the multiblock copolymer chain as well as between the copolymer globules and their homopolymer analogs stresses out the important role of the solvo-philic blocks. The dependence of the above results on the relative ratio of the solvo-phobic over the solvo-philic blocks ($n_A/n_B$), which is equal to 1 in the current study, is an interesting issue, which is under investigation.

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References and Notes

Table 1: The average relative error of the mean energy of $B$-blocks over the five states of conformational interchanges for the $N=500$, $N=1000$ and $N=2000$ multiblock copolymer chains.

<table>
<thead>
<tr>
<th>$N$</th>
<th>$\frac{\langle \Delta E \rangle}{\langle E \rangle_{\nu=5}}$</th>
</tr>
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<tbody>
<tr>
<td>500</td>
<td>0.26</td>
</tr>
<tr>
<td>1000</td>
<td>0.22</td>
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<tr>
<td>2000</td>
<td>0.15</td>
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Figure Captions

Figure 1: Snapshots of configurations of a single multiblock copolymer chain with $n_A = n_B = n = 100$ ($N = 1000$), $m = 5$ at $E_{AA} = 0.10$ for $A$-beads (blue) and $E_{BB} = 0.45$ for $B$-beads (red). In the insets, the possible configurations of the collapsed $B$-blocks (from five individual “globules” to one single globule”) are schematically portrayed.

Figure 2: Number of globules (in the x-axes) as a function of time (configuration number - in the y-axes) for all systems of a single multiblock copolymer chain with (a) $N = 500$; (b) $N = 1000$; (c) $N = 2000$; (d) $N = 3000$ and (e) $N = 5000$ with $n_A = n_B = n = N / 10$ at $E_{AA} = 0.10$ and $E_{BB} = 0.45$.

Figure 3: Probabilities of occurrence for each of the five classes of conformations for all systems of a single multiblock copolymer chain with (a) $N = 500$; (b) $N = 1000$; (c) $N = 2000$; (d) $N = 3000$ and (e) $N = 5000$ with $n_A = n_B = n = N / 10$ at $E_{AA} = 0.10$ and $E_{BB} = 0.45$.

Figure 4: (a) Number of globules (in the x-axis) as a function of time (configuration number – in the y-axis) for a single multiblock copolymer chain of $N = 5000$ with $n_A = n_B = n = 50$ at $E_{AA} = 0.10$ and $E_{BB} = 0.45$; The initial state of the simulation was a state with three globules. (b) The corresponding probabilities for the detected conformations.

Figure 5: Mean energy values of $B$-blocks for configurations with one to five globules of a single multiblock copolymer chain with (a) $N = 500$; (b) $N = 1000$; (c) $N = 2000$; (d) $N = 3000$ and (e) $N = 5000$ with $n_A = n_B = n = N / 10$ at $E_{AA} = 0.10$ and $E_{BB} = 0.45$; error bars are set to signify the minimum and the maximum energy values, which have been calculated for each case.
**Figure 6:** Normalized distributions of the energy of the globules formed by the $B$-blocks for all cases of globule formation (one to five globules) for a single multiblock copolymer chain with $N = 1000$, $n_A = n_B = n = 100$ at $E_{AA} = 0.10$ and $E_{BB} = 0.45$.

**Figure 7:** Distribution of the distances between the centers of mass of all pairs of $B$-blocks for all cases of globule formation (one to five globules) for a single multiblock copolymer chain with (a) $N = 500$; (b) $N = 1000$; (c) $N = 2000$; (d) $N = 3000$ and (e) $N = 5000$ with $n_A = n_B = n = N / 10$ at $E_{AA} = 0.10$ and $E_{BB} = 0.45$. Vertical lines correspond to a distance of $2R_{gn}$ for each system correspondingly.

**Figure 8:** Segment density distribution of the globule, which is formed by the solvophobic parts of a single multiblock copolymer chain as a function of the distance from the center of mass of the globule. (a) Comparison among globules consisting of all five $B$-blocks for chains with $N = 500$ (containing 250 units), 1000 (containing 500 units) and 2000 (containing 1000 units), together with a globule formed by a homopolymer with 1000 units. (b) Comparison between equivalent globules consisting of one or more $B$-block together with the globule of the homopolymer analog (all containing 500 units). (c) Comparison among copolymer globules with various numbers of units ($500, 1000, 2000$ and $5000$ as in the caption).

**Figure 9:** Mean value of the radius of gyration of the globules consisting of one to five $B$-blocks as a function of the number of $B$ units in a single globule, averaged over the corresponding configurations of each case, for a single multiblock copolymer chain of all systems ($N = 500, 1000, 2000, 3000, 5000$); values for the radius of gyration of globules formed by homopolymer analogs are also included. Vertical lines are to guide the eye to the set of values being compared.
Figure 1
Figure 2
Figure 3
Figure 4
Figure 5
Figure 6
Figure 7
Figure 8
Figure 9

Figure 9