Coil-Globule Transition and Knottedness
in Homo- and Heteropolymers

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Abstract: The aim of this numerical investigation is twofold. First, we give an estimate for the coil-globule transition temperature of single random heteropolymers described by the HP model (50% H and 50% P). In addition, we examine the degree of knottedness in homopolymers (100% H) as a function of temperature, and show that in globular states, knots are less abundant in heteropolymers.

1 Determination of the Θ-point

In this study we consider single homopolymer chains consisting of monomers of type H and single heteropolymer chains consisting of monomers of type H (hydrophobic) and P (polar). Polymer chains are described as self-avoiding walks on a cubic lattice with attractive ($\epsilon_{HH} = -1$) or neutral ($\epsilon_{HP} = \epsilon_{PP} = 0$) interactions between neighboring nonbonded monomers. This well-established model [1] captures certain aspects of proteins, in particular the formation of the hydrophobic core. The new version of the pruned-enriched Rosenbluth method with importance sampling (nPERMis) [2, 3] is employed for all simulations.

At high temperatures or good solvent conditions, the free energy of a single polymer chain is dominated by entropy and the chain resides in a stretched coil-like state. At low temperatures or bad solvent conditions, energetic interactions between the beads become more important and the chain collapses to a globular state. The temperature at which the collapse occurs depends on the size of the chain, but can be extrapolated to the thermodynamic limit ($N \to \infty$) which is known as the Θ-point. Estimates for the Θ-point are obtained in two ways (Fig. 1). First, we determine the transition temperature $T^{C_v}(N)$ as the temperature at which the specific heat $C_v(N, T)$ reaches its maximum and extrapolate to T_Θ [4]:

$$T^{C_v}(N) = T_\Theta^{C_N} - \frac{a_1}{\sqrt{N}} + \frac{a_2}{N}. \tag{1}$$

Alternatively, the transition temperature for a chain of size $N = (N_1 + N_2)/2$ can be determined by the crossing of the radii of gyration $R_{gyr}^2(N_1, T)$ and $R_{gyr}^2(N_2, T)$. As suggested in [5], we extrapolate

$$T^{R_{gyr}}(N) = T_\Theta^{R_{gyr}} - c_1 N^{-1/2}. \tag{2}$$

The best estimate of the Θ-temperature ($T_\Theta = 3.717(3)$) for the homopolymer model used in this work was given by Grassberger et. al. [6], who studied significantly larger chains. We obtain $T_\Theta^{C_N} = 3.66 \pm 0.1$ and $T^{R_{gyr}}(N) = 3.78 \pm 0.1$ which is in reasonable agreement with the previous result and confirms our methodology.

We have also applied this approach to an ensemble of random heteropolymers of chain lengths $N = 100, 150, \ldots, 500$ which contain 50% H and 50% P. Extrapolating these finite-size results we get $T_\Theta^{C_N} = 1.33 \pm 0.2$ and $T^{R_{gyr}}(N) = 1.27 \pm 0.09$. Note that obtaining $C_v(N, T)$

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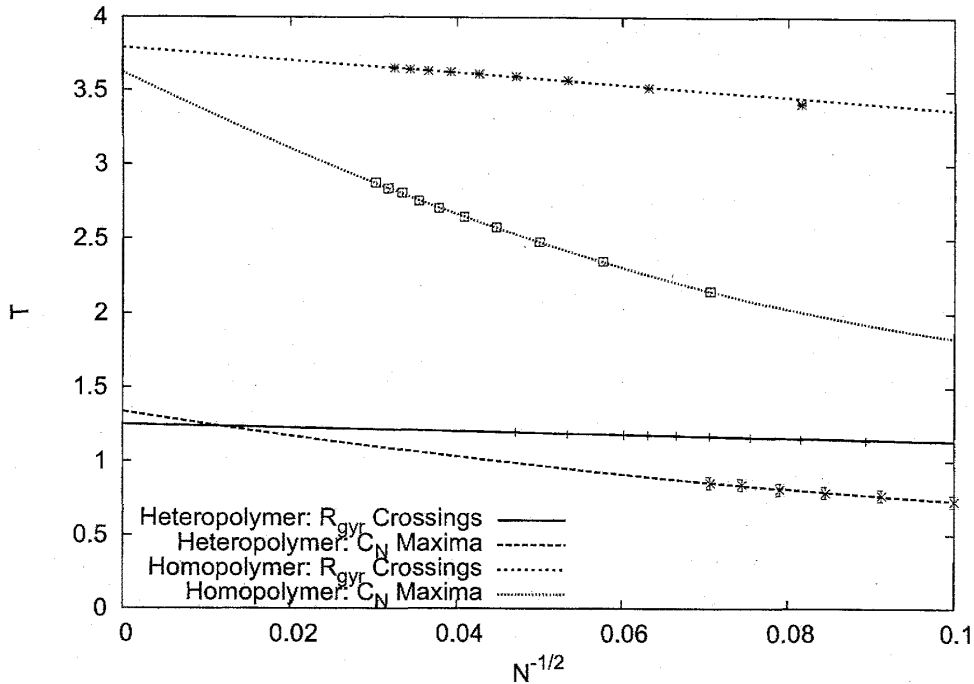Figure 1: Θ-point determination using the maxima of the specific heat as well as the scaling behavior of the radius of gyration for homo- (100% H, upper lines) and heteropolymers (50% H and 50% P, lower lines).

and $R_{gyr}^2(N,T)$ is nontrivial for an ensemble of heteropolymers and quite demanding from a computational point of view. Therefore, our estimates are not very precise and further inquiries are certainly warranted.

2 Knots in Homo- and Heteropolymers

In the following we would like to investigate topological properties of random heteropolymers and compare those to homopolymers of similar density. Our study is motivated by the rarity of knots in experimentally determined protein structures [7, 8, 9, 10, 11] which is in contrast to the apparent abundance of knots in homopolymers [12, 13, 9]. Of course, this investigation can only be understood as a first step towards understanding the sparseness of knots in proteins. Our toy model only accounts for hydrophobic effects – it neither considers specific sequences, secondary structure nor kinetics.

Even though knots are only well-defined in closed curves, we can introduce the concept of knottedness in a statistical sense by connecting the end points in a clear-cut manner. As shown in previous work [13, 14], the exact form of the closure only plays a minor role. Here, we draw two lines outward starting at the termini in the direction of the connection line between the center of mass and the respective ends. These two lines are joined by a big loop, and the structure is classified by the determination of its Alexander polynomial [14, 15].

First, we would like to describe the typical behavior observed in homopolymer chains (100% H). Figure 2 shows the probability of observing an unknot, a trefoil knot (3_1) and a figure-eight knot (4_1) for a homopolymer of size $N = 500$. At high temperatures, the chain behaves like a self-avoiding walk and tends to be unknotted. At low temperatures, globular states form and almost 60% of all configurations contain a knot. In between we observe a smooth transition
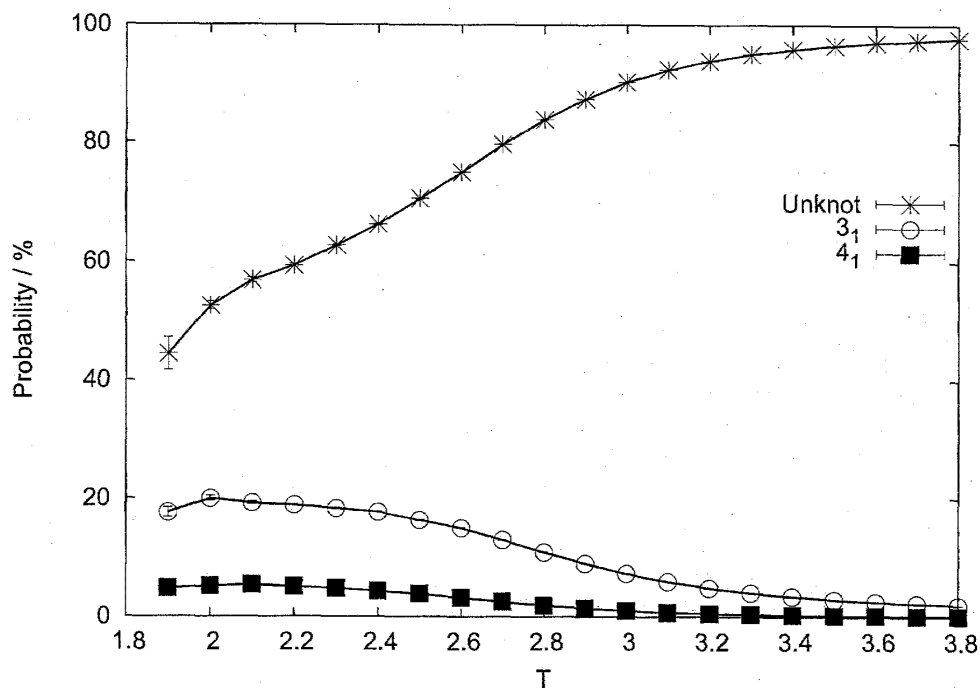
Figure 2: Temperature dependence of knot probabilities for homopolymer chains of size $N = 500$.
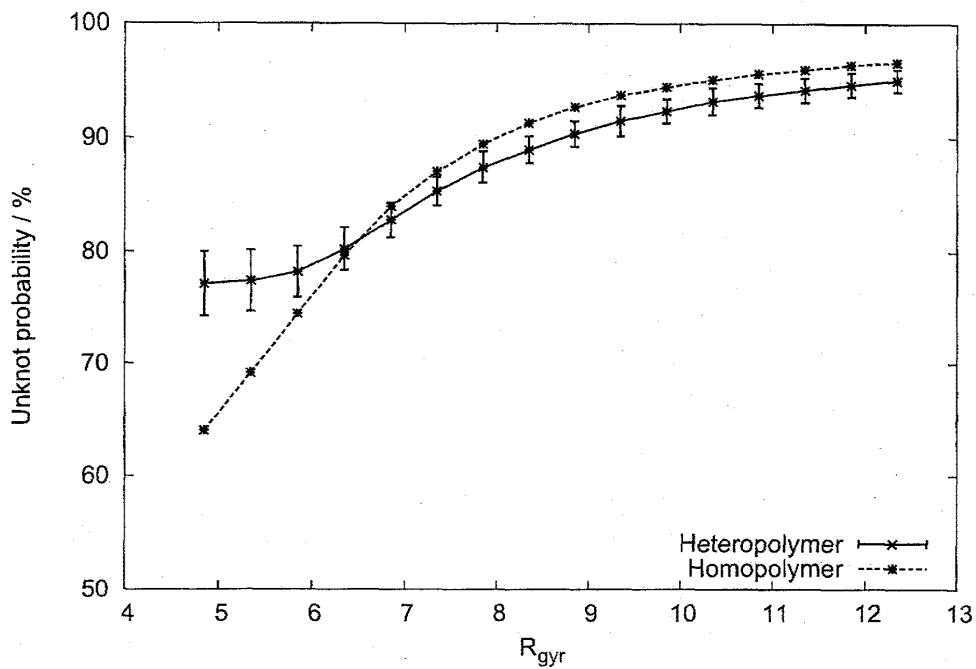

Figure 3: Unknot probabilities for homo- and heteropolymers ($N = 500$) as a function of the radius of gyration. Error bars for heteropolymers display the standard deviation of the mean, not the error of the mean, and give an indication for the spread of knottedness among different heteropolymer sequences. Note that results for homopolymers are not directly comparable to Fig. 2.

from unknotted to knotted states.

Even though nPERMis [2, 3] allows us to simulate globular homopolymers, it fails to generate properly Boltzmann-weighted configurations for globular heteropolymers. In fact, we are unaware of any algorithm which is currently up to this task. In contrast to homopolymers, globular heteropolymers display a broad distribution of weights and averages tend to be dominated by few configurations with high weights. Nevertheless, we try to describe their topological properties at least qualitatively. From each nPERMis run we choose one configuration and disregard its weight, i.e. each configuration contributes equally. This way, we have generated 50000 configurations of size N=500 for 100 random sequences at temperatures T=0.55, 0.6, 0.7, 0.8 0.9 and 1. For homopolymers 200000 configurations have been created at T=1.9, 2.1, 2.3, 2.5, 2.7, 2.9 and 3.1. Configurations are binned according to their radius of gyration (bin width ΔR_{gyr}=0.5) and averages are computed for each bin.

For large radii of gyration, which correspond to elevated temperatures, homo- and heteropolymers behave similarly, and only few configurations are knotted. In globular states, however, we observe considerably less knots in heteropolymers than in homopolymers. This difference can be attributed to a higher level of order within the heteropolymer globule. In homopolymers, strands can go back and forth through the core. In heteropolymers, a hydrophobic core forms which restricts the arrangement of the remaining parts of the chain.

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